

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 16:01:16 : Search time 81 seconds  
(without alignments)  
21.555 Million cell updates/sec

Title: US-09-787-443-20  
Perfect score: 11  
Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 274822

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :			
A_Geneseq_19Jun03:*			
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24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:	62	4

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	21	NCAM Igl binding p
2	11	100.0	11	23	Human neural cell
3	5	45.5	13	23	Human keratinocyte
4	5	45.5	13	23	Human keratinocyte
5	5	45.5	13	23	Human keratinocyte
6	5	45.5	13	23	Human keratinocyte
7	5	45.5	13	23	Human keratinocyte
8	4	36.4	8	20	Granulocyte colony
9	4	36.4	8	20	perception sensiti

10	4	36.4	8	21	AAV2044
11	4	36.4	8	22	AAV274
12	4	36.4	8	22	AAE3104
13	4	36.4	8	22	AAE3104
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86	4	36.4	10	22	AAW81446	Ranget cyclic pept	159	4	36.4	14	24	AAW24441	Arabitopsis thalia
87	4	36.4	10	22	AAW81938	Human D40 associat	160	4	36.4	14	24	AAW24442	Arabitopsis thalia
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106	4	36.4	11	17	AAE55318	Human retinoic act	179	4	36.4	14	24	AAW24441	Arabitopsis thalia
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108	4	36.4	11	21	AAW88558	NCAM Ig1 binding p	181	4	36.4	14	24	AAW24441	Arabitopsis thalia
109	4	36.4	11	21	AAW51589	HIV-1 derived Gp12	182	4	36.4	14	24	AAW24442	Arabitopsis thalia
110	4	36.4	11	22	AAE08102	Peptide #1 from hu	183	4	36.4	14	24	AAW24441	Arabitopsis thalia
111	4	36.4	11	22	AAW99418	Staphylokinase 1-c	184	4	36.4	14	24	AAW24442	Arabitopsis thalia
112	4	36.4	11	22	AAW50076	csk tyrosine kinas	185	4	36.4	14	24	AAW24441	Arabitopsis thalia
113	4	36.4	11	23	AAO18012	Human immunoglobul	186	4	36.4	14	24	AAW24442	Arabitopsis thalia
114	4	36.4	11	23	ABB74327	Bipartite/split nu	187	4	36.4	14	24	AAW24441	Arabitopsis thalia
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116	4	36.4	11	23	ABW74590	Transcription fact	189	4	36.4	14	24	AAW24441	Arabitopsis thalia
117	4	36.4	12	6	AAW50865	Synthetic peptide	190	4	36.4	14	24	AAW24442	Arabitopsis thalia
118	4	36.4	12	16	AAW79721	Optimal peptide su	191	4	36.4	14	24	AAW24441	Arabitopsis thalia
119	4	36.4	12	18	AAW24439	Nucleic acid (NA)	192	4	36.4	14	24	AAW24442	Arabitopsis thalia
120	4	36.4	12	18	AAW3100	c-Abl substrate	193	4	36.4	14	24	AAW24441	Arabitopsis thalia
121	4	36.4	12	19	AAW62021	Peptide substrate	194	4	36.4	14	24	AAW24442	Arabitopsis thalia
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123	4	36.4	12	21	AAW12833	Optimised Abl pept	196	4	36.4	14	24	AAW24442	Arabitopsis thalia
124	4	36.4	12	21	AAW18075	Human lactoferrin	197	4	36.4	14	24	AAW24441	Arabitopsis thalia
125	4	36.4	12	21	AAW67922	Synthetic abt. opti	198	4	36.4	14	24	AAW24442	Arabitopsis thalia
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130	4	36.4	12	23	AAW51963	V-Abl tyrosine kin	203	4	36.4	14	24	AAW24441	Arabitopsis thalia
131	4	36.4	12	23	AAW76109	Nociceptin-like pe	204	4	36.4	14	24	AAW24442	Arabitopsis thalia
132	4	36.4	12	23	ABB74314	Simple nuclear loc	205	4	36.4	14	24	AAW24441	Arabitopsis thalia
133	4	36.4	12	24	AAE12316	Arabitopsis thalia	206	4	36.4	14	24	AAW24442	Arabitopsis thalia
134	4	36.4	13	16	AAW70135	NACP peptide 2, S	207	4	36.4	14	24	AAW24441	Arabitopsis thalia
135	4	36.4	13	16	AAW66182	Cardiac troponin I	208	4	36.4	14	24	AAW24442	Arabitopsis thalia
136	4	36.4	13	18	AAW24445	Nucleic acid (NA)	209	4	36.4	14	24	AAW24441	Arabitopsis thalia
137	4	36.4	13	18	AAW24440	Nucleic acid (NA)	210	4	36.4	14	24	AAW24442	Arabitopsis thalia
138	4	36.4	13	18	AAW24441	Nucleic acid (NA)	211	4	36.4	14	24	AAW24441	Arabitopsis thalia
139	4	36.4	13	18	AAW24431	K6, a nucleic acid	212	4	36.4	14	24	AAW24442	Arabitopsis thalia
140	4	36.4	13	19	AAW20517	Human neurofilamen	213	4	36.4	14	24	AAW24441	Arabitopsis thalia
141	4	36.4	13	19	AAW65142	Partial sequence o	214	4	36.4	14	24	AAW24442	Arabitopsis thalia
142	4	36.4	13	21	AAW65753	RNA binding peptid	215	4	36.4	14	24	AAW24441	Arabitopsis thalia
143	4	36.4	13	22	AAW06090	K8 polylysine pept	216	4	36.4	14	24	AAW24442	Arabitopsis thalia
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145	4	36.4	13	22	AAW36920	Polylysine peptide	218	4	36.4	14	24	AAW24442	Arabitopsis thalia
146	4	36.4	13	23	ABP52549	CXC chemokine rece	219	4	36.4	14	24	AAW24441	Arabitopsis thalia
147	4	36.4	13	23	ABP52550	CXC chemokine rece	220	4	36.4	14	24	AAW24442	Arabitopsis thalia
148	4	36.4	13	23	ABP52552	CXC chemokine rece	221	4	36.4	14	24	AAW24441	Arabitopsis thalia
149	4	36.4	13	23	AAO18024	Human immunoglobul	222	4	36.4	14	24	AAW24442	Arabitopsis thalia
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151	4	36.4	13	23	AAO19336	Cysteine-X-Cysteine	224	4	36.4	14	24	AAW24442	Arabitopsis thalia
152	4	36.4	13	23	AAO19337	Cysteine-X-Cysteine	225	4	36.4	14	24	AAW24441	Arabitopsis thalia
153	4	36.4	13	23	AAO19339	Cysteine-X-Cysteine	226	4	36.4	14	24	AAW24442	Arabitopsis thalia
154	4	36.4	13	23	AAE17225	Peptide comprising	227	4	36.4	14	24	AAW24441	Arabitopsis thalia
155	4	36.4	13	23	AAE17227	Peptide comprising	228	4	36.4	14	24	AAW24442	Arabitopsis thalia











PF 05-FEB-2002; 2002WO-EP01175.  
XX  
PR 06-FEB-2001; 2001EP-0102574.  
PR 19-FEB-2001; 2001EP-0103954.  
XX  
PA (MERE ) MERCK PATENT GMBH.  
XX  
XX Carr FJ, Carter G, Jones T, Williams S;  
XX WPI: 2002-657523/70.  
XX  
PT New modified molecule having the biological activity of keratinocyte  
PT growth factor (KGF) and being non-immunogenic, for reducing propensity  
PT of the polypeptide to elicit an immune response upon administration to  
PT a human subject .  
XX  
XX Claim 6: Page 12; 40pp: English.  
XX  
CC The invention relates to modified molecules having the biological  
CC activity of keratinocyte growth factor (KGF) and being non-immunogenic or  
CC less immunogenic than any non-modified molecule having the same  
CC biological activity when used in vivo. The modified peptides can then  
CC elicit an immune response upon administration to a human subject. The  
CC invention also relates to identifying potential T-cell epitopes within  
CC the amino acid sequence of the protein and determining binding of the  
CC peptides to major histocompatibility complex (MHC) molecules using in  
CC vitro or in silico techniques or biological assays, and designing new  
CC sequence variants with one or more amino acids within the identified  
CC potential T-cell epitopes modified to reduce or eliminate the activity of  
CC the T-cell epitope. This sequence represents a human KGF T-cell epitope  
CC with MHC Class II binding potential.  
XX  
SQ Sequence 13 AA:  
  
Query Match: 45.5%; Score 5; EB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 KKEQK 7  
Db 9 KKEQK 13  
  
RESULT 6  
ABG79752  
ID ABG79752 standard; Peptide: 13 AA.  
XX  
AC ABG79752:  
XX  
XX 15-NOV-2002 (first entry)  
XX  
XX Human keratinocyte growth factor (KGF) T-cell epitope #46.  
XX  
XX Human: keratinocyte growth factor; KGF; Major histocompatibility complex;  
KW MHC; immunomodulatory; T-cell epitope.  
XX  
XX Homo sapiens.  
XX  
XX WO200262842-A1.  
XX  
XX 15-AUG-2002.  
XX  
XX 05-FEB-2002; 2002WO-EP01175.  
XX  
PR 06-FEB-2001; 2001EP-0102574.  
PR 19-FEB-2001; 2001EP-0103954.  
XX  
XX (MERE ) MERCK PATENT GMBH.  
XX  
XX Carr FJ, Carter G, Jones T, Williams S;  
XX WPI: 2002-657523/70.  
XX  
XX

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CC biological activity when used in vivo. The modified peptides can then  
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CC invention also relates to identifying potential T-cell epitopes within  
CC the amino acid sequence of the protein and determining binding of the  
CC peptides to major histocompatibility complex (MHC) molecules using in  
CC vitro or in silico techniques or biological assays, and designing new  
CC sequence variants with one or more amino acids within the identified  
CC potential T-cell epitopes modified to reduce or eliminate the activity of  
CC the T-cell epitope. This sequence represents a human KGF T-cell epitope  
CC with MHC Class II binding potential.  
XX  
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Query Match: 45.5%; Score 5; EB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 KKEQK 7  
Db 9 KKEQK 13  
  
RESULT 7  
AAB94294  
ID AAB94294 standard; Peptide: 13 AA.  
XX  
AC AAB94294:  
XX  
XX 02-FEB-2002 (first entry)  
XX  
XX Granulocyte colony stimulating factor receptor binding peptide #99  
XX  
XX G-CSF; granulocyte colony stimulating factor receptor; cytokine;  
KW hematopoietic; with T-lymphocyte receptor; proliferation; AIDS.  
KW neutrophil; different; hematopoietic; acquired; immunodeficiency; specific;  
KW chemotherapy; induced; non-specific; immunity; acquired; proliferation;  
KW depressed; neutrophil; colony; stimulation;  
XX  
XX Syn' factor.  
XX  
XX W20020679-A2  
XX  
XX XI JAN-20-02  
XX  
XX 20-FEB-2001; 2001EP-0102574  
XX  
XX 20-FEB-2001; 2001EP-0103954  
XX  
XX (MERE ) MERCK PATENT GMBH.  
XX  
XX WPI: 2002-657523/70.  
XX  
XX Carr FJ, Carter G, Jones T, Williams S;  
XX WPI: 2002-657523/70.  
XX  
XX 05-FEB-2002; 2002WO-EP01175.  
XX  
PR 06-FEB-2001; 2001EP-0102574.  
PR 19-FEB-2001; 2001EP-0103954.  
XX  
XX (MERE ) MERCK PATENT GMBH.  
XX  
XX Carr FJ, Carter G, Jones T, Williams S;  
XX WPI: 2002-657523/70.  
XX  
XX The invention relates to compounds comprising a peptide chain  
XX approximately 1 to 40 amino acids in length that binds to granulocyte

CC colony stimulating factor receptor (G-CSFR). The compounds contain  
 CC specific sequences of the generic peptides appearing as AAW78446  
 CC and the generic sequences XV\_1XV\_2XV\_3XV\_4XV\_5XV\_6XV\_7XV\_8 (where  
 CC XV\_1 = E, C, Q, V or Y; XV\_2 = E, A, L, M, S, W or G; XV\_3 = K, R or T;  
 CC XV\_4 = L, A or Q; XV\_5 = R, A, M, H, E, V, L, G, D, Q or S; XV\_6 = E or  
 CC V; XV\_7 = A or G; and XV\_8 = R, H, G or D) and XVI\_1XVI\_2XVI\_3XVI\_4XVI\_5  
 CC XVI\_6XVI\_7XVI\_8XVI\_9 (where XVI\_1 = A, E or G; XVI\_2 = E, H or D;  
 CC XVI\_3 = R or G; XVI\_4 = K, Y, M, N, Q, R, B, L, S or P; XVI\_5 = A, S or  
 CC P; XVI\_6 = E, D, T, Q, K or A; XVI\_7 = R, W, K, L, S, A or G; XVI\_8 = R  
 CC or E; and XVI\_9 = W, G or R). The compounds are used for treating  
 CC conditions associated with depressed neutrophil count, e.g. chemotherapy  
 CC induced neutropenia, AIDS-induced neutropenia or chemotherapy-induced  
 CC pneumonia-induced pneumonia. The compounds are useful as *in vitro* and  
 CC tools for understanding the biological role of granulocyte colony  
 CC stimulating factor (G-CSF) a haematopoietic growth factor and  
 CC cytokine that stimulates neutrophil proliferation and differentiation,  
 CC including evaluation of many factors thought to influence, and be  
 CC influenced by, production of white blood cells, in the development of  
 CC compounds that bind to G-CSFR, as reagents for detecting G-CSF receptor  
 CC or related receptor on living cells, fixed cells, in biological fluids, in  
 CC tissue homogenates or in purified natural biological materials, *in situ*  
 CC staining, fluorescence-activated cell sorting (FACS), western blotting or  
 CC enzyme-linked immunosorbent assay (ELISA), in receptor purification or  
 CC in purifying cells expressing G-CSFR on the cell surface (or inside  
 CC permeabilised cells) as a commercial research reagent for various medical  
 CC and diagnostic uses or to treat a disease that would benefit from the  
 CC ability of a compound to mimic the effects of G-CSF *in vivo*.  
 CC The compounds bind specifically to G-CSFR and allow for studies of  
 CC biological activities mediated by the receptor and for the treatment of  
 CC diseases, disorders and conditions that would benefit from activating or  
 CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of  
 CC the invention.

SQ Sequence 13 AA:

Query Match 45.5%, Score 17, ID 20, Length 10  
 Best Local Similarity 100.0%, Pref. No. 50  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 KKKEQ 6  
 DQ 1 KKKEQ 5

RESULT 8  
 AAW78446  
 ID AAW78446 standard; peptide; b AA.

XX AAW78446;

AC AAW78446;

DT 27 APR 1995 (first entry)

DE Perception sensitivity inhibitory peptide BRL 3 BP.

XX Perception sensitivity inhibitory peptide; receptor; pain;

XX hot plate test.

OS Synthetic.

GS Bos taurus.

XX JPT1021298 A.

PN 26 JAN 1995.

XX 02-JUL-1997; 97JP-0176905.

XX 02-JUL-1997; 97JP-0176905.

XX (EISA) EISA CO LTD.

XX WPI: 1999-163218/14.

PT New perception sensitivity inhibitory peptide - useful for

PT Inhibiting pain and pain sensation. Tested on postoperative pain.  
 XX Example 5; Page 60-61; b AA.  
 TS This peptide represents a peptide with sensitivity inhibitory properties.  
 CC The invention of the peptide is based on the known structure of  
 CC inhibiting peptides and corresponds to the peptide described in the  
 CC inhibiting peptide and amino acid sequence, respectively from a hot plate test.

SQ Sequence b AA

Query Match 45.5%, Score 17, ID 20, Length 10

Best Local Similarity 100.0%, Pref. No. 50

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 KKKEQ 6

DQ 1 KKKEQ 5

RESULT 4

AAW78446

ID AAW78446 standard; peptide; b AA

XX AAW78446;

XX AAW78446;

XX 27 APR 1995 (first entry)

XX Perception sensitivity inhibitory peptide BRL 3 BP.

XX Perception sensitivity inhibitory peptide; receptor; pain;

XX hot plate test.

OS Synthetic.

GS Bos taurus.

XX JPT1021298 A.

PN 26 JAN 1995.

XX 02-JUL-1997; 97JP-0176905.

XX 02-JUL-1997; 97JP-0176905.

XX (EISA) EISA CO LTD.

XX WPI: 1999-163218/14.

PT New perception sensitivity inhibitory peptide - useful for





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XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PI
XX P1 Harley JB, James JA, Scofield RH;
XX XX
XX DR WPI: 2001-335087/35.
XX XX
XX PT Generating systemic lupus erythematosus animal model by immunizing
XX PT non-human animal with non-immunoglobulin peptide having amino acid
XX PT sequence of self-antigen bound by autoantibody population in early
XX PT stage of disease
XX XX
XX PS Claim 10; Column 100; 63pp; English.
XX XX
XX CC The patent discloses a specific method of generating an animal model
XX CC of systemic lupus erythematosus (SLE), comprising immunising a non-
XX CC human animal with non-immunoglobulin peptide which comprises an
XX CC epitope immunoreactive with auto-antibody (AAb) from patient with
XX CC SLE. The epitope includes a region of self-antigen which is bound
XX CC by AAb population present in early stage in patient with SLE. The
XX CC method is used for generating an animal model of SLE. It is useful
XX CC for screening therapeutics effective in treating autoimmune disorders.
XX CC It is useful as a component in a diagnostic assay, as a therapeutic
XX CC (vaccine to block the AAbs produced, by eliciting immune response),
XX CC and in research on the possible causes of the autoimmune diseases.
XX CC The method is used to interrupt the course of an autoimmune response,
XX CC once autoimmunity against the autoantigen is established. The amino
XX CC acid sequences are used to make agents for neutralising circulating
XX CC antibodies or immobilised on substrates in extracorporeal devices for
XX CC specific removal of AAbs. The reagents identified by using the method
XX CC are useful in manufacturing and testing autoantigens. The method is
XX CC useful as models for screening of compounds which induce autoimmunity,
XX CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX CC in diagnosis of autoimmunity and as therapeutics for the treatment of
XX CC autoimmune disorders. The present sequence is a peptide from human ribo-
XX CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX CC of the invention.
XX SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9,3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQK 7
Db 3 KEQK 6
|||||

RESULT 15
AAE08106
ID AAE08106 standard; peptide; 8 AA.
XX AC
XX AC AAE08106;
XX DT 01-NOV-2001 (first entry)
XX DE
XX DE Peptide #5 from human ribonucleoprotein, 60 kD Ro/SSA.
XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
XX KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.
XX OS Homo sapiens.
XX XX
XX PN US6232522-B1.
XX XX
XX PD 15-MAY-2001.
XX XX
XX PF 30-NOV-1993; 93US-0160604.
XX PR
XX PR 31-JAN-1990; 90US-0472947.
XX PR 31-JAN-1991; 91US-0648205.
XX PR 13-APR-1992; 92US-0867819.

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XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PI
XX P1 Harley JB, James JA, Scofield RH;
XX XX
XX DR WPI: 2001-45067/45.
XX XX
XX PT Generating systemic lupus erythematosus animal model by immunizing
XX PT non-human animal with non-immunoglobulin peptide having amino acid
XX PT sequence of self-antigen bound by autoantibody population in early
XX PT stage of disease
XX XX
XX PS Claim 10; Column 100; 63pp; English.
XX XX
XX CC The patent discloses a specific method of generating an animal model
XX CC of systemic lupus erythematosus (SLE), comprising immunising a non-
XX CC human animal with non-immunoglobulin peptide which comprises an
XX CC epitope immunoreactive with auto-antibody (AAb) from patient with
XX CC SLE. The epitope includes a region of self-antigen which is bound
XX CC by AAb population present in early stage in patient with SLE. The
XX CC method is used for generating an animal model of SLE. It is useful
XX CC for screening therapeutics effective in treating autoimmune disorders.
XX CC It is useful as a component in a diagnostic assay, as a therapeutic
XX CC (vaccine to block the AAbs produced, by eliciting immune response),
XX CC and in research on the possible causes of the autoimmune diseases.
XX CC The method is used to interrupt the course of an autoimmune response,
XX CC once autoimmunity against the autoantigen is established. The amino
XX CC acid sequences are used to make agents for neutralising circulating
XX CC antibodies or immobilised on substrates in extracorporeal devices for
XX CC specific removal of AAbs. The reagents identified by using the method
XX CC are useful in manufacturing and testing autoantigens. The method is
XX CC useful as models for screening of compounds which induce autoimmunity,
XX CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX CC in diagnosis of autoimmunity and as therapeutics for the treatment of
XX CC autoimmune disorders. The present sequence is a peptide from human ribo-
XX CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX CC of the invention.
XX SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9,3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQK 7
Db 3 KEQK 6
|||||

RESULT 16
AAE08135
ID AAE08135 standard; peptide; 8 AA.
XX AC
XX AC AAE08135;
XX DT 01-NOV-2001 (first entry)
XX DE
XX DE Peptide #54 from human ribonucleoprotein, 60 kD Ro/SSA.
XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;
XX KW autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.
XX OS Homo sapiens.
XX XX
XX PN US6232522-B1.
XX XX
XX PD 15-MAY-2001.
XX XX
XX PF 30-NOV-1993; 93US-0160604.
XX PR
XX PR 31-JAN-1990; 90US-0472947.
XX PR 31-JAN-1991; 91US-0648205.
XX PR 13-APR-1992; 92US-0867819.

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XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX Harley JB, James JA, Scofield RH;  
 XX WPI: 2001-335087/35.  
 XX  
 XX Generating systemic lupus erythematosus animal model by immunizing  
 XX non-human animal with non-immunoglobulin peptide having amino acid  
 XX sequence of self-antigen bound by autoantibody population in early  
 XX stage of disease  
 XX  
 XX Example 1; Column 15; 63pp; English.  
 XX  
 XX The patent discloses a specific method of generating an animal model  
 XX of systemic lupus erythematosus (SLE), comprising immunising a non-  
 XX human animal with non-immunoglobulin peptide which comprises an  
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 XX method is used for generating an animal model of SLE. It is useful  
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 XX (vaccine to block the AABs produced, by eliciting immune response),  
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 XX in diagnosis of autoimmunity and as therapeutics for the treatment of  
 XX autoimmune disorders. The present sequence is a peptide from human ribo-  
 XX nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification  
 XX of the invention.  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 36.48; Score 4; DB 22; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 4, 30-05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;  
 XX  
 XX QY 7 KORN 10  
 XX III  
 XX DB 5 KORN 8  
 XX  
 XX RESULT 17  
 XX AAE08136  
 XX ID AAE08136 standard; peptide: 8 AA.  
 XX AC AAE08136;  
 XX XX  
 XX DT 01-NOV-2001 (first entry)  
 XX XX  
 XX DE Peptide #35 from human ribonucleoprotein, 60 kD Ro/SSA.  
 XX XX  
 XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;  
 XX autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.  
 XX OS Homo sapiens.  
 XX XX  
 XX PN US6232522-B1.  
 XX XX  
 XX PD 15-MAY-2001.  
 XX XX  
 XX PF 30-NOV-1993; 93US-0150604.  
 XX XX  
 XX PR 31-JAN-1990; 90US-0472947.  
 XX PR 31-JAN-1991; 91US-0648205.  
 XX PR 13-APR-1992; 92US-0867819.

XX  
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX Harley JB, James JA, Scofield RH;  
 XX WPI: 2001-335087/35.  
 XX  
 XX Generating systemic lupus erythematosus animal model by immunizing  
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 XX sequence of self-antigen bound by autoantibody population in early  
 XX stage of disease  
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 XX in diagnosis of autoimmunity and as therapeutics for the treatment of  
 XX autoimmune disorders. The present sequence is a peptide from human ribo-  
 XX nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification  
 XX of the invention.  
 XX  
 XX Sequence 4 AA;  
 XX  
 XX Query Match 66.4%; Score 4; DB 22; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 9, 40-05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;  
 XX  
 XX QY 7 KORN 10  
 XX III  
 XX DB 4 KORN 7  
 XX  
 XX RESULT 18  
 XX AAE08137  
 XX ID AAE08137 standard; peptide: 4 AA.  
 XX AC AAE 41-02;  
 XX XX  
 XX DT 01-NOV-2001 (first entry)  
 XX XX  
 XX DE Peptide #35 from human ribonucleoprotein, 60 kD Ro/SSA.  
 XX XX  
 XX KW Systemic lupus erythematosus; SLE; vaccine; immune response; therapeutic;  
 XX autoimmune disorder; ribonucleoprotein; human; 60 kD Ro/SSA peptide.  
 XX OS Homo sapiens.  
 XX XX  
 XX PN US6232522-B1.  
 XX XX  
 XX PD 15-MAY-2001.  
 XX XX  
 XX PF 4 KORN 1993; 93US-0150604.  
 XX XX  
 XX PR 31-JAN-1990; 90US-0472947.  
 XX PR 31-JAN-1991; 91US-0648205.  
 XX PR 13-APR-1992; 92US-0867819.



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XX PA (OKLA.) OKLAHOMA MEDICAL RES FOUND.
XX PI Harley JB, James JA, Scofield RB;
XX DR WPI: 2001-335087/35.
XX PT Generating systemic lupus erythematosus animal model by immunizing
XX PT non-human animal with non-immunoglobulin peptide having amino acid
XX PT sequence of self-antigen bound by autoantibody population in early
XX PT stage of disease.
XX PS Example 1; Column 15; 63pp; English.
XX CC The patent discloses a specific method of generating an animal model
XX CC of systemic lupus erythematosus (SLE), comprising immunising a non-
XX CC human animal with non-immunoglobulin peptide which comprises an
XX CC epitope immunoreactive with auto-antibody (AAb) from patient with
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XX CC It is useful as a component in a diagnostic assay, as a therapeutic
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XX CC and in research on the possible causes of the autoimmune diseases.
XX CC The method is used to interrupt the course of an autoimmune response,
XX CC once autoimmunity against the autoantigen is established. The amino
XX CC acid sequences are used to make agents for neutralising circulating
XX CC antibodies or immobilised on substrates in ex vivo/peroral devices for
XX CC specific removal of AAbs. The reagents identified by using the method
XX CC are useful in manufacturing and testing autoantigens. The method is
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XX CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX CC in diagnosis of autoimmunity and as therapeutics for the treatment of
XX CC autoimmune disorders. The present sequence is a peptide from human ribo-
XX CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX CC of the invention.
XX SQ Sequence 8 AA:
      Query Match: 36.4%; Score 4; PR 22; Length 6;
      Best Local Similarity 100.0%; Prod. No. 9, 3e-05;
      Matches 4; Conservative 0; Mismatches 0; Gaps 0;
QY 7 QRN 10
DB 3 QRN 6

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XX PA (OKLA.) OKLAHOMA MEDICAL RES F INE.
XX PI Harley JB, James JA, Scofield RB;
XX DR WPI: 2001-335087/35.
XX PT Generating systemic lupus erythematosus animal model by immunizing
XX PT non-human animal with non-immunoglobulin peptide having amino acid
XX PT sequence of self-antigen bound by autoantibody population in early
XX PT stage of disease.
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XX CC human animal with non-immunoglobulin peptide which comprises an
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XX CC SLE. The epitope includes a region of self-antigen which is bound
XX CC by AAb population present in early stage in patient with SLE. The
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XX CC for screening therapeutics effective in treating autoimmune disorders.
XX CC It is useful as a component in a diagnostic assay, as a therapeutic
XX CC (vaccine to block the AAbs produced, by eliciting immune response),
XX CC and in research on the possible causes of the autoimmune diseases.
XX CC The method is used to interrupt the course of an autoimmune response,
XX CC once autoimmunity against the autoantigen is established. The amino
XX CC acid sequences are used to make agents for neutralising circulating
XX CC antibodies or immobilised on substrates in ex vivo/peroral devices for
XX CC specific removal of AAbs. The reagents identified by using the method
XX CC are useful in manufacturing and testing autoantigens. The method is
XX CC useful as models for screening of compounds which induce autoimmunity,
XX CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful
XX CC in diagnosis of autoimmunity and as therapeutics for the treatment of
XX CC autoimmune disorders. The present sequence is a peptide from human ribo-
XX CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification
XX CC of the invention.
XX SQ Sequence 8 AA:
      Query Match: 36.4%; Score 4; PR 22; Length 6;
      Best Local Similarity 100.0%; Prod. No. 9, 3e-05;
      Matches 4; Conservative 0; Mismatches 0; Gaps 0;
QY 7 QRN 10
DB 3 QRN 6

```

XX (KIA-) OKLAHOMA MEDICAL RES FOUND  
 XX  
 PI Bartley JR, James JA, Seefeldt RH;  
 XX  
 XX WPI: 2601-335087/35.  
 XX  
 XX Generating systemic lupus erythematosus animal model by immunizing  
 PT non-human animal with non-immunoglobulin peptide having amino acid  
 PT sequence of self-antigen bound by autoantibody precipitated in early  
 PT stage of disease  
 XX  
 XX Example 1: Column 15: 63pp; English.  
 XX  
 XX The patent discloses a specific method of generating an animal model  
 CC of systemic lupus erythematosus (SLE), comprising immunizing a non-  
 CC human animal with non-immunoglobulin peptide which comprises an  
 CC epitope immunoreactive with auto-antibody (AAB) from patient with  
 CC SLE. The epitope includes a region of self-antigen which is bound  
 CC by AAB population present in early stage in patient with SLE. The  
 CC method is used for generating an animal model of SLE. It is useful  
 CC for screening therapeutics effective in treating autoimmune disorders.  
 CC It is useful as a component in a diagnostic assay, as a therapeutic  
 CC (vaccine to block the AABs produced, by eliciting immune response),  
 CC and in research on the possible causes of the autoimmune diseases.  
 CC The method is used to interrupt the course of an autoimmune response,  
 CC once autoimmunity against the autoantigen is established. The amino  
 CC acid sequences are used to make agents for neutralising circulating  
 CC antibodies or immobilised on substrates in extracellular devices for  
 CC specific removal of AABs. The reagents identified by using the method  
 CC are useful in manufacturing and testing autoantibodies. The method is  
 CC useful as models for screening of compounds which induce autoimmunity,  
 CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful  
 CC in diagnosis of autoimmunity and as therapeutics for the treatment of  
 CC autoimmune disorders. The present sequence is a peptide from human fibro  
 CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification  
 CC of the invention.  
 XX  
 XX Sequence 8 AA:  
 SQ  
 Query Match 36.4% Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9; AA: 3;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KQEN IG  
 Db 1 KURN 4  
 1111  
 1 KURN 4  
 RESULT 21  
 ABG30769  
 ID ABG30769 standard; Peptide: 8 AA.  
 AC  
 XX  
 XX ABG30769;  
 DT 05-NOV-2002 (first entry)  
 XX  
 XX E2F 1/cyclin A interaction inhibitory peptide #19.  
 XX  
 XX Cancer; cytostatic; cyclic; transcription factor; E2F 1; cyclin A; cdk2;  
 KW S phase delay; cell cycle arrest; apoptosis.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified site 1  
 FT /label= OTHER  
 FT /note= Ac-Pro on "Protein"  
 FT Misc difference 5:8  
 FT /note= "Residues form a cyclic strand etc."  
 FT  
 XX W0206250102-A2.  
 PN  
 XX

PI 2601-335087/35.  
 XX  
 XX  
 XX  
 XX (KIA-) OKLAHOMA MEDICAL RES FOUND  
 XX  
 XX WPI: 2601-335087/35.  
 XX  
 XX Generating systemic lupus erythematosus animal model by immunizing  
 PT non-human animal with non-immunoglobulin peptide having amino acid  
 PT sequence of self-antigen bound by autoantibody precipitated in early  
 PT stage of disease  
 XX  
 XX Example 1: Column 15: 63pp; English.  
 XX  
 XX The patent discloses a specific method of generating an animal model  
 CC of systemic lupus erythematosus (SLE), comprising immunizing a non-  
 CC human animal with non-immunoglobulin peptide which comprises an  
 CC epitope immunoreactive with auto-antibody (AAB) from patient with  
 CC SLE. The epitope includes a region of self-antigen which is bound  
 CC by AAB population present in early stage in patient with SLE. The  
 CC method is used for generating an animal model of SLE. It is useful  
 CC for screening therapeutics effective in treating autoimmune disorders.  
 CC It is useful as a component in a diagnostic assay, as a therapeutic  
 CC (vaccine to block the AABs produced, by eliciting immune response),  
 CC and in research on the possible causes of the autoimmune diseases.  
 CC The method is used to interrupt the course of an autoimmune response,  
 CC once autoimmunity against the autoantigen is established. The amino  
 CC acid sequences are used to make agents for neutralising circulating  
 CC antibodies or immobilised on substrates in extracellular devices for  
 CC specific removal of AABs. The reagents identified by using the method  
 CC are useful in manufacturing and testing autoantibodies. The method is  
 CC useful as models for screening of compounds which induce autoimmunity,  
 CC inhibit induction of autoimmunity, suppress autoimmunity. It is useful  
 CC in diagnosis of autoimmunity and as therapeutics for the treatment of  
 CC autoimmune disorders. The present sequence is a peptide from human fibro  
 CC nucleoprotein, 60 kD Ro/SSA. This peptide is used in the exemplification  
 CC of the invention.  
 XX  
 XX Sequence 8 AA:  
 SQ  
 Query Match 36.4% Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9; AA: 3;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KQEN IG  
 Db 1 KURN 4  
 1111  
 1 KURN 4  
 RESULT 21  
 ABG30769  
 ID ABG30769 standard; Peptide: 8 AA.  
 AC  
 XX  
 XX ABG30769;  
 DT 05-NOV-2002 (first entry)  
 XX  
 XX E2F 1/cyclin A interaction inhibitory peptide #19.  
 XX  
 XX Cancer; cytostatic; cyclic; transcription factor; E2F 1; cyclin A; cdk2;  
 KW S phase delay; cell cycle arrest; apoptosis.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified site 1  
 FT /label= OTHER  
 FT /note= Ac-Pro on "Protein"  
 FT Misc difference 5:8  
 FT /note= "Residues form a cyclic strand etc."  
 FT  
 XX W0206250102-A2.  
 PN  
 XX

PT receptor 4 (CXCR4) for preventing or treating AIDS and HIV infection.  
PT comprises binding a molecule to a molecule with a binding property  
XX corresponding to CXCR4

Example 1: Page 20: 92pp: English.

CC The present invention describes a method (M1) for identifying a binding  
CC compound for cysteine-X-cysteine chemokine receptor 4 (CXCR4) comprises  
CC binding a molecule from the library of two or more molecules to the  
CC molecule with a binding property corresponding to CXCR4. (M1) comprises:  
CC (a) providing a library of two or more molecules; (b) providing a  
CC molecule with a binding property corresponding to CXCR4; (c) binding a  
CC molecule from the library of two or more molecules to the molecule with  
CC a binding property corresponding to CXCR4; (d) separating the bound  
CC molecule from the library of two or more molecules; and (e) identifying  
CC the bound molecule as a binding compound for CXCR4. Also described is  
CC a binding compound (I) for CXCR4 identified from M1. (I) has virucide  
CC and anti-HIV activities. A partially purified CXCR4 protein is useful  
CC for carrying out selection, identification and improvement of tight  
CC binding ligands in identifying therapeutically useful compounds.  
CC Therapeutic peptides, peptidomimetics, or small molecule antagonists or  
CC agonists of CXCR4 binding may be used in the prevention and treatment of  
CC AIDS and HIV infection. The present sequence represents a CXCR4 related  
CC peptide which is used in an example from the present invention

XX Sequence: 8 AA:

Query Match 36.4%; Score 4; DB 24; Length 87  
Best Local Similarity 100.0%; Pred. No. 9, 36-001  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KKKE 5  
Db 2 KKKE 5

RESULT 23

AAU78918  
ID AAU78918 standard; Peptide: 8 AA.  
AC AAU78918:  
XX 18-JUN-2002 (first entry)  
XX Lupinus luteus nuclear localisation signal.  
XX Nuclear localisation signal; NLS: lupinus protein delivery;  
XX fusion protein; membrane penetrating peptide.  
XX Lupinus luteus.  
XX W0200218572-A2.  
XX 07-MAR-2002.  
XX 23-AUG-2001; 2001W0-US26421.  
XX 25-AUG-2000; 2000US-227647P.  
XX 07-FER-2000; 2001GB-0003110.  
XX (AVE1) AVENTIS PHARM INC.

PI Guo Y, Morse CC, Yao Z, Keeslet GA.  
XX WPI: 2002-304256/34.  
XX New fusion proteins comprising membrane penetrating peptides, useful as  
XX in vivo, ex vivo or in vitro intracellular carriers of delivery devices  
XX for a compound of interest (e.g. peptide, protein, chemical entity,  
XX nucleic acid)

PS Disclosure: Page 10; 45pp: English.

CC This sequence represents a partially purified protein, which comprises a  
CC membrane penetrating property, and is used in an example from the present  
CC invention. The present invention describes a method (M1) for identifying a binding  
CC compound for cysteine-X-cysteine chemokine receptor 4 (CXCR4) comprises  
CC binding a molecule from the library of two or more molecules to the  
CC molecule with a binding property corresponding to CXCR4. (M1) comprises:  
CC (a) providing a library of two or more molecules; (b) providing a  
CC molecule with a binding property corresponding to CXCR4; (c) binding a  
CC molecule from the library of two or more molecules to the molecule with  
CC a binding property corresponding to CXCR4; (d) separating the bound  
CC molecule from the library of two or more molecules; and (e) identifying  
CC the bound molecule as a binding compound for CXCR4. Also described is  
CC a binding compound (I) for CXCR4 identified from M1. (I) has virucide  
CC and anti-HIV activities. A partially purified CXCR4 protein is useful  
CC for carrying out selection, identification and improvement of tight  
CC binding ligands in identifying therapeutically useful compounds.  
CC Therapeutic peptides, peptidomimetics, or small molecule antagonists or  
CC agonists of CXCR4 binding may be used in the prevention and treatment of  
CC AIDS and HIV infection. The present sequence represents a CXCR4 related  
CC peptide which is used in an example from the present invention

XX Sequence: 8 AA:

Query Match 36.4%; Score 4; DB 24; Length 87  
Best Local Similarity 100.0%; Pred. No. 9, 36-001  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KKKE 5  
Db 2 KKKE 5

RESULT 24

AAU49681  
ID AAU49681 standard; Peptide: 8 AA.  
AC AAU49681:  
XX 20-MAY-2000 (first entry)  
XX Nuclear localisation signal; NLS: lupinus protein delivery;  
XX fusion protein; membrane penetrating peptide.  
XX Lupinus luteus.  
XX W0200218572-A2.  
XX 07-MAR-2002.  
XX 23-AUG-2001; 2001W0-US26421.  
XX 25-AUG-2000; 2000US-227647P.  
XX 07-FER-2000; 2001GB-0003110.  
XX (AVE1) AVENTIS PHARM INC.

PI Guo Y, Morse CC, Yao Z, Keeslet GA.  
XX WPI: 2002-304256/34.  
XX New fusion proteins comprising membrane penetrating peptides, useful as  
XX in vivo, ex vivo or in vitro intracellular carriers of delivery devices  
XX for a compound of interest (e.g. peptide, protein, chemical entity,  
XX nucleic acid)

PS Disclosure: Page 10; 45pp: English.

RESULT 25

AAU49681

ID AAM49686: standard; peptide: 8 AA.  
AC AAM49686:  
XX  
XX 28-MAY-2002 (first entry)  
DT  
XX  
XX Nociceptin peptide analogue SEQ ID No 7.  
DE  
XX  
XX Nociceptin; hypersensitivity inhibitor; analgesic; pain relief.  
KW  
XX  
XX Synthetic.  
OS  
XX JP2001354696-A.  
PN  
XX 25-DEC-2001.  
PD  
XX  
XX 08-JUN-2000; 2000JP-0171386.  
PF  
XX  
XX 08-JUN-2000; 2000JP-0171386.  
PR  
XX  
XX (NNSH ) NIPPON SHINYAKU CO LTD.  
PA  
XX  
XX WPI; 2002-262912/31.  
DR  
XX  
XX Hypersensitivity inhibitory peptides are new  
PT  
XX  
XX Claim 4; Page 6; 8pp; Japanese.  
PS  
XX  
XX This invention describes novel nociceptin analogues which inhibit  
CC nociceptin-induced hypersensitivity and have analgesic activity. The  
CC products of the invention can be used for pain relief. AAM49675-AAM49687  
CC represent nociceptin analogues described in the method of the invention  
XX  
XX  
SQ Sequence 8 AA:

Query Match 36.4%; Score 4; PB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 36-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FOKQ 8  
I I I I  
Db 3 FOKQ 6

RESULT 26  
AAM49686  
ID AAM49686 standard; peptide: 8 AA.  
XX  
XX AAM49686:  
AC  
XX  
XX 28-MAY-2002 (first entry)  
DT  
XX  
XX Nociceptin peptide analogue SEQ ID No 12.  
DE  
XX  
XX Nociceptin; hypersensitivity inhibitor; analgesic; pain relief.  
KW  
XX  
XX Synthetic.  
OS  
XX JP2001354696-A.  
PN  
XX 25-DEC-2001.  
PD  
XX  
XX 08-JUN-2000; 2000JP-0171386.  
PF  
XX  
XX 08-JUN-2000; 2000JP-0171386.  
PR  
XX  
XX (NNSH ) NIPPON SHINYAKU CO LTD.  
PA  
XX  
XX WPI; 2002-262912/31.  
DR  
XX  
XX Hypersensitivity inhibitory peptides are new  
PT  
XX  
XX Example 11; Page 7; 8pp; Japanese.

XX This invention describes novel nociceptin analogues which inhibit  
CC nociceptin-induced hypersensitivity and have analgesic activity. The  
CC products of the invention can be used for pain relief. AAM49675-AAM49687  
CC represent nociceptin analogues described in the method of the invention  
XX  
XX  
SQ Sequence 8 AA:  
Query Match 36.4%; Score 4; PB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 36-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FOKQ 8  
I I I I  
Db 3 FOKQ 6

RESULT 27  
AAM49687  
ID AAM49687 standard; peptide: 8 AA.  
XX  
XX AAM49687:  
AC  
XX  
XX 28-MAY-2002 (first entry)  
DT  
XX  
XX Nociceptin peptide analogue SEQ ID No 8.  
DE  
XX  
XX Nociceptin; hypersensitivity inhibitor; analgesic; pain relief.  
KW  
XX  
XX Synthetic.  
OS  
XX JP2001354696-A.  
PN  
XX 25-DEC-2001.  
PD  
XX  
XX 08-JUN-2000; 2000JP-0171386.  
PF  
XX  
XX 08-JUN-2000; 2000JP-0171386.  
PR  
XX  
XX (NNSH ) NIPPON SHINYAKU CO LTD.  
PA  
XX  
XX WPI; 2002-262912/31.  
DR  
XX  
XX Hypersensitivity inhibitory peptides are new  
PT  
XX  
XX Example 11; Page 7; 8pp; Japanese.

Query Match 36.4%; Score 4; PB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 36-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 FOKQ 8  
I I I I  
Db 3 FOKQ 6

RESULT 28  
AAM49688  
ID AAM49688 standard; peptide: 8 AA.  
XX  
XX AAM49688:  
AC  
XX  
XX 28-MAY-2002 (first entry)  
DT  
XX  
XX Nociceptin peptide analogue SEQ ID No 14  
DE  
XX

KW Nociceptin; hypersensitivity inhibitor; analgesic; pain relief; bovine.  
XX  
OS Bos taurus.  
XX  
PN JP2001354696-A.  
XX  
PD 25-DEC-2001.  
XX  
PF 08-JUN-2000; 2000JP-0171386.  
XX  
PR 08-JUN-2000; 2000JP-0171386.  
XX  
PA (NNSH) NIPPON SHINYAKU CO LTD.  
XX  
DR WPI; 2002-262912/31.  
XX  
PT Hypersensitivity inhibitory peptides are new -  
XX  
PS Example 12; Page 7; 8pp; Japanese.  
XX  
CC This invention describes novel nociceptin analogues which inhibit  
CC nociceptin-induced hypersensitivity and have analgesic activity. The  
CC products of the invention can be used for pain relief. This sequence  
CC represents a bovine nociceptin analogue described in the method of the  
CC invention.  
XX  
SQ Sequence 8 AA:  
Query Match 36.4%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 EQKQ 8  
DB 3 EQKQ 6  
RESULT 29  
AA013980  
ID AA013980 standard; Peptide: 8 AA.  
XX  
AC AA013980;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Cysteine-X-Cysteine chemokine receptor 4 P12 domain binding peptide.  
XX  
KW Cysteine-X-Cysteine Chemokine Receptor 4; CXCR4 binding peptide;  
KW chemoattractant cytokine; human immunodeficiency virus; HIV;  
KW HIV envelope glycoprotein; cellular CD4 receptor; env gene; gp160; gp120;  
KW gp41; CD4+ target cell; HIV-infected cell; CXCR4-binding compound;  
KW acquired immunodeficiency syndrome; AIDS; P12 binding domain;  
KW oriented linear peptide library.  
XX  
OS Synthetic.  
XX  
PN WO200170768-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US09160.  
XX  
PR 21-MAR-2000; 2000US-190945P.  
XX  
PR 21-MAR-2000; 2000US-190956P.  
XX  
PR 21-MAR-2000; 2000US-191299P.  
XX  
PR 20-MAR-2001; 2001US-081344B.  
XX  
PR 20-MAR-2001; 2001US-0813651.  
XX  
PR 20-MAR-2001; 2001US-0813653.  
XX  
PA (CONS-) CONSENSUS PHARM INC.  
XX  
PI Nestor JJ, Wilson CJ, Tan Hehir CA, Kates SA;  
XX

sk WPI; 2002-003533/00.  
XX  
XX Identifying agents that bind to CXCR4 chemokine receptor 4, useful for  
XX treatment and prevention of acquired immunodeficiency syndrome,  
XX comprises screening compound library for members that bind to the  
XX receptor.  
XX  
XX Example 12; Page 10; 8pp; English.  
XX  
XX The invention relates to a method of identifying Cysteine-X-Cysteine  
XX chemokine receptor 4 (CXCR4) binding compounds. The method comprises  
XX testing and selecting compounds in a library for their ability to bind to  
XX CXCR4. Chemokines (chemoattractant cytokines) regulate the movement and  
XX biological activities of leukocytes in many disease states. CXCR4  
XX acts as a co-receptor for the human immunodeficiency virus (HIV). As it  
XX interacts with the HIV envelope glycoproteins and the cellular CD4  
XX receptor, to facilitate HIV entry into cells. The HIV glycoproteins  
XX (encoded by the *env* gene) are translated as a precursor (gp160) which is  
XX subsequently cleaved into gp120 and gp41. gp120 binds to CXCR4 and the  
XX CD4 receptor present on the surface of susceptible CD4+ target cells,  
XX causing the virus to fuse with the cell membranes and thereby  
XX facilitating entry of the virus into the cell. The eventual expression of  
XX the *env* product on the surface of the HIV-infected cell enables the cell  
XX to fuse with uninfected cells, thereby spreading the infection. The  
XX CXCR4-binding compounds of the invention inhibit the entry of HIV into  
XX the CD4+ cell and therefore are useful in the prevention of HIV infection  
XX and the treatment and prevention of acquired immunodeficiency syndrome  
XX (AIDS). The present sequence represents a peptide that binds to the CXCR4  
XX binding domain. P12. This sequence was isolated from an oriented linear  
XX peptide library as part of an example of the invention.  
XX  
XX Sequence 8 AA:  
Query Match 36.4%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 KKKE 6  
DB 2 KKKE 5  
RESULT 30  
AA052777  
ID AA052777 standard; Peptide: 6 AA.  
XX  
AC AA052777;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE P12 domain binding peptide.  
XX  
KW CXCR4; CX chemokine receptor 4; human HIV infected cell;  
KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
KW drug screening; identifying novel binding domain.  
XX  
OS Synthetic.  
XX  
PN WO200171446-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 21-MAR-2001; 2001WO-US09160.  
XX  
PR 21-MAR-2000; 2000US-190945P.  
XX  
PR 21-MAR-2000; 2000US-190956P.  
XX  
PR 21-MAR-2000; 2000US-191299P.  
XX  
PR 20-MAR-2001; 2001US-081344B.  
XX  
PR 20-MAR-2001; 2001US-0813651.  
XX  
PR 20-MAR-2001; 2001US-0813653.  
XX  
PA (CONS-) CONSENSUS PHARM INC.  
XX  
PI Nestor JJ, Wilson CJ, Tan Hehir CA, Kates SA;  
XX

PI Nestor JJ, Wilson CJ, See RH, Tan Behr CA;  
 XX WPI: 2002-010610/01.  
 XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule  
 XX  
 XX Example 1: Page 19; 50pp: English.  
 XX The invention relates to a method for identifying a binding compound  
 CC for CC chemokine receptor 5 (CCR5). The method involves screening a  
 CC library of test molecules (particularly peptides) with immobilised CCR5,  
 CC and then identifying those molecules which bind. The invention also  
 CC relates to CCR5-binding molecules identified using the method of the  
 CC invention, methods for identifying consensus motifs for CCR5-binding  
 CC peptides, a transfer vector encoding tagged CCR5, a computer-aided  
 CC method for determining the relative binding affinity of a test molecule  
 CC to CCR5 and a computer aided drug screening assay that utilises the  
 CC three-dimensional structure of CCR5. Compounds identified using the  
 CC methods of the invention are useful for treating or preventing HIV  
 CC (human immunodeficiency virus) infection or AIDS (acquired  
 CC immunodeficiency syndrome) in a patient. The methods of the invention  
 CC may also be used to identify agonists or antagonists of the interaction  
 CC of CCR5 with its natural ligand, and to determine a binding motif for  
 CC CCR5. Sequences AAM52777-AAM52783 represent peptides or peptide libraries  
 CC able to bind to known protein binding domains which were used in an  
 CC in an exemplification of the invention.  
 XX  
 XX Sequence 8 AA:

QY 2 KKKE 5  
 DB IIII  
 2 KKKE 5

Query Match 36.4%; Score 4; DB 23; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Models 0; Caps 0;

RESULT 31  
 ABR74588  
 ID ABR74588 standard; Peptide; 8 AA.  
 XX  
 XX ABR74588;  
 XX  
 XX 18-APR-2002 (first entry)  
 XX  
 XX Transcription factor nuclear localisation signal peptide SPW ID NO:352.  
 XX Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; antitumor; solid tumor;  
 KW peptide; lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W0200193836-A2.  
 XX  
 XX 13-DEC-2001.  
 XX  
 XX 08-JUN-2001: 2001WO-US18657.  
 XX  
 XX 09-JUN-2000: 2000US-210525P.  
 XX  
 XX (HCU: /) BOULIKAS T.  
 XX  
 XX Boulikas T;  
 XX  
 XX WPI: 2002-164295/21.  
 XX  
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted

PI Liposome complexes

ES Claim 14: Page 24; 50pp: English

XX The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (i) combining  
 CC negatively charged agent with a cationic lipid in a ratio where the  
 CC of the negatively charged agent is neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in situ;  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic  
 CC karyophilic peptide conjugates in a 1:0.6:1 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent *in vivo*, comprising the administration  
 CC of the micelle. ABR74588 represents specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumor activities. The peptide-lipid-polynucleotide conjugates  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The fused and related to the field of gene therapy and is  
 CC directed toward methods for peptide and peptide-lipid polynucleotide  
 CC complexes suitable for delivery of therapeutic agents. The encapsulated  
 CC molecules display therapeutic activity in eradicating solid tumors.  
 CC Encapsulated liposomes containing a fusion protein or protein conjugate  
 CC ABR74588. ABR74588 represents the encapsulation of the present  
 CC invention.

XX Sequence 8 AA.

QY Query Match 36.4%; Score 4; DB 23; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Models 0; Caps 0;

QY 2 KKKE 5  
 DB IIII  
 2 KKKE 5

RESULT 32  
 ABR74588

ID ABR74588 standard; Peptide; 8 AA.

XX  
 XX ABR74588;  
 XX

XX 18-APR-2002 (first entry)

XX Transcription factor nuclear localisation signal peptide SPW ID NO:352.  
 XX Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; antitumor; solid tumor;  
 KW peptide; lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 XX breast carcinoma; prostate carcinoma.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W020193836-A2.  
 XX  
 XX 13-DEC-2001.  
 XX  
 XX 08-JUN-2001: 2001WO-US18657.  
 XX  
 XX 09-JUN-2000: 2000US-210525P.  
 XX  
 XX (HCU: /) BOULIKAS T.  
 XX  
 XX Boulikas T;  
 XX  
 XX WPI: 2002-164295/21.  
 XX  
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted

PS Claim 14: Page 27; 50pp: English.

XX The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (1) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.9 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and anticancer activities. The peptide lipopolymer-nucleic acid complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide lipid-polymeroid  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumors  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;

Query Match 36.43; Score 4; Dh 23; Length 8;

Best Local Similarity 100.0%; Prod. No. 9.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 KKKE 5  
 DB IIII  
 5 KKKE 8

RESULT 33

ABB74530

ID ABB74640 standard; Peptide: 8 AA.

AC ABB74640;

XX 18-APR-2002 (first entry)

XX Transcription factor nuclear localisation signal peptide SEQ ID NO:364.

XX Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; antitumor; solid tumor;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.

XX *Xenopus* sp.

OS

PN W0200193836-A2.

XX 13-DEC-2001.

XX 13-DEC-2001.

XX 08-JUN-2001; 2001WO-US18657.

PF 09-JUN-2000; 2000US-210525P.

PR (B00L/) R001IRAS T.

XX Boudikas T.

XX WPI: 2002-164295/21.

XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with

PT nuclear localization signal/fusogenic peptide conjugates into targeted

PT liposome complexes -

PS Claim 14; Page 77; 107pp; English.

XX The present invention describes a method for producing micelles with

CC entrapped therapeutic agents. The method comprises: (1) combining

XX neoplastic disease, such as a malignant lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (1) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.9 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and anticancer activities. The peptide-lipopolymer-nucleic acid complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide lipid-polymeroid  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumors  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;

Query Match 36.43; Score 4; Dh 23; Length 8;

Best Local Similarity 100.0%; Prod. No. 9.4e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 KKKE 5

DB IIII

5 KKKE 8

RESULT 34

ABB74235

ID ABB74292 standard; Peptide: 8 AA

XX ABB74292;

XX 10-APR-2002 (first entry)

XX Sequence factor nuclear localisation signal peptide SEQ ID NO:364.

XX Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; antitumor; solid tumor;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.

XX *Xenopus* sp.

OS

PN W0200193836-A2.

XX 13-DEC-2001.

XX 13-DEC-2001.

XX 08-JUN-2001; 2001WO-US18657.

PF 09-JUN-2000; 2000US-210525P.

PR (B00L/) R001IRAS T.

XX Boudikas T.

XX WPI: 2002-164295/21.

XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with

PT nuclear localization signal/fusogenic peptide conjugates into targeted

PT liposome complexes -

PS Claim 14; Page 77; 107pp; English.

XX The present invention describes a method for producing micelles with

CC entrapped therapeutic agents. The method comprises: (1) combining





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XX SQ Sequence 9 AA:
Query Match 36.4%, Score 4: 108.16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9, 10-0%;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

OY 4 KEUK 7
DB 4 KEUK 7

RESULT 37
AAW24434
ID AAW24434 standard; peptide: 9 AA.
XX AC
XX AC AAW24434;
XX DT
XX DT 30-SEP-1997 (first entry)
XX DE
XX DE K4, a nucleic acid (NA) binding peptide used in NA delivery to cells.
XX KW Nucleic acid transporter; gene therapy; binding complex; lysis agent;
XX KW JTS-1; K8; alpha helix; endosome; lysosome; nucleic acid;
XX OS Synthetic.
XX PN W09640958-A1.
XX XX
XX PD 19 DEC-1996.
XX PF 23 APR-1996; 96WO-US05679.
XX PR 07 JUN-1995; 95US-0484777.
XX PA (BAY) BAYLOR COLLEGE MEDICINE.
XX P1 Smith LC, Sparrow JT, Woo SL;
XX WPI: 1997-052345/05.
XX PT Nucleic acid transporter useful in gene therapy - contains binding
XX PT complex associated with surface and nuclear ligands and lysis agent
XX PS Disclosure: Page 49; 125pp; English.
XX CC
XX CC AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both
XX CC condensing and stabilising a NA. The peptides can be conjugated to a
XX CC lytic peptide to form a nucleic acid transporter system. The lysis agent
XX CC forms an alpha-helical structure. The transporter system is used to
XX CC deliver nucleic acid to a cell and for treating humans by gene therapy.
XX CC By taking advantage of the characteristics of both the lysis agents
XX CC and the binding molecules, delivery of the nucleic acid is enhanced.
XX CC Specific lysis agents are capable of releasing the nucleic acid
XX CC into the cellular interior from the endosome. Release is efficient
XX CC without endosomal/lysosomal degradation, once released the binding
XX CC complexes help target the nucleic acid to the nucleus.
XX SQ Sequence 9 AA;

Query Match 36.4%, Score 4: 108.16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9, 10-0%;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

OY 1 AKKK 4
DB 4 AKKK 6

RESULT 38
AAW78352
ID AAW78352 standard; peptide: 9 AA.
XX XX
```

```
AC AAW78352.
XX XX
XX 27 APR 1997 (first entry)
XX DE Interleukin-6 (IL-6) is a cytokine that plays a role in the regulation of
XX XX the immune system. It is a member of the interleukin-6 family of
XX KW cytokines. It is a secreted protein that binds to its receptor, the
XX KW IL-6 receptor, and induces the production of other cytokines. It is
XX XX involved in the regulation of the immune system.
XX OS Synthetic.
XX OS IL-6.
XX PN U01241206-A1.
XX DE 26 JAN 1997.
XX PF 02 DEC 1997; 96WO-US05679.
XX PR 07 JUN 1995; 95US-0484777.
XX XX
XX DE (FISA) Interleukin-6 (IL-6) is a cytokine that plays a role in the
XX XX regulation of the immune system. It is a member of the interleukin-6
XX PF family of cytokines. It is a secreted protein that binds to its
XX PF receptor, the IL-6 receptor, and induces the production of other
XX PF cytokines. It is involved in the regulation of the immune system.
XX XX
XX DE Example of a cytokine: Interleukin-6 (IL-6) is a secreted protein
XX XX that plays a role in the regulation of the immune system. It is a
XX XX member of the interleukin-6 family of cytokines. It is a secreted
XX XX protein that binds to its receptor, the IL-6 receptor, and induces
XX XX the production of other cytokines. It is involved in the regulation
XX XX of the immune system.
XX SQ Sequence 9 AA

Query Match 36.4%, Score 4: 108.16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9, 10-0%;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

OY 4 KEUK 7
DB 4 KEUK 7

RESULT 39
AAW85246
ID AAW85246 standard; peptide: 9 AA.
XX AC
XX AC AAW85246
XX DE 10 JUL 2000 (first entry)
XX DE Amino acid sequence: Lysine, Arginine, Lysine, Arginine, Lysine,
XX XX Arginine, Lysine, Arginine, Lysine, Arginine.
XX KW Amino acid sequence: Lysine, Arginine, Lysine, Arginine, Lysine,
XX KW Arginine, Lysine, Arginine, Lysine, Arginine.
XX KW Amino acid sequence: Lysine, Arginine, Lysine, Arginine, Lysine,
XX XX Arginine, Lysine, Arginine, Lysine, Arginine.
XX OS Homo sapiens.
XX OS Homo sapiens.
XX PN W02000000-A1
XX DE 24 SEP 1997; 96WO-US05679.
XX PF 24 SEP 1997; 96WO-US05679.
XX PR (PRIM) PRIM-00000000
XX XX
XX RISS 7;
```

XX WPI: 2000-292880/25.  
 XX New antibodies useful in detecting apoptosis and diagnosis of  
 PT conditions such as cancer, specifically recognize the new amino  
 PT terminus of a protein cleaved by a protease during apoptosis.  
 XX  
 XX Claim 6; Page 40; 6pp; English.  
 XX  
 CC This sequence represents a fragment of the amino terminus sequence of  
 CC poly ADP-ribose polymerase (PARP) after it has been cleaved during  
 CC apoptosis. PARP is an enzyme associated with DNA repair. Cleavage of the  
 CC PARP protein (by a caspase) into fragments contributes to the  
 CC fragmentation of DNA that is characteristic of apoptosis. Identification  
 CC of cells containing PARP fragments is an indication of apoptosis. The  
 CC invention relates to an antibody that is immunoreactive with a neopeptide  
 CC that produced in a cell undergoing apoptosis (e.g. a PARP fragment such as  
 CC that represented by the present sequence). The antibody specifically  
 CC recognises the new amino terminus of a protein cleaved at a cleavage site  
 CC by a protease, and is not immunoreactive with the protein prior to  
 CC cleavage. The antibodies are useful for detecting apoptosis in a cell or  
 CC groups of cells, especially human leukaemia HL60 or Jurkat cells, by  
 CC contacting the antibodies (optionally bound to a hapten, enzyme,  
 CC radioactive, fluorescent or luminescent label) with a protein sample or a  
 CC cell or tissue sample containing the neopeptide and detecting any binding  
 CC activity. The antibody is also useful for diagnosing, from patient cell  
 CC or tissue samples, disorders and diseases associated with apoptosis or  
 CC the inability of cells to undergo apoptosis such as cancer,  
 CC neurodegeneration, autoimmunity or heart disease. The antibodies are also  
 CC useful for screening for inhibitors and/or inducers of apoptosis, by  
 CC exposing two samples to conditions known to activate apoptosis,  
 CC contacting the first sample with a test compound, contacting both samples  
 CC with the antibody and detecting and comparing the binding of the antibody  
 CC to the neopeptide in the two samples.  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 36-95;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKK 4  
 Db 6 AKKK 9  
 RESULT 40  
 ID AAY51591  
 AC AAY51591 standard; peptide; 9 AA.  
 XX  
 XX AAY51591:  
 DT 25-MAY-2000 (first entry)  
 XX  
 XX HIV-1 derived gp120 peptide fragment #3.  
 XX  
 XX Plastic carrier surface; detection: gp120.  
 KW  
 XX Human immunodeficiency virus type 1.  
 OS  
 XX W0200005584-A1.  
 PN  
 XX 03-FEB-2000.  
 PD  
 XX 21-JUL-1999; 99WO-NL00470.  
 PF  
 XX 21-JUL-1998; 98NL-1009703.  
 PR  
 XX (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOEK.  
 PA  
 XX Puljk WC;  
 PT  
 XX WPI: 2000-182757/16.  
 DR

XX Ultra flat plastic carrier surfaces by molding on to smooth  
 PT non adhesive surfaces e.g. glass or glass, and release, can carry  
 PT active groups for molecular biology, also form submicron order size  
 PT wells suitable for micro-printing techniques.  
 XX  
 XX Disclosure: Fig 9, 4pp; English.  
 PS  
 XX  
 CC This invention describes a novel method for the manufacture of an ultra  
 CC flat plastic carrier surface, by molding on to a very smooth auxiliary  
 CC surface, treating the plastic so that the surface roughness of the side  
 CC facing the auxiliary is reduced, and removal coupling of chemical and  
 CC biochemical analyses for examination through active groups on the  
 CC plastic surface. Surface applications of the surface include  
 CC techniques. Examples of applications of the surface include  
 CC investigations of biological materials; peptides, proteins, saccharides,  
 CC RNA, viruses, and lipids; and radiation carrying polymers, e.g. DNA or  
 CC RNA, or their fragments, especially attached via linkers, detection  
 CC and determination of a variety of interest can be carried out as a  
 CC standard procedure, e.g. in SA, fluorescence, color, or radiation, except  
 CC that very small amounts can be assayed at investigated. Consequently,  
 CC the surface can be used in a variety of methods for these purposes. These  
 CC can be applied to a variety of biological materials, e.g. the forming  
 CC surface the plastic surface is so smooth that it can bind very small  
 CC amounts of materials. The surface, which can be detected polymer, even  
 CC when these together in the surface by microscopy and/or photo-  
 CC e.g. a central scanning without interference from bumps and blemishes  
 CC caused had discussing. AAY51591, 9 AA represent peptide fragments  
 CC derived from the human immunodeficiency virus type 1 gp120 protein which  
 CC are used to illustrate the nature of the invention.  
 XX  
 XX Sequence 9 AA:  
 SQ  
 Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 36-95;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKK 4  
 Db 6 AKKK 9  
 RESULT 41  
 ID AAB85065  
 AC AAB85065 standard; peptide; 9 AA.  
 XX  
 XX AAB85065:  
 DT 06-AUG-2000 (first entry)  
 XX  
 XX N terminal S benzyl transfer peptide #5.  
 DE  
 XX Coupling: amine-derivative hydroxy derivative; this ester; two other.  
 KW  
 XX Synthesis  
 XX  
 XX Key: Described/modified  
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PI Galt MJ, Stetsenko D;  
 DR WPI: 2001-367105/38.  
 XX  
 PT Method for coupling molecules, e.g. peptides and oligonucleotides, and  
 PT new intermediates and reagents  
 XX  
 PS Example 3; Page 27; 39pp; English.  
 XX  
 CC The invention relates to methods for coupling molecules. One method of  
 CC linking an amine derivative with a hydroxy derivative comprises reacting  
 CC an alkyl or aryl thio ester with an amino thioether. The compounds of the  
 CC invention are useful e.g. for linking a peptide and an oligonucleotide.  
 CC Sequences AAB8501-59 represent peptide N-terminal S-benzyl thio esters.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 36.4%; Score 4; DR 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKK 4  
 DB 1111  
 2 AKKK 5  
 RESULT 42  
 ID AAB67921  
 XX AAB6792: standard; peptide; 9 AA.  
 AC  
 XX  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Formula for heparin affinity regulatory peptide anlogqueic peptides.  
 XX  
 KW Heparin affinity regulatory peptide; HARP; anlogqueic peptide; HIV;  
 KW immune response; cellular growth; cellular regeneration; muscle cell;  
 KW cicatrization; immunosuppressive disease; human immunodeficiency virus;  
 KW HIV infection; antiviral.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note- "any amino acid; represents 0-20, where the  
 FT sum of the residues represented by amino acids  
 FT 1 and 9 is 0-20, preferably 0-15, and most  
 FT preferably 0-10"  
 FT Misc-difference 9 /note- "any amino acid; represents 0-25, where the  
 FT sum of the residues represented by amino acids  
 FT 1 and 9 is 0-20, preferably 0-15, and most  
 FT preferably 0-10"  
 XX  
 PN W0200127136-A2.  
 XX  
 PD 19-APR-2001.  
 XX  
 XX 06-OCT-2000; 2000WO-FR02786.  
 XX  
 PR 12-OCT-1999; 99FR-0012714.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Barritault D, Achour A, Courty J;  
 XX  
 DR WPI: 2001-281970/29.  
 XX  
 CC New Heparin Affinity Regulatory Peptide anlogqueic peptides, useful for  
 PT regenerating muscle cells, aiding cicatrization, detecting and  
 PT treating immunosuppressive diseases, stimulate immune response and  
 PT tissue regeneration

XX Claim 2; Page 32; 43pp; French.  
 XX  
 CC The present sequence represents a formula for heparin affinity  
 CC regulatory peptide (HARP) anlogqueic peptides that stimulate immune  
 CC response, cellular growth and regeneration. The peptides are useful  
 CC for regeneration cells such as muscle cells, and in aiding  
 CC cicatrization as well as in the treatment of immunosuppressive  
 CC diseases. The peptide activity the replication of human immunodeficiency  
 CC virus (HIV) in vitro and are useful in the detection of HIV infected cells.  
 CC When used with an internal signal, they render the HIV more accessible  
 CC to the antiviral agent, and therefore are more easily destroyed.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 36.4%; Score 4; DR 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKK 4  
 DB 1111  
 2 AKKK 5  
 RESULT 43  
 ID AAB67921  
 XX AAB6792: standard; peptide; 9 AA.  
 AC  
 XX  
 DT 29-JUN-2001 (first entry)  
 XX  
 DE Formula for heparin affinity regulatory peptide anlogqueic peptides.  
 XX  
 KW Heparin affinity regulatory peptide; HARP; anlogqueic peptide; HIV;  
 KW immune response; cellular growth; cellular regeneration; muscle cell;  
 KW cicatrization; immunosuppressive disease; human immunodeficiency virus;  
 KW HIV infection; antiviral.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note- "any amino acid; represents 0-20, where the  
 FT sum of the residues represented by amino acids  
 FT 1 and 9 is 0-20, preferably 0-15, and most  
 FT preferably 0-10"  
 FT Misc-difference 9 /note- "any amino acid; represents 0-25, where the  
 FT sum of the residues represented by amino acids  
 FT 1 and 9 is 0-20, preferably 0-15, and most  
 FT preferably 0-10"  
 XX  
 PN W0200127136-A2.  
 XX  
 PD 19-APR-2001.  
 XX  
 XX 06-OCT-2000; 2000WO-FR02786.  
 XX  
 PR 12-OCT-1999; 99FR-0012714.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Barritault D, Achour A, Courty J;  
 XX  
 DR WPI: 2001-281970/29.  
 XX  
 CC The invention relates to a formula for an immune response stimulating  
 CC peptide having a cell expressing at least one first molecule having a  
 CC motif, and at least one second molecule having a motif, and at least one  
 CC phosphatase 2A regulatory substrate A) and a substrate domain with an

agent that modulates the interaction between the first molecule and the second molecule. Also included are: (1) treating a subject having a condition that would benefit from down-regulation of an immune response, comprises administering an agent that inhibits the interaction between a first molecule and a second molecule described above; (2) identifying a compound that modulates the interaction of CTLA4 and pp2AA, and (3) identifying a compound which modulates the interaction of a molecule comprising at least one CTLA4 lysine rich motif and a pp2AA molecule comprising a pp2AA CTLA4-interacting domain. The methods are useful for modulating an immune response and treating a subject having a condition that would benefit from down-regulation of an immune response, such as autoimmune disorder (e.g. rheumatoid arthritis, myasthenia gravis, autoimmune thyroiditis, systemic lupus erythematosus, type 1 diabetes mellitus, Grave's disease, or multiple sclerosis), a transplant (e.g. a bone marrow transplant, a stem cell transplant, a heart transplant, a lung transplant, a liver transplant, a kidney transplant, a cornea transplant, or a skin transplant), graft versus host disease, an allergy, or an inflammatory disorder. Enhancing an immune response is useful in treating bacterial, viral (e.g. HIV 1 or 2, human immunodeficiency virus, hepatitis B or C) or parasitic infections. The present sequence is a pp2AA-binding peptide from human PAK-1.

Query Match: 36.4%; Score: 4; PB: 23; Length: 9;  
Best local Similarity: 100.0%; Pred. No.: 3, 4, 5, 05;  
Matches: 4; Conservative: 0; Mismatches: 0; Labels: 0; Days: 0;

RESULT 44	
ABG32828	
ID	ARG32828 standard; Peptide: 9 AA.
XX	
AC	ARG32828:
XX	
DT	29-Nov-2002 (first entry)
XX	
DE	PP2AA-binding peptide from mouse HPX #2.
XX	
KW	Cytotoxic T-lymphocyte associated protein; CytAA;
KW	protein phosphatase 2; PP2AA; immune response regulation; gene therapy;
KW	autoimmune disorder; rheumatoid arthritis; myasthenia gravis
KW	autoimmune thyroiditis; systemic lupus erythematosus; Grave's disease;
KW	type I diabetes mellitus; multiple sclerosis; transplant;
KW	graft versus host disease; allergy; inflammatory disorder;
KW	bacterial infection; viral infection; HIV; parasitic infection;
KW	human immunodeficiency virus; hepatitis; mouse; HPX

[illegible]

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Wing 43. Tail 24. Culmen 4.  
Tarsus 16. Middle toe 10.5.

[illegible]

XX Deriving DNA binding protein sequence binding to target regulatory  
PT sequence comprises selecting sequence for protein, mutating it, and  
PT providing to cell having reporter/seperator gene and screening for gene  
PT expression.  
XX  
XX Example 5: Page 47: 90pp: English.  
XX  
XX The invention relates to methods for identification and production of  
CC new DNA binding proteins that up or down regulate the expression of pre-  
CC determined target genes. Such genes include DNA sequences that encode  
CC proteins that regulate such target genes as well as gene constructs  
CC and biological materials that contain such DNA binding proteins and/  
CC or their DNA sequences. The method is useful for deriving a gene  
CC sequence of a new DNA binding protein that can bind to a target  
CC regulatory sequence where the gene sequence derived is useful as a  
CC tool for controlling gene expression and as therapeutics, the present  
CC sequence is a nuclear localisation signal. (NLS) peptide used to  
CC illustrate the method of the invention.  
XX  
SQ Sequence 9 AA:

Query Match: 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; Mismatches 0; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
QY 1 AKKK 4  
DB 2 AKKK 5

RESULT 46  
AA018023  
ID AA018023 standard: Peptide: 9 AA.  
XX  
XX AA018024:  
XX 30-AUG-2002 (first entry)  
XX Human immunoglobulin E epitope SEQ ID No: 15.  
XX Allergy: immunoglobulin E; IgE; vaccine: immunogen; epitope: human;  
KW non-anaphylactogenic; anti-allergic.  
XX Homo sapiens.  
XX WO200234288-A2.  
XX 02-MAY-2002.  
XX 24-OCT-2001: 2001WO-EP12392.  
XX 27-OCT-2000: 2000GB-0026334.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX Vinals Pe Bassols YC;  
XX WPI: 2002-479702/51.  
XX New peptides epitopes and mimotopes derived from IgE (seq-Id) for  
PT treating or preventing allergies, for typing circulating anti IgE, or  
PT for diagnosing atopy  
XX  
XX Claim 1: Page 5: 28pp: English.  
XX The present invention provides peptide epitopes derived from human  
CC immunoglobulin E (IgE), which are non-anaphylactogenic and can be used  
CC as immunogens to diagnose and treat allergies. The present sequence is  
CC an epitope of the invention.  
XX  
SQ Sequence 9 AA:

Query Match: 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; Mismatches 0; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
QY 7 KURN 10  
DB 2 KURN 5  
RESULT 47  
AA018024  
ID AA018024 standard: Peptide: 9 AA.  
XX  
XX AA018024:  
XX 02-SEP-2002 (first entry)  
XX Human IgE epitope: Peptide: SEQ ID No: 300.  
XX Immunogen: human IgE; vaccine: immunogen; epitope: late of the molecule;  
KW vaccine: anti-allergic.  
XX Homo sapiens.  
XX WO200234288-A2.  
XX 28-SEP-2002.  
XX 02-AUG-2002: 2002WO-EP12392.  
XX 22-AUG-2002: 2002WO-EP12392.  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (WPI ) 2002-479702/51.  
XX Epi-Id: M. Vinals Pe Bassols YC;  
XX WPI: 2002-479702/51.  
XX Compounds for use in treatment for treatment of allergy, comprises  
PT a substance that is a polyclonal IgE and immunogen carried  
XX Claim 4: Page 15: 11p: English.  
XX The present invention relates to compounds suitable for use in vaccines,  
CC where the substance comprises a d-substance and a cyclised peptide and an  
CC immunogen carrier. The compounds can be used in the treatment of  
CC allergies. The present sequence is a cyclic peptide immunogen derived  
CC from human IgE (IdE) suitable for use in the invention.  
XX  
SQ Sequence 9 AA:  
Query Match: 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; Mismatches 0; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
QY 7 KURN 1  
DB 2 KURN 5  
RESULT 48  
AA018026  
ID AA018026 standard: Peptide: 9 AA.  
XX  
XX AA018026:  
XX 06-SEP-2002 (first entry)  
XX Human IgE associated peptide: SEQ ID No: 119.  
XX IgE, and late of the molecule, and human cancer, cancer, cytostatic, HLA;  
KW human immunoglobulin E epitope: human cancer, cancer, cytostatic, HLA;

KW cervical cancer; epithelioid cancer; promyelocytic leukemia;  
KW oesophageal cancer; pancreatic cancer; malignant melanoma; lung cancer;  
KW oral carcinoma; breast cancer; metrorrhinoma; ovarian cancer;  
KW gliocytoma; colon cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200220560-A1.  
XX  
PD 14 MAR-2002.  
XX  
XX 07 SEP-2001: 2001WO-JP07784.  
XX  
XX 08-SEP-2000: 2000JP-0274218.  
XX  
XX (NISC) JAPAN SCI & TECHNOLOGY CORP.  
XX Takimoto M, Kuzumaki N, Sato N, Sahara H;  
XX WPI: 2002-292253/33.  
XX Human cancer-testis antigen D40 and encoded gene, useful in diagnosis  
XX and immunotherapy for cancer  
XX  
XX Claim 14: Page 109; 151pp; Japanese.  
XX This invention describes a novel gene encoding the human protein antigen,  
XX D40 which is expressed in testis and various cancers over a broad range  
XX and which has cytostatic activity. Peptides derived from this protein  
XX can bind with human leucocyte antigen (HLA) class I and can be used for  
XX detecting cytotoxic T cells or their precursor cells. The antigen is  
XX useful in diagnosis and immunotherapy for cancer, including cervical  
XX cancer, epithelioid cancer, promyelocytic leukemia, oesophageal cancer,  
XX pancreatic cancer, malignant melanoma, lung cancer, oral carcinoma,  
XX breast cancer, metrorrhinoma, ovarian cancer, gliocytoma and colon  
XX cancer. AAM49813-AAM50030 represent peptides associated with the human  
XX D40 antigen described in the disclosure of the invention.  
SQ Sequence 9 AA:  
Query Match 36.4%; Score 4; EB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9;36.05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 5 EOKQ 8  
Db 3 EOKQ 6  
RESULT 49  
AAM50020  
ID AAM50020 standard: peptide; 9 AA.  
XX  
AC AAM50020:  
XX  
XX 05-JUL-2002 (first entry)  
XX  
XX Human D40 associated peptide SEQ ID NO 211.  
XX  
XX D40: antigen; cancer-testis antigen; human; cancer; cytostatic; HLA;  
XX human leucocyte antigen class I cytotoxic T cell; immunotherapy;  
XX cervical cancer; epithelioid cancer; promyelocytic leukemia;  
KW oesophageal cancer; pancreatic cancer; malignant melanoma; lung cancer;  
KW oral carcinoma; breast cancer; metrorrhinoma; ovarian cancer;  
KW gliocytoma; colon cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200220560-A1.  
XX  
PD 14 MAR-2002.  
XX  
XX 07-SEP-2001: 2001WO-JP07784.  
XX

XX  
XX 08-SEP-2001: 2001WO-JP07784.  
XX  
XX (NISC) JAPAN SCI & TECHNOLOGY CORP.  
XX  
XX Takimoto M, Kuzumaki N, Sato N, Sahara H;  
XX WPI: 2002-292253/33.  
XX  
XX Human cancer-testis antigen D40 and encoded gene, useful in diagnosis  
XX and immunotherapy for cancer  
XX  
XX Claim 14: Page 109; 151pp; Japanese.  
XX This invention describes a novel gene encoding the human protein antigen,  
XX D40 which is expressed in testis and various cancers over a broad range  
XX and which has cytostatic activity. Peptides derived from this protein  
XX can bind with human leucocyte antigen (HLA) class I and can be used for  
XX detecting cytotoxic T cells or their precursor cells. The antigen is  
XX useful in diagnosis and immunotherapy for cancer, including cervical  
XX cancer, epithelioid cancer, promyelocytic leukemia, oesophageal cancer,  
XX pancreatic cancer, malignant melanoma, lung cancer, oral carcinoma,  
XX breast cancer, metrorrhinoma, ovarian cancer, gliocytoma and colon  
XX cancer. AAM49813-AAM50030 represent peptides associated with the human  
XX D40 antigen described in the disclosure of the invention.  
XX  
XX Sequence 9 AA:  
XX  
XX Query Match 36.4%; Score 4; EB 23; Length 9;  
XX Best Local Similarity 100.0%; Pred. No. 9;36.05;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX Oy 5 EOKQ 8  
XX Db 3 EOKQ 6  
XX  
XX RESULT 50  
XX AAM500278  
XX ID AAM500278 standard: peptide; 9 AA.  
XX  
XX AC AAM500278:  
XX  
XX 07-JUL-2002 (first entry)  
XX  
XX Human D40 associated peptide SEQ ID NO 211.  
XX  
XX D40: antigen; cancer-testis antigen; human; cancer; cytostatic;  
XX  
XX HLA; human leucocyte antigen class I cytotoxic T cell; immunotherapy;  
XX cervical cancer; epithelioid cancer; promyelocytic leukemia;  
KW oesophageal cancer; pancreatic cancer; malignant melanoma; lung cancer;  
KW oral carcinoma; breast cancer; metrorrhinoma; ovarian cancer;  
KW gliocytoma; colon cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200220560-A1.  
XX  
PD 14 MAR-2002.  
XX  
XX 07-SEP-2001: 2001WO-JP07784.  
XX

CC The present invention relates to the isolation of novel human genes  
CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The  
CC gene encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding  
CC PHOR1-F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6  
CC polynucleotide and polypeptide sequences are useful in diagnostic and  
CC therapeutic methods, and compositions for various cancers such as  
CC prostate cancer. The sequences are useful for inhibiting the growth of  
CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating  
CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof  
CC can be used to elicit an immune response. AA091563-AA092962 represent  
CC PHOR1-A11 or PHOR1-F5D6 peptides tested for HLA binding.

xx  
SQ Sequence 9 AA:

Query Match 36.4%; Score 4; DB 24; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KEOK 7  
| | | |  
Db 5 KEOK 8

Search completed: September 30, 2003, 17:03:05  
Job time : 86 secs





103	2	18.2	16	2	154523	alpha-actinin-1	172	1.3	1.3	1.3	Human
104	2	18.2	10	2	S65387	alpha-actinin-2	172	1.3	1.3	1.3	Human
105	2	18.2	10	2	S65385	alpha-actinin-3	172	1.3	1.3	1.3	Human
106	2	18.2	10	2	PH0900	alpha-actinin-4	172	1.3	1.3	1.3	Human
107	2	18.2	10	2	PH0927	alpha-actinin-5	172	1.3	1.3	1.3	Human
108	2	18.2	10	2	PH0933	alpha-actinin-6	172	1.3	1.3	1.3	Human
109	2	18.2	10	2	PH0925	alpha-actinin-7	172	1.3	1.3	1.3	Human
110	2	18.2	10	2	PH0926	alpha-actinin-8	172	1.3	1.3	1.3	Human
111	2	18.2	10	2	PH0923	alpha-actinin-9	172	1.3	1.3	1.3	Human
112	2	18.2	10	2	PH0948	alpha-actinin-10	172	1.3	1.3	1.3	Human
113	2	18.2	10	2	PC4374	alpha-actinin-11	172	1.3	1.3	1.3	Human
114	2	18.2	10	2	S52645	alpha-actinin-12	172	1.3	1.3	1.3	Human
115	2	18.2	10	2	PA0216	alpha-actinin-13	172	1.3	1.3	1.3	Human
116	2	18.2	10	2	S50220	alpha-actinin-14	172	1.3	1.3	1.3	Human
117	2	18.2	10	2	A44871	alpha-actinin-15	172	1.3	1.3	1.3	Human
118	2	18.2	10	2	PC0788	alpha-actinin-16	172	1.3	1.3	1.3	Human
119	2	18.2	10	2	PC0785	alpha-actinin-17	172	1.3	1.3	1.3	Human
120	2	18.2	10	2	PC0783	alpha-actinin-18	172	1.3	1.3	1.3	Human
121	2	18.2	10	2	PC0783	alpha-actinin-19	172	1.3	1.3	1.3	Human
122	2	18.2	10	2	PC0783	alpha-actinin-20	172	1.3	1.3	1.3	Human
123	2	18.2	10	2	PC0783	alpha-actinin-21	172	1.3	1.3	1.3	Human
124	2	18.2	10	2	PC0783	alpha-actinin-22	172	1.3	1.3	1.3	Human
125	2	18.2	10	2	PC0783	alpha-actinin-23	172	1.3	1.3	1.3	Human
126	2	18.2	10	2	PC0783	alpha-actinin-24	172	1.3	1.3	1.3	Human
127	2	18.2	10	2	PC0783	alpha-actinin-25	172	1.3	1.3	1.3	Human
128	2	18.2	10	2	PC0783	alpha-actinin-26	172	1.3	1.3	1.3	Human
129	2	18.2	10	2	PC0783	alpha-actinin-27	172	1.3	1.3	1.3	Human
130	2	18.2	10	2	PC0783	alpha-actinin-28	172	1.3	1.3	1.3	Human
131	2	18.2	10	2	PC0783	alpha-actinin-29	172	1.3	1.3	1.3	Human
132	2	18.2	10	2	PC0783	alpha-actinin-30	172	1.3	1.3	1.3	Human
133	2	18.2	10	2	PC0783	alpha-actinin-31	172	1.3	1.3	1.3	Human
134	2	18.2	10	2	PC0783	alpha-actinin-32	172	1.3	1.3	1.3	Human
135	2	18.2	10	2	PC0783	alpha-actinin-33	172	1.3	1.3	1.3	Human
136	2	18.2	10	2	PC0783	alpha-actinin-34	172	1.3	1.3	1.3	Human
137	2	18.2	10	2	PC0783	alpha-actinin-35	172	1.3	1.3	1.3	Human
138	2	18.2	10	2	PC0783	alpha-actinin-36	172	1.3	1.3	1.3	Human
139	2	18.2	10	2	PC0783	alpha-actinin-37	172	1.3	1.3	1.3	Human
140	2	18.2	10	2	PC0783	alpha-actinin-38	172	1.3	1.3	1.3	Human
141	2	18.2	10	2	PC0783	alpha-actinin-39	172	1.3	1.3	1.3	Human
142	2	18.2	10	2	PC0783	alpha-actinin-40	172	1.3	1.3	1.3	Human
143	2	18.2	10	2	PC0783	alpha-actinin-41	172	1.3	1.3	1.3	Human
144	2	18.2	10	2	PC0783	alpha-actinin-42	172	1.3	1.3	1.3	Human
145	2	18.2	10	2	PC0783	alpha-actinin-43	172	1.3	1.3	1.3	Human
146	2	18.2	10	2	PC0783	alpha-actinin-44	172	1.3	1.3	1.3	Human
147	2	18.2	10	2	PC0783	alpha-actinin-45	172	1.3	1.3	1.3	Human
148	2	18.2	10	2	PC0783	alpha-actinin-46	172	1.3	1.3	1.3	Human
149	2	18.2	10	2	PC0783	alpha-actinin-47	172	1.3	1.3	1.3	Human
150	2	18.2	10	2	PC0783	alpha-actinin-48	172	1.3	1.3	1.3	Human
151	2	18.2	10	2	PC0783	alpha-actinin-49	172	1.3	1.3	1.3	Human
152	2	18.2	10	2	PC0783	alpha-actinin-50	172	1.3	1.3	1.3	Human
153	2	18.2	10	2	PC0783	alpha-actinin-51	172	1.3	1.3	1.3	Human
154	2	18.2	10	2	PC0783	alpha-actinin-52	172	1.3	1.3	1.3	Human
155	2	18.2	10	2	PC0783	alpha-actinin-53	172	1.3	1.3	1.3	Human
156	2	18.2	10	2	PC0783	alpha-actinin-54	172	1.3	1.3	1.3	Human
157	2	18.2	10	2	PC0783	alpha-actinin-55	172	1.3	1.3	1.3	Human
158	2	18.2	10	2	PC0783	alpha-actinin-56	172	1.3	1.3	1.3	Human
159	2	18.2	10	2	PC0783	alpha-actinin-57	172	1.3	1.3	1.3	Human
160	2	18.2	10	2	PC0783	alpha-actinin-58	172	1.3	1.3	1.3	Human
161	2	18.2	10	2	PC0783	alpha-actinin-59	172	1.3	1.3	1.3	Human
162	2	18.2	10	2	PC0783	alpha-actinin-60	172	1.3	1.3	1.3	Human
163	2	18.2	10	2	PC0783	alpha-actinin-61	172	1.3	1.3	1.3	Human
164	2	18.2	10	2	PC0783	alpha-actinin-62	172	1.3	1.3	1.3	Human
165	2	18.2	10	2	PC0783	alpha-actinin-63	172	1.3	1.3	1.3	Human
166	2	18.2	10	2	PC0783	alpha-actinin-64	172	1.3	1.3	1.3	Human
167	2	18.2	10	2	PC0783	alpha-actinin-65	172	1.3	1.3	1.3	Human
168	2	18.2	10	2	PC0783	alpha-actinin-66	172	1.3	1.3	1.3	Human
169	2	18.2	10	2	PC0783	alpha-actinin-67	172	1.3	1.3	1.3	Human
170	2	18.2	10	2	PC0783	alpha-actinin-68	172	1.3	1.3	1.3	Human
171	2	18.2	10	2	PC0783	alpha-actinin-69	172	1.3	1.3	1.3	Human
172	2	18.2	10	2	PC0783	alpha-actinin-70	172	1.3	1.3	1.3	Human
173	2	18.2	10	2	PC0783	alpha-actinin-71	172	1.3	1.3	1.3	Human
174	2	18.2	10	2	PC0783	alpha-actinin-72	172	1.3	1.3	1.3	Human
175	2	18.2	10	2	PC0783	alpha-actinin-73	172	1.3	1.3	1.3	Human





A:Molecule type: protein  
 A:Residues: 1-9 <ARN>  
 A:Experimental source: heart  
 C:Genetics:  
 A:Genome: nuclear  
 C:Function:  
 A:Pathway: oxidative phosphorylation; respiratory chain  
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 27.3%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2,46-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQ 6  
 DB 1 KEQ 3

## RESULT 3

PC7076  
 spectrin alpha chain, non-erythroid - mouse (fragment)  
 N:Alternate names: fodrin alpha chain  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
 C:Accession: PC7076  
 R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
 Electrophoresis 21, 1853-1871, 2000  
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of  
 A:Reference number: PC7072  
 A:Accession: PC7076  
 A:Molecule type: protein  
 A:Residues: 1-9 <FS>  
 A:Experimental source: strain C57BL/6Cr Slc, male; brain; striatum  
 C:Keywords: brain

Query Match 27.3%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2,46-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4  
 DB 6 KKK 8

## RESULT 4

PD0441  
 translation elongation factor TU-like protein p43, mitochondrial - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 21-Aug-1998  
 C:Accession: PD0441  
 R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.;  
 submitted to JEPID, August 1998  
 A:Description: Proteome analysis of mouse brain.  
 A:Reference number: PD0441  
 A:Accession: PD0441  
 A:Molecule type: protein  
 A:Residues: 1-11 <KAW>  
 A:Experimental source: striatum  
 C:Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3,46-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 4 AKK 6

## RESULT 5

E64573  
 hypothetical protein HP0429 - Helicobacter pylori (strain 26695)  
 C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1997  
 C:Accession: E64573  
 R:Torby, J.F.; White, G.; Kozlov, A.P.; Clayton, R.A.; Sutton, G.; Fleischmann  
 Peterson, S.; Loftus, B.; Richardson, J.; Dodson, R.; Khalak, H.; Glisdek, A.; Mc  
 son, J.D.; Kelley, J.M.; Collins, M.B.; Weidman, J.M.; Fujii, C.; Rozen, S.; White  
 Nature 388, 539-547, 1997  
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, R.G.; Chase  
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori  
 A:Reference number: A6452; WU09704467; PMID:9252185  
 A:Accession: E64573  
 A:Status: preliminary  
 A:Molecule type: RNA  
 A:Residues: 1-12 <FS>  
 A:Cross-references: R:AB00651; R:AB006111; NID:0243336; P1IN:AA009221; P1D:022

Query Match 27.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3,46-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKE 6  
 DB 4 KKE 8

## RESULT 6

A00763  
 sucrose 6-phosphate hydrolase (EC 3.2.2.22) - lactococcus lactis subsp. lactis (strain  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 12-Sep-1997  
 C:Accession: A00763  
 R:Tagesson, J.; Nyberg, N.Y.; Strickell, L.L.; Dockershort, J.A.;  
 J. Biol. Chem. 269, 14523-14526, 1994  
 A:Title: Transposon encoded surface metabolism in lactococcus lactis, fermenting  
 A:Reference number: Abstract Biochemistry 11; PMID:1659362  
 A:Accession: A00763  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <FS>  
 C:Keywords: 4-phosphosucrose hydrolase

Query Match 27.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3,46-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKE 9  
 DB 4 KKE 8

## RESULT 7

PI0083  
 protein GAG6022 - Arabidopsis thaliana (strain Columbia)  
 C:Species: Arabidopsis thaliana (mouse ear cross)  
 C:Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 06-Jun-1997  
 C:Accession: PI0083  
 R:Tsugita, A.; Kamo, M.; Kawakami, T.; Uchida, Y.;  
 submitted to JEPID, August 1998  
 A:Description: Arabidopsis thaliana electrophoresis of plant proteins and standard protein  
 A:Reference number: PI0083  
 A:Accession: PI0083  
 A:Molecule type: protein  
 A:Residues: 1-12 <FS>  
 A:Experimental source: plant

Query Match 27.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3,46-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FOK 7  
 DB 7 FOK 9

RESULT 8  
 S23168  
 Z: protein - guinea pig (fragment)  
 C: Species: Cavia porcellus (guinea pig)  
 C: Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
 C: Accession: S23168  
 R: Nicollier, M.; Roblin, S.; Cypriani, B.; Remy-Martin, J.P.; Adessi, G.L.  
 Eur. J. Biochem. 205, 1137-1144, 1992  
 A: Title: Purification and characterization of a binding protein related to the 2 class 2  
 A: Reference number: S23168; MUID:92249119; PMID:1576997  
 A: Accession: S23168  
 A: Molecule type: protein  
 A: Residues: 1-12 <NIC>  
 A: Experimental source: liver  
 C: Function:  
 A: Description: binds dehydroepiandrosterone sulfate, estrone sulfate, oleic acid, cholest  
 C: Keywords: liver; steroid binding  
  
 Query Match 27.3%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; gaps 0;  
  
 QY 6 OKQ 8  
 DB 10 OKQ 12  
  
 RESULT 9  
 A33208  
 calreticulin, hepatic - bovine (fragment)  
 C: Species: Bos primigenius taurus (cattle)  
 C: Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 31-Oct-1997  
 C: Accession: A33208  
 R: Milner, R.E.; Baksh, S.; Shemanko, C.; Carpenter, M.R.; Smillie, L.; Vance, J.E.; Opas  
 J. Biol. Chem. 266, 7155-7165, 1991  
 A: Title: Calreticulin, and not calsequestrin, is the major calcium binding protein of sm  
 A: Reference number: A33208; MUID:91201375; PMID:2016321  
 A: Accession: A33208  
 A: Status: preliminary  
 A: Molecule type: protein  
 A: Residues: 1-13 <ML>  
 C: Superfamily: calreticulin  
 C: Keywords: liver  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; gaps 0;  
  
 QY 4 KEQ 6  
 DB 7 KEQ 9  
  
 RESULT 10  
 T08533  
 hypothetical protein X - Enterobacter aerogenes plasmid 8751  
 C: Species: Enterobacter aerogenes  
 C: Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jun-2000  
 C: Accession: T08533  
 R: Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.  
 Plasmid 46, 95-111, 1996  
 A: Title: Conservation of the genetic switch between replication and transfer genes of 13  
 A: Reference number: 216434; MUID:97118926; PMID:8954891  
 A: Accession: T08533  
 A: Status: preliminary; translated from GR/EMBL/DBJ  
 A: Molecule type: DNA  
 A: Residues: 1-13 <THO>  
 A: Cross-references: EMBL:067194; NID:q1572549; FIEN:AA764477.1; PMID:q1572582  
 C: Genetics:  
 A: Genome: plasmid 8751  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; gaps 0;  
  
 QY 1 AKK 3  
 DB 6 AKK 8  
  
 RESULT 11  
 S22955  
 hypothetical protein X - Escherichia coli plasmid 4901  
 C: Species: Escherichia coli  
 C: Date: 11-Dec-1994 #sequence\_revision 24-Sep-1994 #text\_change 08-Dec-1995  
 C: Accession: S22955  
 R: Zaeveloff, G.; Falsgaard, W.; Strick, P.; Bolzer, D.; Klever, M.; Knip, V.; Bakka  
 DNA Seq. 1, 303-323, 1991  
 A: Title: Nucleotide sequence and organization of genes flanking the transfer origin  
 A: Reference number: S22955; MUID:92056349; PMID:1665937  
 A: Accession: S22955  
 A: Molecule type: DNA  
 A: Residues: 1-13 <ZF>  
 A: Cross-references: EMBL:067194; NID:q1572549; FIEN:AA764477.1; PMID:q1572582  
 C: Genetics:  
 A: Genome: plasmid  
 A: Start codon: TTT  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; gaps 0;  
  
 QY 1 AKK 3  
 DB 6 AKK 8  
  
 RESULT 12  
 A86126  
 hypothetical protein X - Escherichia coli (strain 017 H7, strain 017 H7)  
 C: Species: Escherichia coli  
 C: Date: 16-Feb-2000 #sequence\_revision 17-Feb-2000 #text\_change 12-Sep-2001  
 C: Accession: A86126  
 R: Perna, N.T.; Park, H.; Burland, V.; Mau, B.; Glasner, J.; Fink, S.; Lau, A.; Mo  
 Miller, L.; Gattler, K.; Paulsen, O.; White, O.; Salzberg, S.L.; Peterson, K.; Aki  
 Nature 409, 529-534, 2001  
 A: Title: Genome sequence of enterobacterial Escherichia coli strain  
 A: Reference number: A86126; MUID:97046746; PMID:11206581  
 A: Accession: A86126  
 A: Status: preliminary  
 A: Molecule type: DNA  
 A: Residues: 1-13 <SH>  
 A: Cross-references: EMBL:067194; NID:q1572549; FIEN:AA764477.1; PMID:q1572582  
 A: Experimental source: strain 017 H7; Escherichia coli  
 C: Genetics:  
 A: Genome: 758kb  
  
 Query Match 27.3%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; gaps 0;  
  
 QY 1 AKK 3  
 DB 6 AKK 8  
  
 RESULT 13  
 QW45V  
 mastoparan - yellow (baked) (Western blotting)  
 C: Species: Wistar-Kyoto  
 C: Date: 24-Sep-1994 #sequence\_revision 24-Sep-1994 #text\_change 08-Dec-1995  
 C: Accession: QW45V  
 R: Hirata, Y.; Yasutake, T.; Yoshida, H.; Nakajima, T.; Fujino, M.; Kitada, M.  
 Chem. Pharm. Bull. 42, 1942-1944, 1994  
 A: Title: A new mastoparan-related peptide mastoparan in the venom of Vespa  
 A: Reference number: QW45V; MUID:92056349; PMID:543862

A:Accession: A01776  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 A:Note: the active peptide was also synthesized  
 C:Comment: This cytoactive peptide from wasp venom induces mast cell degranulation. The  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4e-03;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 14  
 QMWHMM  
 mastoparan M - hornet (Vespa mandarinia)  
 N:Alternate names: mast cell-degranulating peptide  
 C:Species: Vespa mandarinia  
 C:Date: 04-Dec-1986 #sequence\_revision: 04-Dec-1986 #text\_change: 08-Dec-1995  
 C:Accession: A01777  
 R:Rital, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 Biomed. Res. 2, 447-449, 1981  
 A:Title: A new mast cell degranulating peptide, mastoparan M, is the venom of the hornet  
 A:Reference number: A01777  
 A:Accession: A01777  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation and  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end; venom  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4e-03;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 15  
 QMWHXX  
 mastoparan X - hornet (Vespa xanthoptera)  
 C:Species: Vespa xanthoptera  
 C:Date: 24-Sep-1987 #sequence\_revision: 24-Sep-1991 #text\_change: 08-Dec-1995  
 C:Accession: A01778  
 R:Rital, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 Chem. Pharm. Bull. 27, 1945-1946, 1979  
 A:Title: A new mast cell degranulating peptide homologous to mastoparan in the venom of  
 A:Reference number: A01778; MUID:80155338; PMID:540603  
 A:Accession: A01778  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation.  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4e-03;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 16  
 QMWHLL  
 mastoparan L - hornet (Vespa mandarinia)  
 C:Species: Vespa mandarinia  
 C:Date: 26-Sep-1990 #sequence\_revision: 26-Sep-1990 #text\_change: 08-Dec-1995  
 C:Accession: A01779  
 R:Rital, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 J. Biol. Chem. 265, 1133-1137, 1990  
 A:Title: Isolation and characterization of a new mast cell degranulating peptide from hornet venom  
 A:Reference number: A01779  
 A:Accession: A01779  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This peptide from hornet venom induces mast cell degranulation.  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4e-03;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 17  
 QMWHLL  
 mastoparan L - hornet (Vespa mandarinia)  
 C:Species: Vespa mandarinia  
 C:Date: 26-Sep-1990 #sequence\_revision: 26-Sep-1990 #text\_change: 08-Dec-1995  
 C:Accession: A01779  
 R:Rital, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 J. Biol. Chem. 265, 1133-1137, 1990  
 A:Title: Isolation and characterization of a new mast cell degranulating peptide from hornet venom  
 A:Reference number: A01779  
 A:Accession: A01779  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 C:Comment: This peptide from hornet venom induces mast cell degranulation.  
 C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end  
 F:14/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4e-03;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
 III  
 DB 10 AKK 12

RESULT 18  
 S6662  
 xylose 1,4-beta xylosidase (EC 3.2.1.35)  
 N:Alternate names: beta xylosidase  
 C:Species: Thermotoga sp.  
 A:Accession: A01780  
 C:Date: 29-Mar-1999 #sequence\_revision: 29-Mar-1999 #text\_change: 08-Dec-1995  
 A:Accession: A01780  
 R:Rital, Y.; Kuwada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 A:Title: Thermotoga xylosidase and beta xylosidase from Thermotoga sp.  
 A:Reference number: A01780; PMID:842876  
 A:Accession: A01780  
 A:Molecule type: protein  
 A:Residues: 1-14 <HR>  
 A:Experimental: used as substrate for xylosidase  
 C:Comment: A thermophilic xylosidase and xylosidase from Thermotoga sp.  
 C:Function: hydrolase  
 A:Note: plays an important role in the catabolism of end-product inhibition of xylosidase

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4e-03;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
 III  
 DB 10 AKK 12

C:Keywords: glycosidase; hydrolase; polysaccharide deacetylase

Query Match 27.3%, Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4e-04;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
DB 1 AKK 3

#### RESULT 19

S13864

methy coenzyme M reductase (EC 1.8.1.1) [1: alpha chain - Methanobacterium thermoautotrophicum]

C:Species: Methanobacterium thermoautotrophicum

A:Variety: strain Marburg

C:Date: 14-Mar-1997 #sequence\_revision 13-Sep-1998 #text\_change 30-Oct-1998

C:Accession: S13864

R:Rospert, S.; Linder, D.; Ellermann, J.; Trauer, R.K.

Eur. J. Biochem. 194, 871-877, 1990

A:Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium thermophilum

A:Reference number: S13864; MUID:91098170; PMID:2269436

A:Accession: S13864

A:Molecule type: protein

A:Residues: 1-14 <ROS>

A:Experimental source: strain Marburg

C:Keywords: methanogenesis; oxidoreductase

Query Match 27.3%, Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4e-04;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKK 4  
DB 12 KKK 14

#### RESULT 20

B34135

DNA-binding protein q - Crithidia fasciculata mitochondrion (fragment)

C:Species: mitochondrion Crithidia fasciculata

C:Date: 30-Sep-1991 #sequence\_revision 10-Sep-1991 #text\_change 07-Jun-1999

C:Accession: B34135

R:Tittawalla, I.

FEBS Lett. 260, 57-61, 1990

A:Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata

A:Reference number: A34135

A:Accession: B34135

A:Molecule type: protein

A:Residues: 1-14 <TIT>

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Keywords: mitochondrion

Query Match 27.3%, Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4e-04;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
DB 6 AKK 8

#### RESULT 21

S14336

mastoparan B - hornet (Vespa basalis)

C:Species: Vespa basalis

C:Date: 14-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Apr-1999

C:Accession: S14336

R:Ho, C.H.; Hwang, L.L.

Biochem. J. 274, 453-456, 1991

A:Title: Structure and biological activities of a new mastoparan isolated from the venom

A:Reference number: S14336

A:Accession: S14336

A:Molecule type: protein

A:Residues: 1-14 <ROS>

A:Experimental source: strain Marburg

C:Keywords:

A:Description: possesses a potent formylating activity which acts in synergy with the formylating activity of mastoparan to induce a potent cytotoxic effect

A:Keywords: mastoparan; cytotoxicity; status: experimental

Query Match 27.3%, Score 4; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 4e-04;

Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3  
DB 1 AKK 1

#### RESULT 22

S21747

human and sheep erythropoietin (EC 3.4.1.1) [1: cytochrome b2]

C:Species: erythropoietin

C:Date: 14-Mar-1997 #sequence\_revision 14-Mar-1997 #text\_change 14-Mar-1997

C:Accession: S21747

R:Gold, P.; Puri, R.; Zetterstrom, M.W.

Proc Natl Acad Sci USA 87, 1111-1115, 1990

A:Title: A human erythropoietin gene, an extremely heterogeneous cDNA family, and a human erythropoietin gene

A:Reference number: S21747; MUID:91098170; PMID:169155

A:Accession: S21747

A:Molecule type: protein

A:Residues: 1-14 <ROS>

A:Experimental source: strain Marburg

C:Keywords: erythropoietin

Query Match 27.3%, Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4e-04;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KKK 3  
DB 2 KKK 4

#### RESULT 23

B34208

crithidia fasciculata (Crithidia fasciculata)

C:Species: Crithidia fasciculata (Crithidia fasciculata)

C:Date: 30-Sep-1991 #sequence\_revision 10-Sep-1991 #text\_change 12-Apr-1999

C:Accession: B34208

R:Rospert, S.; Linder, D.; Ellermann, J.; Trauer, R.K.; Hwang, L.L.

Eur. J. Biochem. 194, 871-877, 1990

A:Title: Two genetically distinct methyl-coenzyme M reductases in Methanobacterium thermophilum

A:Reference number: A34208; MUID:91098170; PMID:2269436

A:Accession: B34208

A:Molecule type: protein

A:Residues: 1-14 <ROS>

A:Experimental source: strain Marburg

C:Keywords: erythropoietin

Query Match 27.3%, Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4e-04;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KKK 3  
DB 2 KKK 4

#### RESULT 24

A00156

cellulase (EC 3.2.1.4) [1: structure (fragment)]

N:Alternative names: ends 1-4 beta-D-glucosidase





Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QR 9  
 DB 6 QR 7

RESULT 30  
 S43971  
 tumor-associated antigen MUT2 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
 C:Accession: S43971  
 R:Mandelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.  
 Nature 369, 67-71, 1994  
 A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine  
 A:Reference number: S43971; PMID:9421781; PMID:9164742  
 A:Accession: S43971  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <MAN>  
 C:Superfamily: unassigned animal pept.des

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 EQ 6  
 DB 2 EQ 3

RESULT 31  
 S43972  
 tumor-associated antigen MUT2 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
 C:Accession: S43972  
 R:Mandelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.  
 Nature 369, 67-71, 1994  
 A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine  
 A:Reference number: S43971; PMID:9421781; PMID:9164742  
 A:Accession: S43972  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <MAN>  
 C:Superfamily: unassigned animal pept.des

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 EQ 6  
 DB 2 EQ 3

RESULT 32  
 S37141  
 rpsA protein - Erwinia chrysanthemi  
 C:Species: Erwinia chrysanthemi  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
 C:Accession: S37141  
 R:Doullie, A.; Toussaint, A.; Faelen, M.  
 submitted to the EMBL Data Library, August 1993  
 A:Description: Identification of the integration host factor genes of E. chrysanthemi.  
 A:Reference number: S37139  
 A:Accession: S37141  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <DOU>

Accession references: EMBL: X74760; NCBI: 349964; EION: CAA52769.1; PDB: 1fj0

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AK 2  
 DB 5 AK 6

RESULT 33  
 S70727  
 IgGF protein: Shigella flexneri (fragment)  
 C:Species: Shigella flexneri  
 C:Date: 15-Feb-1997 #sequence\_revision 15-Mar-1997 #text\_change 08-Oct-1999  
 C:Accession: S70727  
 R:Allapure, A.; Sussanetti, L.; Wenzel, R.; Barzu, S.; Meunier, J.; Halpin, A.;  
 Mol. Microbiol. 12, 301-310, 1994  
 A:Title: Mx13, a protein that is involved in the secretion of Shigella spp. 190, causes  
 A:Reference number: S70727; PMID:1251111; PMID:8755365  
 A:Accession: S70727  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-4 ALL  
 A:Superfamily: unassigned animal pept.des

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KO 8  
 DB 2 KO 3

RESULT 34  
 A39308  
 glycine reductase (G1-4799) sulphydryl protein G, alpha chain - Clostridium stick  
 C:Species: Clostridium sticklandii  
 C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 15-Apr-1997  
 C:Accession: A39308  
 R:Staden, J.; Davis, J.N.  
 J. Biol. Chem. 266, 2437-2456, 1991  
 A:Title: Glycine reductase from Clostridium sticklandii: properties and characterization of the rbcA  
 A:Reference number: A39308; PMID:247341; PMID:194245  
 A:Accession: A39308  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <SDA>  
 C:Function:  
 A:Description: Glycine reductase complex catalyzes the reductive decarboxylation of glycine  
 C:Keywords: Amino acid reductase

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 NA 11  
 DB 3 NA 6

RESULT 35  
 C61512  
 variant surface glycoprotein M1.1-1.4 - Trypanosoma brucei (flagrant)  
 C:Species: Trypanosoma brucei  
 C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1999  
 C:Accession: C61512  
 R:Holder, A.A.; Cross, J.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A:Title: glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C:term  
 A:Reference number: A61512; MUID:81172836; PMID:6163983  
 A:Accession: C61512

A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <HOL>  
 C:Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NA 11  
 II  
 DB 4 NA 5

RESULT 36  
 A21440  
 variant surface glycoprotein pSLcl - Trypanosoma brucei (fragment)  
 C:Species: Trypanosoma brucei  
 C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Mar 1998  
 C:Accession: A21440  
 R:Parsons, M.; Nelson, R.G.; Watkins, K.F.; Agabian, N.  
 Cell 38, 309-316, 1984  
 A:Title: Trypanosoma mRNAs share a common 5' spliced leader sequence.  
 A:Reference number: A90853; MUID:84282716; PMID:6088073  
 A:Accession: A21440  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <PAR>  
 A:Cross-references: GB:K02195; NID:q162150; PID:q162151  
 C:Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KE 5  
 II  
 DB 4 KE 5

RESULT 37  
 B27867  
 homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)  
 C:Species: Drosophila melanogaster  
 C>Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 23-Feb-1997  
 C:Accession: B27867  
 R:Saari, G.; Bientz, M.  
 EMBO J. 6, 1775-1778, 1987  
 A:Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.  
 A:Reference number: A91072  
 A:Accession: B27867  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <SAR>  
 C:Genetics:  
 A:Gene: FlyBase:Ubx  
 A:Cross-references: FlyBase:FBgn0003944  
 C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 6  
 II  
 DB 6 EQ 7

RESULT 38  
 A61467  
 penalbumin - Adelle penguin (fragment)

C:Species: pygoscolis adelle (Adelle penguin)  
 C>Date: 07-Oct-1994 #sequence\_revision 04-Nov-1994 #text\_change 04-Sep 1995  
 C:Accession: A61467  
 R:Seegal, D.L.; Amichini, R.; de V. K.; Allissey, R.S.; Peckey, R.E.  
 J. Protein Chem. 2, 43-52, 1993  
 A:Title: Sulfhydryl proteins of penumbra and white ovalbumin and penalbumin. C:term  
 A:Reference number: A61467  
 A:Accession: A61467  
 A:Molecule type: protein  
 A:Residues: 1-8 <SAR>  
 C:Keywords: egg white; fly; penguin

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NA 11  
 II  
 DB 7 NA 5

RESULT 39  
 P14234  
 14 heavy chain (beta) and 14 light chain (alpha) human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 10-Aug-1999  
 C:Accession: P14234  
 R:Yamada, M.; Wasserman, K.; Rederbach, K.A.; Stane, S.; Catlett, A.J.; Roeder, G.  
 J. Exp. Med. 173, 445-462, 1991  
 A:Title: Prediction of the structure of a specific immunoglobulin heavy chain diversity  
 A:Reference number: P14234; MUID:1895102; PMID:1895102  
 A:Accession: P14234  
 A:Molecule type: DNA  
 A:Residues: 1-8 <VAR>  
 A:Experimental source: N. Y. H. H. H.  
 C:Keywords: immunoglobulin; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 5  
 II  
 DB 7 EQ 6

RESULT 40  
 I48434  
 apolipoprotein A1 (mouse (Mus musculus))  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1990 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I48434  
 R:Ko, M.S.; Ward, A.; Bickel, C.; Bickel, M.; Takahashi, N.; Morozaki, Y.; Radom  
 Mamm. Genome 5, 349-355, 1994  
 A:Title: Gene for apolipoprotein A1 (ApoA) from the mouse genome by PCR  
 A:Reference number: I48434; MUID:1895102; PMID:854349  
 A:Accession: I48434  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Cross-references: EMBL:U00001; NID:q162150; PID:q162151  
 A:Residues: 1-8 <SAR>

Query Match 18.2%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2  
 II  
 DB 7 AK 5

RESULT 41

A54823  
 Olfactory receptor 17 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 28-Apr-1995 #sequence\_revision 28 Apr-1995 #text\_change 17-Mar-1999  
 C:Accession: A54823  
 R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 76, 823-834, 1994  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A:Reference number: A54823; MUID:94373818; PMID:8087849  
 A:Accession: A54823  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <CH>

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 II  
 DB 4 RN 5

RESULT 42  
 PN0043  
 phosphatidylinositol amine-binding protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 20-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998  
 C:Accession: PN0043  
 R:Kato, H.  
 Kawasaki 19kkaishi 22, 245-259, 1996  
 A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cell  
 A:Reference number: PN0041  
 A:Accession: PN0043  
 A:Molecule type: protein  
 A:Residues: 1-8 <KAT>  
 A:Experimental source: neuroblastoma cell  
 C:Comment: The molecular mass is 23.500 and the pI is 4.4. The amino-terminus is blocked  
 C:Keywords: Brain

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 6  
 II  
 DB 3 EQ 4

RESULT 43  
 I48935  
 apolipoprotein A-II - western wild mouse (fragment)  
 C:Species: Mus spretus (western wild mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I48935  
 R:KO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maeyaki, Y.; Nadeau, J.H.  
 Mamm. Genome 5, 349-355, 1994  
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
 A:Reference number: I48934; MUID:94319082; PMID:8043449  
 A:Accession: I48935  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <RES>  
 A:Cross-references: EMBL:005692; NID:q497011; FIDN:AR604743; FID:q42827

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2  
 II  
 DB 7 AK 8

RESULT 44  
 R64823  
 Olfactory receptor 17 - western wild mouse (fragment)  
 C:Species: Mus spretus (western wild mouse)  
 C>Date: 28-Apr-1995 #sequence\_revision 28 Apr-1995 #text\_change 17-Mar-1999  
 C:Accession: R64823  
 R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 76, 823-834, 1994  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression  
 A:Reference number: A54823; MUID:94373818; PMID:8087849  
 A:Accession: R64823  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-8 <CH>

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 II  
 DB 4 RN 5

RESULT 45  
 A63347  
 Cytochrome P450 A1 - rat (fragment)  
 C:Species: Rattus norvegicus (R. norvegicus)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1996  
 C:Accession: A63347  
 R:Shimono, H.; Suda, A.; Ogata, S.; Nadeau, J.H.; Axel, R.  
 Brain Metal Disphos. 19, 241-255, 1991  
 A:Title: Purification and characterization of liver microsomal cytochrome P450 A1  
 A:Reference number: A63347; MUID:94373818; PMID:1676625  
 A:Accession: A63347  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <SH>

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KF 3  
 II  
 DB 6 KF 2

RESULT 46  
 I47642  
 Olfactory receptor 17 - western wild mouse (fragment)  
 C:Species: Rattus sp. (R. sp.)  
 C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 28-Feb-1997  
 C:Accession: I47642  
 R:Raney, J.P.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 76, 823-834, 1994  
 A:Title: Allelic inactivation regulates olfactory receptor gene expression  
 A:Reference number: I47642; MUID:94373818; PMID:841429  
 A:Accession: I47642  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <RES>  
 A:Cross-references: EMBL:005692; NID:q497011; FIDN:AR604743; FID:q42827

Query Match 18.2% Score 2: DB 2: Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10



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OM protein - protein search, using sw model

Run on: September 30, 2003, 17:01:41 : Search time 23 seconds

(without alignments)  
22.491 Million cell updates/sec

Title: US-09-787-443-20

Perfect score: 11

Sequence: 1 AKKKEQKORNA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 707

Minimum OR seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	9	1	COXE_THUOB
2	3	27.3	9	1	P80975 trunnus obe
3	3	27.3	10	1	P82661 panagrellus
4	3	27.3	12	1	XYNR_DICB4
5	3	27.3	13	1	RS19_GLYEP
6	3	27.3	13	1	CRTC_BOVIN
7	3	27.3	14	1	MAST_VESBA
8	3	27.3	14	1	MAST_VESCR
9	3	27.3	14	1	MAST_VESLE
10	3	27.3	14	1	MAST_VESMA
11	3	27.3	14	1	MCRX_METTM
12	3	27.3	14	1	TKN1_PANMA
13	3	27.3	15	1	COX1_THUOB
14	3	27.3	15	1	GR78_HORSE
15	3	27.3	15	1	UC08_MAIZE
16	2	18.2	8	1	B44K_PORGI
17	2	18.2	8	1	FAR1_PENMO
18	2	18.2	8	1	FAR1_HOMAM
19	2	18.2	8	1	FAR4_HOMAM
20	2	18.2	8	1	NPB_BOVIN
21	2	18.2	8	1	NS1_MYCTU
22	2	18.2	8	1	RS1_ERMCH
23	2	18.2	9	1	CCAP_CARMA
24	2	18.2	9	1	CONO_CONGE
25	2	18.2	9	1	CONO_CONST
26	2	18.2	9	1	FAR6_MACRS
27	2	18.2	9	1	LMIP_LOCHI
28	2	18.2	9	1	LPCA_STAUA
29	2	18.2	9	1	NEOU_CAVPO
30	2	18.2	9	1	OXYT_EISFO
31	2	18.2	9	1	OXYT_OCTVU
32	2	18.2	9	1	RS10_SERMA
33	2	18.2	9	1	RT33_BOVIN

34	2	18.2	9	1	CHYE_PIL
35	2	18.2	9	1	U_NG_BIRAN
36	2	18.2	9	1	CAIS_SHEEP
37	2	18.2	9	1	CAIS_WMY
38	2	18.2	9	1	CAIS_WMY
39	2	18.2	9	1	CAIS_WMY
40	2	18.2	9	1	CAIS_WMY
41	2	18.2	9	1	CAIS_WMY
42	2	18.2	9	1	CAIS_WMY
43	2	18.2	9	1	CAIS_WMY
44	2	18.2	9	1	CAIS_WMY
45	2	18.2	9	1	CAIS_WMY
46	2	18.2	9	1	CAIS_WMY
47	2	18.2	9	1	CAIS_WMY
48	2	18.2	9	1	CAIS_WMY
49	2	18.2	9	1	CAIS_WMY
50	2	18.2	9	1	CAIS_WMY
51	2	18.2	9	1	CAIS_WMY
52	2	18.2	9	1	CAIS_WMY
53	2	18.2	9	1	CAIS_WMY
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55	2	18.2	9	1	CAIS_WMY
56	2	18.2	9	1	CAIS_WMY
57	2	18.2	9	1	CAIS_WMY
58	2	18.2	9	1	CAIS_WMY
59	2	18.2	9	1	CAIS_WMY
60	2	18.2	9	1	CAIS_WMY
61	2	18.2	9	1	CAIS_WMY
62	2	18.2	9	1	CAIS_WMY
63	2	18.2	9	1	CAIS_WMY
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66	2	18.2	9	1	CAIS_WMY
67	2	18.2	9	1	CAIS_WMY
68	2	18.2	9	1	CAIS_WMY
69	2	18.2	9	1	CAIS_WMY
70	2	18.2	9	1	CAIS_WMY
71	2	18.2	9	1	CAIS_WMY
72	2	18.2	9	1	CAIS_WMY
73	2	18.2	9	1	CAIS_WMY
74	2	18.2	9	1	CAIS_WMY
75	2	18.2	9	1	CAIS_WMY
76	2	18.2	9	1	CAIS_WMY
77	2	18.2	9	1	CAIS_WMY
78	2	18.2	9	1	CAIS_WMY
79	2	18.2	9	1	CAIS_WMY
80	2	18.2	9	1	CAIS_WMY
81	2	18.2	9	1	CAIS_WMY
82	2	18.2	9	1	CAIS_WMY
83	2	18.2	9	1	CAIS_WMY
84	2	18.2	9	1	CAIS_WMY
85	2	18.2	9	1	CAIS_WMY
86	2	18.2	9	1	CAIS_WMY
87	2	18.2	9	1	CAIS_WMY
88	2	18.2	9	1	CAIS_WMY
89	2	18.2	9	1	CAIS_WMY
90	2	18.2	9	1	CAIS_WMY
91	2	18.2	9	1	CAIS_WMY
92	2	18.2	9	1	CAIS_WMY
93	2	18.2	9	1	CAIS_WMY
94	2	18.2	9	1	CAIS_WMY
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97	2	18.2	9	1	CAIS_WMY
98	2	18.2	9	1	CAIS_WMY
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100	2	18.2	9	1	CAIS_WMY
101	2	18.2	9	1	CAIS_WMY
102	2	18.2	9	1	CAIS_WMY
103	2	18.2	9	1	CAIS_WMY
104	2	18.2	9	1	CAIS_WMY
105	2	18.2	9	1	CAIS_WMY
106	2	18.2	9	1	CAIS_WMY

107	2	18.2	15	1	EF1A_MICCR	P81266 microplis	180	9.1	1	PL14_MALV	P82929 bos tauris
108	2	18.2	15	1	FIBA_ANAPL	P12501 anas platyr	181	9.1	1	EF1A_MALV	P8632 zea mays
109	2	18.2	15	1	LEC2_PSOCC	P22585 psophocarp	182	9.1	1	EF1A_MALV	P8644 mus muscu
110	2	18.2	15	1	MAT2_BACIO	P80072 bacillus th	183	9.1	1	EF1A_MALV	P6576 zea mays
111	2	18.2	15	1	MCA2_RHOOP	P56870 rhodococcu	184	9.1	1	EF1A_MALV	P6582 zea mays
112	2	18.2	15	1	MCRA_METTE	P22948 methanosarc	185	9.1	1	EF1A_MALV	P8195 perkinsus a
113	2	18.2	15	1	MM01_RAT	P81563 rattus norv	186	9.1	1	EF1A_MALV	P8181 carotinus m
114	2	18.2	15	1	NI51_ANAVA	P44507 anabaena va	187	9.1	1	EF1A_MALV	P8184 carotinus m
115	2	18.2	15	1	NU03_SOLTU	P80263 solanum tub	188	9.1	1	EF1A_MALV	P8274 schizanthu
116	2	18.2	15	1	NU08_SOLTU	P89731 solanum tub	189	9.1	1	EF1A_MALV	P8375 schizanthu
117	2	18.2	15	1	ONC1_ONCMY	P83287 oncorhynch	190	9.1	1	EF1A_MALV	P8332 clostridiu
118	2	18.2	15	1	PGK1_PHPA	P80659 physcomitre	191	9.1	1	EF1A_MALV	P8347 cocus zoot
119	2	18.2	15	1	PGS5_PELAC	P80504 pelobacter	192	9.1	1	EF1A_MALV	P8416 nepenthes
120	2	18.2	15	1	R13A_SPIOL	P82454 spicacilus ol	193	9.1	1	EF1A_MALV	P8339 toxostoma
121	2	18.2	15	1	RS10_BACST	P59683 bacillus st	194	9.1	1	EF1A_MALV	P8178 toxostoma
122	2	18.2	15	1	RS20_BACST	P59681 bacillus st	195	9.1	1	EF1A_MALV	P8186 calliphora
123	2	18.2	15	1	RT32_BOVIN	P82927 bos taurus	196	9.1	1	EF1A_MALV	P8187 calliphora
124	2	18.2	15	1	THL1_CLOPA	P81347 clostridium	197	9.1	1	EF1A_MALV	P8183 paracatellus
125	2	18.2	15	1	UC01_MAIZE	P83637 zea mays (m	198	9.1	1	EF1A_MALV	P8184 calliphora
126	2	18.2	15	1	UC13_MAIZE	P80619 zea mays (m	199	9.1	1	EF1A_MALV	P8324 paracatellus
127	2	18.2	15	1	UC17_MAIZE	P80623 zea mays (m	200	9.1	1	EF1A_MALV	P8363 paracatellus
128	2	18.2	15	1	UC27_MAIZE	P82633 zea mays (m	201	9.1	1	EF1A_MALV	P8363 calliphora
129	2	18.2	15	1	UN01_PINPS	P81106 pinus pinas	202	9.1	1	EF1A_MALV	P8373 paracatellus
130	2	18.2	15	1	UN04_PINPS	P81673 pinus pinas	203	9.1	1	EF1A_MALV	P8373 ascaris suu
131	2	18.2	15	1	URE2_MORMO	P17338 morganella	204	9.1	1	EF1A_MALV	P8370 calliphora
132	2	18.2	15	1	VORA_METTM	P80907 methanobact	205	9.1	1	EF1A_MALV	P8370 paracatellus
133	1	9.1	8	1	ACL1_THUAL	P18091 thymus alb	206	9.1	1	EF1A_MALV	P8363 calliphora
134	1	9.1	8	1	ACT1_CARMA	P80709 carcinus ma	207	9.1	1	EF1A_MALV	P8363 calliphora
135	1	9.1	8	1	AKH3_GRYB1	P83086 gryllus bim	208	9.1	1	EF1A_MALV	P8363 calliphora
136	1	9.1	8	1	AKH1_EIBAG	P25418 ciolliula a	209	9.1	1	EF1A_MALV	P8363 calliphora
137	1	9.1	8	1	AKH1_MEIML	P25423 melolontha	210	9.1	1	EF1A_MALV	P8363 calliphora
138	1	9.1	8	1	AKH1_TABAT	P14595 tabanus atr	211	9.1	1	EF1A_MALV	P8363 calliphora
139	1	9.1	8	1	AL12_CARMA	P81615 carcinus ma	212	9.1	1	EF1A_MALV	P8363 calliphora
140	1	9.1	8	1	AL15_CARMA	P8318 carotinus ma	213	9.1	1	EF1A_MALV	P8363 calliphora
141	1	9.1	8	1	AL17_CARMA	P81820 carcinus ma	214	9.1	1	EF1A_MALV	P8363 calliphora
142	1	9.1	8	1	ALL1_CYDPO	P82152 cydia pomon	215	9.1	1	EF1A_MALV	P8363 calliphora
143	1	9.1	8	1	ALL3_CYDPO	P82154 cydia pomon	216	9.1	1	EF1A_MALV	P8363 calliphora
144	1	9.1	8	1	ALL4_CALVO	P41840 calliphora	217	9.1	1	EF1A_MALV	P8363 calliphora
145	1	9.1	8	1	ALL5_CYDPO	P82155 cydia pomon	218	9.1	1	EF1A_MALV	P8363 calliphora
146	1	9.1	8	1	ALL6_CYDPO	P82156 cydia pomon	219	9.1	1	EF1A_MALV	P8363 calliphora
147	1	9.1	8	1	ALL7_CYDPO	P82157 cydia pomon	220	9.1	1	EF1A_MALV	P8363 calliphora
148	1	9.1	8	1	ALL8_CARMA	P81839 carcinus ma	221	9.1	1	EF1A_MALV	P8363 calliphora
149	1	9.1	8	1	ALL9_CARMA	P81811 carcinus ma	222	9.1	1	EF1A_MALV	P8363 calliphora
150	1	9.1	8	1	ANG2_BOTJA	P81812 carcinus ma	223	9.1	1	EF1A_MALV	P8363 calliphora
151	1	9.1	8	1	CAD1_ENTFA	P14268 entelococcu	224	9.1	1	EF1A_MALV	P8363 calliphora
152	1	9.1	8	1	CLP1_THICU	P83488 tiliobacilli	225	9.1	1	EF1A_MALV	P8363 calliphora
153	1	9.1	8	1	COXG_RAT	P82430 rattus norv	226	9.1	1	EF1A_MALV	P8363 calliphora
154	1	9.1	8	1	FAR1_PANKE	P41872 panagrelus	227	9.1	1	EF1A_MALV	P8363 calliphora
155	1	9.1	8	1	FAR2_MACRS	P84275 macrobrachi	228	9.1	1	EF1A_MALV	P8363 calliphora
156	1	9.1	8	1	FAR3_MACRS	P84277 macrobrachi	229	9.1	1	EF1A_MALV	P8363 calliphora
157	1	9.1	8	1	FAR4_ASCSU	P84279 ascaris suu	230	9.1	1	EF1A_MALV	P8363 calliphora
158	1	9.1	8	1	FAR5_CALVO	P41563 calliphora	231	9.1	1	EF1A_MALV	P8363 calliphora
159	1	9.1	8	1	FUSS_PUSSO	P81910 fusarium so	232	9.1	1	EF1A_MALV	P8363 calliphora
160	1	9.1	8	1	GLUR_HUMAN	P82729 homo sapien	233	9.1	1	EF1A_MALV	P8363 calliphora
161	1	9.1	8	1	HTE1_PERAM	P84548 periplaneta	234	9.1	1	EF1A_MALV	P8363 calliphora
162	1	9.1	8	1	HTE2_PERAM	P84549 periplaneta	235	9.1	1	EF1A_MALV	P8363 calliphora
163	1	9.1	8	1	HTE3_PERAM	P84550 periplaneta	236	9.1	1	EF1A_MALV	P8363 calliphora
164	1	9.1	8	1	ICK1_LEUMA	P21419 leucophaea	237	9.1	1	EF1A_MALV	P8363 calliphora
165	1	9.1	8	1	ICK2_LEUMA	P21420 leucophaea	238	9.1	1	EF1A_MALV	P8363 calliphora
166	1	9.1	8	1	ICK3_LEUMA	P21421 leucophaea	239	9.1	1	EF1A_MALV	P8363 calliphora
167	1	9.1	8	1	ICK4_LEUMA	P21422 leucophaea	240	9.1	1	EF1A_MALV	P8363 calliphora
168	1	9.1	8	1	ICK5_LEUMA	P19588 leucophaea	241	9.1	1	EF1A_MALV	P8363 calliphora
169	1	9.1	8	1	ICK6_LEUMA	P19589 leucophaea	242	9.1	1	EF1A_MALV	P8363 calliphora
170	1	9.1	8	1	ICK7_LEUMA	P19590 leucophaea	243	9.1	1	EF1A_MALV	P8363 calliphora
171	1	9.1	8	1	ICK8_LEUMA	P22396 leucophaea	244	9.1	1	EF1A_MALV	P8363 calliphora
172	1	9.1	8	1	LPK2_LOCHI	P13049 leucophaea	245	9.1	1	EF1A_MALV	P8363 calliphora
173	1	9.1	8	1	LPM5_STAEP	P82421 staphylococ	246	9.1	1	EF1A_MALV	P8363 calliphora
174	1	9.1	8	1	ORMY_ORCHI	P82455 oriconectes	247	9.1	1	EF1A_MALV	P8363 calliphora
175	1	9.1	8	1	PLP2_BRANA	P81707 brassica na	248	9.1	1	EF1A_MALV	P8363 calliphora
176	1	9.1	8	1	PKP2_PERAM	P82692 periplaneta	249	9.1	1	EF1A_MALV	P8363 calliphora
177	1	9.1	8	1	PKP3_PERAM	P82618 periplaneta	250	9.1	1	EF1A_MALV	P8363 calliphora
178	1	9.1	8	1	RPCH_PANBO	P83939 pandalus bo	251	9.1	1	EF1A_MALV	P8363 calliphora
179	1	9.1	8	1	RS7_MYCIT	P83564 mycobacteri	252	9.1	1	EF1A_MALV	P8363 calliphora







Best Local Similarity 100.0%; Pred. No. 1, 100.0%;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 REQ 6  
DB 1 REQ 3

## RESULT 2

## FAR5\_PANPE

ID FAR5\_PANPE STANDARD: PRT: 9 AA.

AC P62561: 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE PMFamide-like neuropeptide pp5 (AMRNA\_VKF amide).  
OS Panagrellus redivivus  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Aphelinoidea  
OC Panagrolaimidae; Panagrolaimidae; Panagrolaimus  
OX NCBI\_TaxID:6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffit C.L., Marks N.J., Hallon D.W., Thomson D.P., Brady T.B.,  
RA Maule A.G.;  
RT \*Isolation, characterization and pharmacology of PMFamide-related  
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.\*  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (PMFAMIDE RELATED PEPTIDE)  
CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD\_RES 9 AMIDATION.

SQ SEQUENCE 9 AA: 1077 MW: AOD11C72DB45436 CR64:

Query Match 27.3%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1, 100.0%;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RNA 11  
DB 3 RNA 5

## RESULT 3

## XYNB\_DICR4

ID XYNB\_DICR4 STANDARD: PRT: 10 AA.

AC P80717: 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 28-FEB-2003 (Rel. 41, last annotation update)  
DE Eudo-1.4-beta-xylanase B (EC 3.2.1.8) (Xylanase B)  
DE (1.4-beta-D-xylan xylohydrolase B) (Fragment)  
OS Dictyoglomus sp. (strain B4A)  
OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus  
OX NCBI\_TaxID:69007;  
RN [1]  
RP SEQUENCE.

RA Adensen A.K., Jacobsen S., Ahning B.K.  
RL Submitted (OCT-1996) to the SWISS-PROT data bank  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4 beta-D xylosidic  
CC linkages in xylans.  
CC -!- PATHWAY: Xylan degradation.  
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL  
CC HYDROLASES).  
DR InterPro: IPR001000; Glyco\_hydro.10.  
DR PROSITE: PS00591; GLYCOSYL\_HYDROL\_F10; PARTIAL.  
KW Xylan degradation; Hydrolase; Glycosidase.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA: 1144 MW: 4554322AA72041A3 CR664:

Query Match 27.3%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1, 100.0%;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 1

DB 1 AKK 1

## RESULT 4

## FAR5\_PANPE

ID FAR5\_PANPE STANDARD: PRT: 9 AA.

AC P62561: 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE PMFamide-like neuropeptide pp5 (AMRNA\_VKF amide).  
OS Panagrellus redivivus  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Aphelinoidea  
OC Panagrolaimidae; Panagrolaimidae; Panagrolaimus  
OX NCBI\_TaxID:6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffit C.L., Marks N.J., Hallon D.W., Thomson D.P., Brady T.B.,  
RA Maule A.G.;  
RT \*Isolation, characterization and pharmacology of PMFamide-related  
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.\*  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (PMFAMIDE RELATED PEPTIDE)  
CC FAMILY.

KW Neuropeptide; Amidation.  
FT MOD\_RES 9 AMIDATION.  
SQ SEQUENCE 9 AA: 1077 MW: AOD11C72DB45436 CR64:

Query Match 27.3%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1, 100.0%;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 1  
DB 1 AKK 1

Query Match 27.3%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1, 100.0%;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 1  
DB 1 AKK 1

## RESULT 5

## FAR5\_PANPE

ID FAR5\_PANPE STANDARD: PRT: 9 AA.

AC P62561: 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE PMFamide-like neuropeptide pp5 (AMRNA\_VKF amide).  
OS Panagrellus redivivus  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Aphelinoidea  
OC Panagrolaimidae; Panagrolaimidae; Panagrolaimus  
OX NCBI\_TaxID:6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffit C.L., Marks N.J., Hallon D.W., Thomson D.P., Brady T.B.,  
RA Maule A.G.;  
RT \*Isolation, characterization and pharmacology of PMFamide-related  
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.\*  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (PMFAMIDE RELATED PEPTIDE)  
CC FAMILY.

KW Neuropeptide; Amidation.  
FT MOD\_RES 9 AMIDATION.  
SQ SEQUENCE 9 AA: 1077 MW: AOD11C72DB45436 CR64:

RA Vance J.E., Opas M., Michalak M.:  
 RT "Calreticulin, and not calsequestrin, is the major calicium-binding  
 RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic  
 RT reticulum".  
 RL J. Biol. Chem. 266:7155-7165(1991).  
 CC -|- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -|- SUBUNIT: Monomer (By similarity).  
 CC -|- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -|- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 DR PIR: A33208.  
 DR InterPro: IPR001580; Calreticulin.  
 DR PROSITE: PS00803; CALRETICULIN\_1; PARTIAL.  
 DR PROSITE: PS00804; CALRETICULIN\_2; PARTIAL.  
 DR PROSITE: PS00805; CALRETICULIN\_REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1557 MW; C85DDA6996CA1339 CR'64;

Query Match 27.3%; Score 3; LR 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQ 6  
 DB 7 KRG 9

## RESULT: 6

MAST\_VESHA  
 ID MAST\_VESBA STANDARD: PRT: 14 AA  
 AC P21654;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan B.  
 OS Vespa basalis (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eurytomera;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID:7444;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Venom;  
 RX MEDLINE=91174755; PubMed=2006909;  
 RA Lo C.-L., Hwang L.-L.;  
 RT "Structure and biological activities of a new mastoparan isolated  
 RT from the venom of the hornet Vespa basalis".  
 RL Biochem. J. 274:453-456(1991).  
 CC -|- FUNCTION: Mast cell degranulating peptide. Activates B proteins  
 CC that couple to phospholipase C.  
 DR PIR: S14336; S14336.  
 DR Mast cell degranulation; Amidation.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA; 1613 MW; D35944CAB3A19A2 CR'64;

Query Match 27.3%; Score 3; LR 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 10 AKK 12

## RESULT: 7

MAST\_VESCR  
 ID MAST\_VESCR STANDARD: PRT: 14 AA  
 AC P01516;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan C.

OS Vespa cralpa (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eurytomera;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID:7444;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Venom;  
 RX MEDLINE=8428944; PubMed=1000000;  
 RA Arakawa A.; Pissinatti;  
 RT "Isolation and characterization of two new peptides, mastoparan C and  
 RT calreticulin, from the venom of the European hornet, Vespa cralpa".  
 RL J. Biol. Chem. 266:10000-10004(1991).  
 CC -|- FUNCTION: Mast cell degranulating peptide. Activates B proteins  
 CC that couple to phospholipase C.  
 DR PIR: A01776; A01776.  
 DR Mast cell degranulation; Amidation.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA; 1613 MW; D35944CAB3A19A2 CR'64;

Query Match 27.3%; Score 3; LR 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 10 AKK 12

MAST\_VESLE  
 ID MAST\_VESLE STANDARD: PRT: 14 AA  
 AC P21654;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan B.  
 OS Vespa basalis (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eurytomera;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespidae;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID:7444;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Venom;  
 RX MEDLINE=91174755; PubMed=2006909;  
 RA Lo C.-L., Hwang L.-L.;  
 RT "Structure and biological activities of a new mastoparan isolated  
 RT from the venom of the hornet Vespa basalis".  
 RL Biochem. J. 274:453-456(1991).  
 CC -|- FUNCTION: Mast cell degranulating peptide. Activates B proteins  
 CC that couple to phospholipase C.  
 DR PIR: A01776; A01776.  
 DR Mast cell degranulation; Amidation.  
 FT MOD\_RES 14 14  
 SQ SEQUENCE 14 AA; 1613 MW; D35944CAB3A19A2 CR'64;

Query Match 27.3%; Score 3; LR 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
 DB 10 AKK 12

MAST\_VESMA  
 ID MAST\_VESMA STANDARD: PRT: 14 AA  
 AC P01516;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mastoparan C.



Zhu Y.O., Zou G., Tsou K.:  
A "Isolation and structure of ranamargaric, a new tachykinin from the  
T T skin of Chinese frog *Rana margaritacea*." Sci. China, Ser. B, Chem. Life Sci. 32:570-574 (1989).  
L N (2)

P SYNTHESIS.  
X MEDLINE=90253600; PubMed=2340087;  
X Lu Y.A., Peng J.L., Zhu Y.Q., Wu S.X., Tian S.H., Zou G.;  
T "Synthesis and biological activity of a new frog skin peptide.

1. ramamargarin. \*;  
2. Sci. China, Ser. B, Chem. Life Sci. 33:170-177(1990).  
3. -1- FUNCTION: PACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS.  
4. C EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
5. C SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
6. C MUSCLES.

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Query Match      27.38; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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y 1 AKK 3  
 |||  
 b 7 AKK 9

RESULT 13

	OXL_THUCB	STANDARD:	PRT;	15 AA.
D	COX1_THUCB			
C	P80978:			
D	01-NOV-1997	(Rel. 35, Created)		
T	01-NOV-1997	(Rel. 35, Last sequence update)		
T	01-NOV-1997	(Rel. 35, Last annotation update)		
E	Cytochrome c oxidase polypeptide VIC-2 (EC 1.9.3.1) (Fragments).			
S	Thunnus obesus (Blueeye tuna).			
C	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
C	Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neocentropo-			
C	deus: Acanthomorpha: Acanthopterygii: Perciformes: Scombroidei:			
C	Scombridae: Thunnus.			
X	NCBI_TaxID=8241;			
X	11			

Query Match 27.38; Score 3; DS 1; Length 15;  
Best local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

[illegible]

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RESULT 14
GR78 WURSE
13 GR78 WURSE STANLEY, 1977 15 2A
14 P14392;
15 AC 01 AUG-1990 (Ref. 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 8
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Query Match	Q <sub>1</sub> Length	Q <sub>2</sub> Length	Q <sub>3</sub> Length	Q <sub>4</sub> Length	Q <sub>5</sub> Length
Best Local Size	10,000	100,000	1,000,000	10,000,000	100,000,000
Matches	4	4	4	4	4
Corresponding	4	4	4	4	4
Index	4	4	4	4	4

$$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$$
[illegible][illegible]

DR Maize-2DPAGE: P80614; COLEOPTILE.

DR MaizeUB: 123934; -

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DR Maize-2DPAGE: P80614; COLEOPTILE.

DR MaizeUB: 123934; -

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RESULT 16

B44K\_P0RG1

AC P81865

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 44 kDa immunogenic protein (Fragment).

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales.

OC Porphyromonadaceae; Porphyromonadaceae.

OX NCBI\_TaxID=837

RN [1]

RP SEQUENCE.

RC STRAIN=VEB 3492.

RX MEDLINE=20198497; PubMed=10731616;

RA Norris J.M., Love D.N.;

RT "Serum antibody responses of cats to soluble whole cell antigens of

RT teline Porphyromonas gingivalis."

RL Vet. Microbiol. 73:37-49(2000).

CC -i- SIMILARITY: P.GINGIVALIS HEMAGGLUTININ A.

KW Antigen.

FT NON\_TER

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DR Maize-2DPAGE: P80614; COLEOPTILE.

DR MaizeUB: 123934; -

FT NON\_TER 1

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RESULT 17

FAP1\_PENMG

ID FAP1\_PENMG

AC P8116

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FMRamide-like neuropeptide FLP1 (GPRN-like analog).

OS Penaeus monodon (Penaeid shrimp).

OC Fukuyota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Decapodiformata; Penaeoidea;

OC Penaeidae; Penaeus.

OX NCBI\_TaxID=6687

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Eyestalk;

RX MEDLINE=21956277; PubMed=11959015;

RA Sithigorngul P., Pupem J., Krungkarn C., Longyan S.,

RA Chaivithangkura P., Sithigorngul W., Petsom A.;

RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk

RT of the giant tiger prawn Penaeus monodon."

RL Comp. Biochem. Physiol. 131B:325-337(2002).

CC -i- SUBCELLULAR LOCATION: Secreted.

CC -i- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.

CC -i- SIMILARITY: P8116; FAP1\_PENMG (FMRAMIDE RELATED PEPTIDE)

FW Neuroptera: Acanthoptera

FW NEUTER 8

FW NEUTER 8

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RT substances from the lobster nervous system: isolated and sequenced.
RL J. Comp. Neurol. 266:15-26(1987).
CC - FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
CC NEUROMUSCULAR JUNCTIONS.
CC - FUNCTION: BELONGS TO THE FAPR (PENTAPEPTIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA: 1067 MW: 1200472964540451 (P0004)
SQ SEQUENCE 8 AA: 1067 MW: 1200472964540451 (P0004)

Query Match: 18.2% Score 2: 1P 1: 1067 MW:
Best Local Similarity 100.0% Pred. No. 1: 3-065
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 9 RN 1C
DB 3 RN 4

RESULT 20
NPB_BOVIN STANDARD: PRT: 8 AA
AC P25507:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovia; Bos; Bos.
OC Ruminantia; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE.
RC MEDLINE:86067985; PubMed:3865193;
RX Yang H.-Y.T., Pratta W., Majano E.A., Costa E.;
RA "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine."
RL Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761(1995);
CC - FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR: B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA: 1062 MW: 870416776967296454;
SQ SEQUENCE 8 AA: 1062 MW: 870416776967296454;

Query Match: 18.2% Score 2: 1P 1: 1067 MW:
Best Local Similarity 100.0% Pred. No. 1: 3-065
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 8 OR 9
DB 6 OR 7

RESULT 21
NS3_MYCTU STANDARD: PRT: 8 AA
AC P81152:
DT 15-JUN-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40 kDa non-secretory protein 3 (Fragment)
OS Mycobacterium tuberculosis
CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetaceae;
CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID:1773;
RN [1]
RP SEQUENCE.
RC STRAIN:H37RV;
RA Prasad H.K., Annapurna P.S.;

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RT substances from the lobster nervous system: isolated and sequenced.
RL J. Comp. Neurol. 266:15-26(1987).
CC - FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
CC NEUROMUSCULAR JUNCTIONS.
CC - FUNCTION: BELONGS TO THE FAPR (PENTAPEPTIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA: 1067 MW: 1200472964540451 (P0004)
SQ SEQUENCE 8 AA: 1067 MW: 1200472964540451 (P0004)

Query Match: 18.2% Score 2: 1P 1: 1067 MW:
Best Local Similarity 100.0% Pred. No. 1: 3-065
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 9 RN 1C
DB 3 RN 4

RESULT 20
NPB_BOVIN STANDARD: PRT: 8 AA
AC P25507:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovia; Bos; Bos.
OC Ruminantia; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE.
RC MEDLINE:86067985; PubMed:3865193;
RX Yang H.-Y.T., Pratta W., Majano E.A., Costa E.;
RA "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine."
RL Proc. Natl. Acad. Sci. U.S.A. 92:7757-7761(1995);
CC - FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR: B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA: 1062 MW: 870416776967296454;
SQ SEQUENCE 8 AA: 1062 MW: 870416776967296454;

Query Match: 18.2% Score 2: 1P 1: 1067 MW:
Best Local Similarity 100.0% Pred. No. 1: 3-065
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps

QY 8 OR 9
DB 6 OR 7

RESULT 21
NS3_MYCTU STANDARD: PRT: 8 AA
AC P81152:
DT 15-JUN-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40 kDa non-secretory protein 3 (Fragment)
OS Mycobacterium tuberculosis
CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetaceae;
CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID:1773;
RN [1]
RP SEQUENCE.
RC STRAIN:H37RV;
RA Prasad H.K., Annapurna P.S.;

```

OS Spodoptera eridania (Southern armyworm);  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Brachyura; Portunoidae; Portunidae; Carcinus;  
 OX NCHI\_TaxID-6759, 7130, 7067, 37547;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES-C.maenas: TISSUE-Pericardial organs;  
 RA Stangier J., Hilbich C., Reyreuther K., Keller K.  
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
 RT shore crab Carcinus maenas";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987)  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES-M.sexata;  
 RA MEDLINE-93050243; PubMed-1426284;  
 RX Cheung C.C., Loi P.K., Sylvestre A.W., Lee T.P., Tuller K.J.;  
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Barker M.,  
 RA Schooley D.A.;  
 RT "Isolation and identification of a cardioactive peptide from tobacco  
 RT moth and Spodoptera eridania";  
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993)  
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO AND CIRCULATORY;  
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
 CC INTO THE HEMOLYPH.  
 CC PIR: A26363; A26363;  
 DR PIR: S27233; S27233;  
 KW Neuropeptide; Amidation;  
 FT DISULFID 3 9  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 959 MW: 65826.1970L44EB9 3694;  
 Query Match 18.28; Score 2; BB 1; Length 9;  
 Best Local Similarity 100.00; Prod. No. 1.10-08;  
 Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0

QY 10 NA 1;  
 DB 4 NA 5

RESULT 24  
 CONO\_CONGE STANDARD: PRT: 1 AA:  
 AC P05486;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lys-conopressin G.  
 OS Conus geographus (Geography cone)  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Mollusca; Trochostomata;  
 OC Apodastropoda; Caenogastropoda; Sorbecorcula; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus  
 OX NCHI\_TaxID-6491;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE-88058932; PubMed-3680288;  
 RA Cruz L.J., de Santos V., Zafaralla G., Kamilla G.A., Zeikus R.D.,  
 RA Gray W.K., Olivera B.M.;  
 RT "Invertebrate vasopressin/oxytocin homologs: characterization of  
 RT peptides from Conus geographus and Conus striatus venoms";  
 RL J. Biol. Chem. 262:15821-15824(1987)  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE-89024586; PubMed-3052286;  
 RA Gray W.R., Olivera B.M., Cruz L.J.

PI "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
 RC shore crab Carcinus maenas";  
 RA Stangier J., Hilbich C., Reyreuther K., Keller K.  
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
 RT shore crab Carcinus maenas";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987)  
 RN [2]  
 RP SEQUENCE.  
 RC MEDLINE-93050243; PubMed-1426284;  
 RX Cheung C.C., Loi P.K., Sylvestre A.W., Lee T.P., Tuller K.J.;  
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Barker M.,  
 RA Schooley D.A.;  
 RT "Isolation and identification of a cardioactive peptide from tobacco  
 RT moth and Spodoptera eridania";  
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993)  
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO AND CIRCULATORY;  
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
 CC INTO THE HEMOLYPH.  
 CC PIR: A26363; A26363;  
 DR PIR: S27233; S27233;  
 KW Neuropeptide; Amidation;  
 FT DISULFID 3 9  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 959 MW: 65826.1970L44EB9 3694;  
 Query Match 18.28; Score 2; BB 1; Length 9;  
 Best Local Similarity 100.00; Prod. No. 1.10-08;  
 Matches 2; Conservative 0; Mismatches 0; Labels 0; Gaps 0

QY 10 NA 1;  
 DB 4 NA 5

RESULT 24  
 CONO\_CONGE STANDARD: PRT: 1 AA:  
 AC P05486;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lys-conopressin G.  
 OS Conus geographus (Geography cone)  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Mollusca; Trochostomata;  
 OC Apodastropoda; Caenogastropoda; Sorbecorcula; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus  
 OX NCHI\_TaxID-6491;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE-88058932; PubMed-3680288;  
 RA Cruz L.J., de Santos V., Zafaralla G., Kamilla G.A., Zeikus R.D.,  
 RA Gray W.K., Olivera B.M.;  
 RT "Invertebrate vasopressin/oxytocin homologs: characterization of  
 RT peptides from Conus geographus and Conus striatus venoms";  
 RL J. Biol. Chem. 262:15821-15824(1987)  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE-89024586; PubMed-3052286;  
 RA Gray W.R., Olivera B.M., Cruz L.J.





QY 2 KK 3  
 DB 2 KK 3

RESULT 29  
 NEUO\_CAVPO STANDARD: PRT: 9 AA.  
 AC P34966;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neuromedin U-9 (NMU-9).  
 GN NMU.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Small intestine;  
 RX MEDLINE=90341105; PubMed=2381877;  
 RA Murphy K., Turner C.A., Furness J.B., Parker L., Giraud A.,  
 RT "Isolation and microsequence analysis of a novel form of neuromedin U  
 from guinea pig small intestine.";  
 RL Peptides 11:613-617(1990).  
 CC -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES  
 CC -!- SELECTIVE VASOCONSTRICTION.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NMU FAMILY.  
 DR InterPro: IPR001942; NMU.  
 DR Pfam: PF02070; NMU; 1.  
 DR PROSITE: PS00967; NMU; 1.  
 DR Antidation: Hormone.  
 KW MOD\_RES 9 AMIDATION.  
 FT MOD\_RES 9 AA: IECF177409K72928 (Rel. 41).  
 SQ SEQUENCE 9 AA: 1169 MW: IECF177409K72928 (Rel. 41).

Query Match: 18.2% Score 21 DB 1: Length 9;  
 Best local Similarity 100.0%; Pred. No. 1: 0-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 DB 8 RN 9

RESULT 30  
 OXYT\_ELSFO STANDARD: PRT: 9 AA.  
 AC P42968;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Annetocin.  
 OS Eisenia foetida (Common brandling worm) (Common dung worm).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;  
 OC Lumbricina; Lumbricidae; Eisenia.  
 OX NCBI\_TaxID=6396;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=94121650; PubMed=8292046;  
 RA Gumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Matsukata H.,  
 RA Nomoto K.;  
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,  
 RT Eisenia foetida.";  
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).  
 CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO  
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE  
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH  
 CC NEPHRIDIAL FUNCTION.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: PC2021; PC2021.

DR INTERPRO: IPR001942; NMU.  
 DR Pfam: PF02070; NMU; 1.  
 DR PROSITE: PS00967; NMU; 1.  
 KW Hormone; Antidation.  
 FT MOD\_RES 9 AA: AMIDATION.  
 SQ SEQUENCE 9 AA: IECF177409K72928 (Rel. 41).  
 QY 9 RN 10  
 DB 8 RN 9

Query Match: 18.2% Score 21 DB 1: Length 9;  
 Best local Similarity 100.0%; Pred. No. 1: 0-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 DB 8 RN 9

RESULT 31  
 OXYT\_ELSFO STANDARD: PRT: 9 AA.  
 AC P42968;  
 DT 01-MAR-1992 (Rel. 27, Created)  
 DT 01-MAR-1992 (Rel. 27, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cephalotoxin.  
 OS Octopus vulgaris (Cuttlefish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Cephalopoda; Nautilus;  
 OC Cephalopoda; Cephalopoda; Cephalopoda; Cephalopoda; Cephalopoda;  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Small intestine;  
 RX MEDLINE=94121650; PubMed=8292046;  
 RA Gumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Matsukata H.,  
 RA Nomoto K.;  
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,  
 RT Eisenia foetida.";  
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).  
 CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO  
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE  
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH  
 CC NEPHRIDIAL FUNCTION.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: PC2021; PC2021.

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed, usagc by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL: AF058451; AAC14294.1; -  
 CC HAHAB; MF\_00508; -; 1.  
 CC InterPro: IPR001848; Ribosomal\_S10.  
 CC DR PROSITE: PS00361; RIBOSOMAL\_S10; PARTIAL.  
 CC KW Ribosomal protein.  
 CC FT NON\_TER 9  
 CC SEQUENCE 9 AA; 1214 MW; DE3944094416C456 CRC64;

Query Match 18.2% Score 2; PB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 QR 9  
 DB 4 QR 5

RESULT 33  
 RT33\_BOVIN  
 ID RT33\_BOVIN STANDARD; PRI; 9 AA.  
 AC P82926;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MPP-S34) (Fragment).  
 GN MRPS33.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=21276436; PubMed=11279123;  
 RA Koc E.C., Burkhardt W., Blackburn K., Mesley A., Sproemelli L.L.;  
 RT "The small subunit of the mammalian mitochondrial ribosome:  
 RT Identification of the full complement of ribosomal proteins present".  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC Ribosome; protein; Mitochondrion.  
 FT NON\_TER 1  
 FT NON\_TER 9  
 FT SEQUENCE 9 AA; 1032 MW; D341D73776D80589 CRC64;

Query Match 18.2% Score 2; PB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AK 2  
 DB 8 AK 9

RESULT 34  
 THYF\_PIG  
 ID THYF\_PIG STANDARD; PRI; 9 AA.  
 AC P01255;

DT 21-JUL-1998 (Rel. 41, Created)  
 DT 21-JUL-1998 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Thymine factor.  
 CC  
 CC SCS Scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Suidae; Sus.  
 CC NCBI\_TaxID=9913;  
 CC  
 CC SEQUENCE  
 CC MEDLINE=7602673; PubMed=34442;  
 CC Fleury J.M., Fardoux M., Bloch Y., Bach J.-F.;  
 CC "Structural study of thymine factor: a peptide isolated  
 CC from pig serum. II. Amino acid sequence".  
 CC J. Biol. Chem. 269:4064-4067(1994).  
 CC -!- MISCELLANEOUS: HEAVY METAL ION SENSITIVE(S) AND PHYSIOLOGICAL  
 CC ACTIVITIES OF THIS PROTEIN HAVE NOT BEEN DETERMINED.  
 CC FIP\_A0124; VF03.  
 CC KW Peptide; Thymine factor.  
 CC FT NON\_TER 1  
 CC SEQUENCE 9 AA; 1199 MW; D11941624422 CRC64;

Query Match 18.2% Score 2; PB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AK 2  
 DB 2 AK 4

RESULT 35  
 HLA\_HUMAN  
 ID HLA\_HUMAN STANDARD; PRI; 9 AA.  
 AC P31429;  
 DT 01-JUL-1993 (Rel. 23, Created)  
 DT 01-JUL-1993 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2L page of liver tissue (Spot 106) (Fragment)  
 OS Homo sapiens (human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94147960; PubMed=844076;  
 RA Hughes G.J., Fritzsche S., Boudry N., Boudry C., Schreier J.P.;  
 RA Classon G.B., Boudry A., Agnew B.D., Boudryasser D.F.;  
 RT "Human liver proteome map of 2L tissue".  
 RL Electrophoresis 14:116-122(1993).  
 CC -!- MISCELLANEOUS: ON THE 2L PAGE OF THE DETERMINED PAGE THIS CAN BE  
 CC IDENTIFIED AS 6. THE MW IS 15.4 K.  
 CC SWISS-PROT: P31429; HUMAN.  
 FT NON\_TER 9  
 FT SEQUENCE 9 AA; 1199 MW; D11941624422 CRC64;

Query Match 18.2% Score 2; PB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AK 4  
 DB 6 AK 1

RESULT 36  
 CATH\_SHEEP  
 ID CATH\_SHEEP STANDARD; PRI; 10 AA.  
 AC P84255;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).  
 GN CISH.  
 OS Ovis aries (sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Artiodactyla; Perissodactyla;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID:9940;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Placenta;  
 RX MEDLINE:22394055; PubMed:12563652;  
 RA El Amir B., Remy B., Sousa N.M., Joris B., Joris N.B., Joranyi Z.,  
 KA Moko H.B., Beckers J.-P.M.P.;  
 RT "Isolation and partial characterization of three pregnancy-associated  
 RT glycoproteins from the ewe placenta.";  
 RL Mol. Reprod. Dev. 64:199-206(2004).  
 CC 1- FUNCTION: Thiol protease which is believed to participate in  
 CC intracellular degradation and turnover of proteins; has also been  
 CC implicated in tumor invasion and metastasis;  
 CC 1- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves Arg-Arg-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin B). In  
 CC addition to being an endopeptidase, shows peptidyl dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC 1- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked  
 CC by a disulfide bond (by similarity).  
 CC 1- SUBCELLULAR LOCATION: Lysosomal (by similarity).  
 CC 1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 11.  
 DR InterPro: IPR000169; Shprot\_acsite.  
 DR PROSITE: PS00640; THIOL\_PROTEASE\_ASN; PARTIAL.  
 DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA: 1177 MW: 879578;MDANALYSE:CR664;

Query Match 18.2% Score 21 OR 11 Length 192  
 Best Local Similarity 100.0% Pred. No. 1,16(14)  
 Matches 2: Conservative G: Mismatches 6: Indels 0: Gaps 0:

OY 5 EQ 6  
 DB 1  
 1 EQ 10

RESULT 47  
 COXA\_OXCY  
 ID COXA\_OXCY STANDARD: PRT: 10 AA.  
 AC P60428;  
 DT 01-OCT-1994 (rel. 30, Created)  
 DT 01-OCT-1994 (rel. 30, Last sequence update)  
 DT 30-MAY-2000 (rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment)  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Procarangiopterygii; Salmoniformes; Salmonidae; Oncorhynchus;  
 OX NCBI\_TaxID:8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Liver;  
 RX MEDLINE:94217150; PubMed:8181469;  
 RA Freund K., Kadenbach B.;  
 RT "Identification of tissue-specific isoforms for subunits VB and VII  
 RT of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).  
 CC 1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
 CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT  
 CC 1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferrioxycyclochrome  
 CC c + 2 H(2)O.  
 CC 1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
 DR PIR: S43625; S43625.

KW Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Cytochrome c oxidase subunit VB).  
 FI NCBI\_TaxID:8022;  
 SQ SEQUENCE 10 AA: 1177 MW: 879578;MDANALYSE:CR664;  
 Query Match 18.2% Score 21 OR 11 Length 192  
 Best Local Similarity 100.0% Pred. No. 1,16(14)  
 Matches 2: Conservative G: Mismatches 6: Indels 0: Gaps 0:  
 OY 5 EQ 6  
 DB 1  
 1 EQ 10  
 RESULT 47  
 COXA\_OXCY  
 ID COXA\_OXCY STANDARD: PRT: 10 AA.  
 AC P60428;  
 DT 01-OCT-1994 (rel. 30, Created)  
 DT 01-OCT-1994 (rel. 30, Last sequence update)  
 DT 30-MAY-2000 (rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment)  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Procarangiopterygii; Salmoniformes; Salmonidae; Oncorhynchus;  
 OX NCBI\_TaxID:8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE: Liver;  
 RX MEDLINE:94217150; PubMed:8181469;  
 RA Freund K., Kadenbach B.;  
 RT "Identification of tissue-specific isoforms for subunits VB and VII  
 RT of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).  
 CC 1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
 CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT  
 CC 1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferrioxycyclochrome  
 CC c + 2 H(2)O.  
 CC 1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
 DR PIR: S43625; S43625.



OC Methanobacteriaceae: Methanothermobacter:  
 OX NCBI\_TaxID=79929;  
 RN 111  
 RP SEQUENCE  
 RX MEDLINE=97261844; PubMed=9108258;  
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.J.  
 RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases  
 in Methanobacterium thermoautotrophicum";  
 RL Eur. J. Biochem. 244:862-868(1997).  
 CC -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin + acetyl-  
 CoA + CO(2) + reduced ferredoxin;  
 CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE  
 CC GAMMA CHAIN.  
 CC -1- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature  
 CC of 80 degrees Celsius.  
 CC Oxidoreductase.  
 KW NON\_TER 10 10  
 FT SEQUENCE 10 AA: 1232 MW: 167010DAPPHPPPPGAPK664;  
 SQ  
 Query Match 18.2%; Score 2; LPI 1; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 1; LPI=04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 EQ 6  
 11  
 DB 5 EQ 6  
 11  
 RESULT 44  
 PSBF\_CAPAN  
 ID PSBF\_CAPAN STANDARD: PRT: 10 AA.  
 AC Q03367;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cytochrome b559 beta subunit (PS1) reaction center subunit V1  
 DE (Fragment).  
 GN PSBF.  
 OS Capsicum annuum (Bell pepper).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Capsicum.  
 OX NCBI\_TaxID=4072;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Lamuyo; TISSUE=fruit, and leaf;  
 RX MEDLINE=93099270; PubMed=1463853;  
 RA Kuntz M., Camara B., Weil J.-H., Schantz P.J.  
 RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA  
 RT editing also occurs in non-photosynthetic chloroplasts";  
 RL Plant Mol. Biol. 20:1185-1188(1992).  
 CC -1- FUNCTION: This b-type cytochrome is tightly associated with the  
 CC reaction center of photosystem II and possibly is part of the  
 CC water-oxidation complex.  
 CC -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.  
 CC -1- SIMILARITY: Belongs to the psbE / psbF family.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL: X65570; CAA46539.1; -  
 DR PIR: S28055; S28055.  
 DR HAMAP: MF\_006433; -; 1.  
 DR InterPro: IPR006216; Cyt\_b559.  
 DR PROSITE: PS00537; CYTOCHROME\_B559; PARTIAL.  
 KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.  
 FT NON\_TER 1 1

FT TRANSMEM 1 1  
 FT DOMAIN 1 1  
 SO SEQUENCE 10 AA: 1232 MW: 167010DAPPHPPPPGAPK664;  
 Query Match 18.2%; Score 2; LPI 1; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 1; LPI=04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 EQ 6  
 11  
 DB 5 EQ 6  
 11  
 RESULT 44  
 PSBF\_CAPAN  
 ID PSBF\_CAPAN STANDARD: PRT: 10 AA.  
 AC Q03367;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cytochrome b559 beta subunit (PS1) reaction center subunit V1  
 DE (Fragment).  
 GN PSBF.  
 OS Capsicum annuum (Bell pepper).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Capsicum.  
 OX NCBI\_TaxID=4072;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Lamuyo; TISSUE=fruit, and leaf;  
 RX MEDLINE=93099270; PubMed=1463853;  
 RA Kuntz M., Camara B., Weil J.-H., Schantz P.J.  
 RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA  
 RT editing also occurs in non-photosynthetic chloroplasts";  
 RL Plant Mol. Biol. 20:1185-1188(1992).  
 CC -1- FUNCTION: This b-type cytochrome is tightly associated with the  
 CC reaction center of photosystem II and possibly is part of the  
 CC water-oxidation complex.  
 CC -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.  
 CC -1- SIMILARITY: Belongs to the psbE / psbF family.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL: X65570; CAA46539.1; -  
 DR PIR: S28055; S28055.  
 DR HAMAP: MF\_006433; -; 1.  
 DR InterPro: IPR006216; Cyt\_b559.  
 DR PROSITE: PS00537; CYTOCHROME\_B559; PARTIAL.  
 KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.  
 FT NON\_TER 1 1

OC Stolidobranchia; Pyridae; Halocynthia.  
 OX NCHI\_TaxID=7729;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RA MEDLINE=96321313; PubMed=8759296;  
 RX Shishikura F., Abe T., Ohtake S.-I., Tanaka K.  
 RT "Purification and characterization of a 58,000 Da proteinase  
 inhibitor from the hemolymph of a solitary ascidian, Halocynthia  
 roretzi".  
 RL Comp. Biochem. Physiol. 114B:1-9(1996).  
 CC - FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.  
 CC - SUBUNIT: Monomer.  
 CC - SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro: IPR000215; Serpin.  
 DK PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Serpin; Serine protease inhibitor; Glycine; Glycyl-L-proline; Plasma.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA: 1104 MW: 4225074518187AA3 CP004.

Query Match 18.2% Score 21 DR 11 Length 10  
 Best Local Similarity 100.0% Prod. No. 11044  
 Matches 23 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KK 3  
 DB 2 KK 3

RESULT 47  
 SYK\_CAMUP STANDARD: PRT: 10 AA:  
 AC Q46464;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lysyl-tRNA synthetase (EC 6.1.1.6) (lysine-tRNA ligase) (LysE)  
 DE (Fragment).  
 GS Campylobacter upsaliensis.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteretes;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=28080;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43954;  
 RX MEDLINE=97149302; PubMed=8996110;  
 RA Bourke B., Rashid S.T., Binham H.L., Chan V.L.  
 RT "Characterization of Campylobacter upsaliensis 1st and 1st  
 localization in a highly conserved region of the Campylobacter  
 genome".  
 RL Gene 181:219-224(1996).  
 CC - CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) -> diphosphate  
 + L-lysyl-tRNA(Lys).  
 CC - COFACTOR: Binds 3 magnesium ions per subunit (by similarity).  
 CC - SUBUNIT: Homodimer (by similarity).  
 CC - SUBCELLULAR LOCATION: Cytoplasmic.  
 CC - SIMILARITY: Belongs to class II aminoacyl-tRNA synthetase family.  
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 CC EMBL: L77076; AAB41342.1;  
 DR HAMAP: MF\_00252;  
 DR InterPro: IPR0006195; tRNA\_LIGASE\_II.  
 DR PROSITE: PS50862; AA\_TRNA\_LIGASE\_II; PARTIAL.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Lysase; ATP binding;  
 Metal-binding; Magnesium.

QY 2 KK 3  
 DB 2 KK 3

Query Match 18.2% Score 21 DR 11 Length 10  
 Best Local Similarity 100.0% Prod. No. 11044  
 Matches 23 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KK 3  
 DB 2 KK 3

RESULT 48  
 SYK\_CAMUP STANDARD: PRT: 10 AA:  
 AC Q46464;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lysyl-tRNA synthetase (EC 6.1.1.6) (lysine-tRNA ligase) (LysE)  
 DE (Fragment).  
 GS Campylobacter upsaliensis.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteretes;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=28080;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43954;  
 RX MEDLINE=97149302; PubMed=8996110;  
 RA Bourke B., Rashid S.T., Binham H.L., Chan V.L.  
 RT "Characterization of Campylobacter upsaliensis 1st and 1st  
 localization in a highly conserved region of the Campylobacter  
 genome".  
 RL Gene 181:219-224(1996).  
 CC - CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) -> diphosphate  
 + L-lysyl-tRNA(Lys).  
 CC - COFACTOR: Binds 3 magnesium ions per subunit (by similarity).  
 CC - SUBUNIT: Homodimer (by similarity).  
 CC - SUBCELLULAR LOCATION: Cytoplasmic.  
 CC - SIMILARITY: Belongs to class II aminoacyl-tRNA synthetase family.  
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 or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC EMBL: L77076; AAB41342.1;  
 DR HAMAP: MF\_00252;  
 DR InterPro: IPR0006195; tRNA\_LIGASE\_II.  
 DR PROSITE: PS50862; AA\_TRNA\_LIGASE\_II; PARTIAL.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Lysase; ATP binding;  
 Metal-binding; Magnesium.

```
RN SEQUENCE.
RP STRAIN-L2/434/Bu;
RA Bini L., Santucci A., Maqi B., Martocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christlanen G., Birkelund S., Virolan E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
DR Siena-2DPAGE: P38007;
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1243 MW: DAD39A33304B5439 CRC664;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
DB 7 KK 8

RESULT 50
ASL2_BACSE
1D ASL2_BACSE STANDARD: PRT: 11 AA.
AC P83147;
DT 28 FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidiales;
OC Bacteroidaceae; Bacteroides.
OX NCRI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN-H-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.-S., Kim D.-H.;
RT *Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6, its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA: 1195 MW: D79D897C7AA451AD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 QR 9
DB 10 QR 11
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 17:03:12 : Search time 92 seconds  
(without alignments)  
10.854 Million cell updates/sec

Title: US-09-787-443-20

Perfect score: 11

Sequence: 1 AKKKEQKQRNA 11

Scoring table: OLIGO  
Gapex 60.0, Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1454

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database:

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	15	4 Q90C17	Q90C17 homo sapien
2	4	36.4	15	10 Q9S016	Q9S016 myzsa sativ
3	3	27.3	9	11 Q99MG3	Q99MG3 mus muscul
4	3	27.3	11	4 Q9H4H5	Q9H4H5 homo sapien
5	3	27.3	12	2 Q6VIX8	Q6VIX8 thelmus the
6	3	27.3	12	16 Q25179	Q25179 helicobacte
7	3	27.3	13	2 Q50117	Q50117 mycobacteri
8	3	27.3	13	4 Q9H4C1	Q9H4C1 homo sapien
9	3	27.3	13	8 Q9T569	Q9T569 zea mays (m
10	3	27.3	13	16 Q8X4F5	Q8X4F5 escherichia
11	3	27.3	14	1 Q9UWM2	Q9UWM2 pyrococcus
12	3	27.3	14	2 Q56750	Q56750 western x p
13	3	27.3	14	2 Q46291	Q46291 canadian pc
14	3	27.3	14	4 Q96Q50	Q96Q50 homo sapien
15	3	27.3	14	4 Q15222	Q15222 homo sapien
16	3	27.3	14	13 P82831	P82831 rana luteiv

17	3	27.3	3	2	15 Q9H12	Q9H12 escherichia
18	3	27.3	3	2	4 Q9H85	Q9H85 rhodospirillum
19	3	27.3	3	4	4 Q9H82	Q9H82 homo sapien
20	3	27.3	3	4	4 Q9H80	Q9H80 homo sapien
21	3	27.3	3	5	5 Q9H804	Q9H804 rana luteiv
22	3	27.3	3	5	5 Q9H803	Q9H803 homo sapien
23	3	27.3	3	5	5 Q9H802	Q9H802 homo sapien
24	3	27.3	3	15	15 Q9S016	Q9S016 myzsa sativ
25	3	27.3	3	15	15 Q9S016	Q9S016 myzsa sativ
26	3	27.3	3	15	15 Q9S016	Q9S016 myzsa sativ
27	3	27.3	3	3	3 Q9H801	Q9H801 escherichia
28	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
29	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
30	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
31	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
32	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
33	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
34	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
35	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
36	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
37	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
38	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
39	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
40	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
41	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
42	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
43	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
44	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
45	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
46	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
47	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
48	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
49	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
50	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
51	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
52	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
53	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
54	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
55	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
56	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
57	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
58	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
59	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
60	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
61	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
62	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
63	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
64	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
65	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
66	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
67	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
68	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
69	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
70	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
71	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
72	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
73	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
74	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
75	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
76	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
77	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
78	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
79	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
80	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
81	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
82	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
83	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
84	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
85	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
86	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
87	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
88	3	27.3	3	3	3 Q9H800	Q9H800 escherichia
89	3	27.3	3	3	3 Q9H800	Q9H800 escherichia



90	2	18.2	10	2	Q8VN85	Q8x85 bacitracin	18.2	1	Q8X85	Q8x85 bacitracin
91	2	18.2	10	2	Q8X3M2	Q8x32 streptococ	18.2	1	Q8X32	Q8x32 streptococ
92	2	18.2	10	2	Q54217	Q54217 staphylococ	18.2	1	Q54217	Q54217 staphylococ
93	2	18.2	10	2	Q8RS01	Q8RS01 bacitracin	18.2	1	Q8RS01	Q8RS01 bacitracin
94	2	18.2	10	2	Q8S3J6	Q8S3J6 escherichia	18.2	1	Q8S3J6	Q8S3J6 escherichia
95	2	18.2	10	2	Q60194	Q60194 spirillum	18.2	1	Q60194	Q60194 spirillum
96	2	18.2	10	2	Q60192	Q60192 spirillum	18.2	1	Q60192	Q60192 spirillum
97	2	18.2	10	2	Q8RSN1	Q8RSN1 clostridium	18.2	1	Q8RSN1	Q8RSN1 clostridium
98	2	18.2	10	2	Q8RSN3	Q8RSN3 clostridium	18.2	1	Q8RSN3	Q8RSN3 clostridium
99	2	18.2	10	2	Q44693	Q44693 bacillus am	18.2	1	Q44693	Q44693 bacillus am
100	2	18.2	10	2	Q51812	Q51812 escherichia	18.2	1	Q51812	Q51812 escherichia
101	2	18.2	10	2	Q8JNC9	Q8JNC9 streptococ	18.2	1	Q8JNC9	Q8JNC9 streptococ
102	2	18.2	10	2	Q8RT11	Q8RT11 anaplasma p	18.2	1	Q8RT11	Q8RT11 anaplasma p
103	2	18.2	10	2	Q8AE19	Q8AE19 streptococ	18.2	1	Q8AE19	Q8AE19 streptococ
104	2	18.2	10	2	Q8JOC7	Q8JOC7 bacillus ce	18.2	1	Q8JOC7	Q8JOC7 bacillus ce
105	2	18.2	10	2	Q8JOC2	Q8JOC2 anaplasma sp	18.2	1	Q8JOC2	Q8JOC2 anaplasma sp
106	2	18.2	10	3	Q8JOC2	Q8JOC2 anaplasma sp	18.2	1	Q8JOC2	Q8JOC2 anaplasma sp
107	2	18.2	10	4	Q8NERG	Q8NERG homo sapien	18.2	1	Q8NERG	Q8NERG homo sapien
108	2	18.2	10	4	Q8QMK9	Q8QMK9 homo sapien	18.2	1	Q8QMK9	Q8QMK9 homo sapien
109	2	18.2	10	4	Q8QCS3	Q8QCS3 homo sapien	18.2	1	Q8QCS3	Q8QCS3 homo sapien
110	2	18.2	10	4	Q8QDE8	Q8QDE8 homo sapien	18.2	1	Q8QDE8	Q8QDE8 homo sapien
111	2	18.2	10	4	Q8QOT9	Q8QOT9 homo sapien	18.2	1	Q8QOT9	Q8QOT9 homo sapien
112	2	18.2	10	4	Q8QPC6	Q8QPC6 homo sapien	18.2	1	Q8QPC6	Q8QPC6 homo sapien
113	2	18.2	10	4	Q8QX85	Q8QX85 homo sapien	18.2	1	Q8QX85	Q8QX85 homo sapien
114	2	18.2	10	4	Q8NPG7	Q8NPG7 homo sapien	18.2	1	Q8NPG7	Q8NPG7 homo sapien
115	2	18.2	10	4	Q8MCP1	Q8MCP1 heliconius	18.2	1	Q8MCP1	Q8MCP1 heliconius
116	2	18.2	10	5	Q8WPI6	Q8WPI6 c. koe-eura	18.2	1	Q8WPI6	Q8WPI6 c. koe-eura
117	2	18.2	10	5	Q8WUN7	Q8WUN7 c. koe-eura	18.2	1	Q8WUN7	Q8WUN7 c. koe-eura
118	2	18.2	10	5	Q8WPE7	Q8WPE7 strobilaria	18.2	1	Q8WPE7	Q8WPE7 strobilaria
119	2	18.2	10	5	Q8WTS4	Q8WTS4 sus scrofa	18.2	1	Q8WTS4	Q8WTS4 sus scrofa
120	2	18.2	10	6	Q8TR06	Q8TR06 bos taurus	18.2	1	Q8TR06	Q8TR06 bos taurus
121	2	18.2	10	6	Q8MJ78	Q8MJ78 bos taurus	18.2	1	Q8MJ78	Q8MJ78 bos taurus
122	2	18.2	10	6	Q8SPN6	Q8SPN6 capra hircu	18.2	1	Q8SPN6	Q8SPN6 capra hircu
123	2	18.2	10	6	Q8MJ52	Q8MJ52 capra hircu	18.2	1	Q8MJ52	Q8MJ52 capra hircu
124	2	18.2	10	6	Q8J205	Q8J205 capra hircu	18.2	1	Q8J205	Q8J205 capra hircu
125	2	18.2	10	7	Q8SHF5	Q8SHF5 papio anub	18.2	1	Q8SHF5	Q8SHF5 papio anub
126	2	18.2	10	7	Q8SHF6	Q8SHF6 papio anub	18.2	1	Q8SHF6	Q8SHF6 papio anub
127	2	18.2	10	7	Q8SHF6	Q8SHF6 papio anub	18.2	1	Q8SHF6	Q8SHF6 papio anub
128	2	18.2	10	7	Q8SHF7	Q8SHF7 papio anub	18.2	1	Q8SHF7	Q8SHF7 papio anub
129	2	18.2	10	7	Q8SHF4	Q8SHF4 papio anub	18.2	1	Q8SHF4	Q8SHF4 papio anub
130	2	18.2	10	7	Q8SHG0	Q8SHG0 homo sapien	18.2	1	Q8SHG0	Q8SHG0 homo sapien
131	2	18.2	10	8	Q8WFT6	Q8WFT6 diadema ant	18.2	1	Q8WFT6	Q8WFT6 diadema ant
132	2	18.2	10	8	Q8J2P4	Q8J2P4 ratius sp	18.2	1	Q8J2P4	Q8J2P4 ratius sp
133	2	18.2	10	8	Q8J1G3	Q8J1G3 saccharomye	18.2	1	Q8J1G3	Q8J1G3 saccharomye
134	2	18.2	10	8	Q8WFI5	Q8WFI5 diadema ant	18.2	1	Q8WFI5	Q8WFI5 diadema ant
135	2	18.2	10	8	Q8H0H4	Q8H0H4 ananotryum	18.2	1	Q8H0H4	Q8H0H4 ananotryum
136	2	18.2	10	9	Q8J217	Q8J217 lactococcus	18.2	1	Q8J217	Q8J217 lactococcus
137	2	18.2	10	10	Q8S926	Q8S926 glycyne max	18.2	1	Q8S926	Q8S926 glycyne max
138	2	18.2	10	10	Q8J212	Q8J212 spinacia ol	18.2	1	Q8J212	Q8J212 spinacia ol
139	2	18.2	10	10	Q8J213	Q8J213 spinacia ol	18.2	1	Q8J213	Q8J213 spinacia ol
140	2	18.2	10	11	Q8QVE8	Q8QVE8 mus sp. pro	18.2	1	Q8QVE8	Q8QVE8 mus sp. pro
141	2	18.2	10	11	Q8QVE7	Q8QVE7 mus sp. pro	18.2	1	Q8QVE7	Q8QVE7 mus sp. pro
142	2	18.2	10	11	Q8J115	Q8J115 mus masculu	18.2	1	Q8J115	Q8J115 mus masculu
143	2	18.2	10	11	Q8Q580	Q8Q580 mus masculu	18.2	1	Q8Q580	Q8Q580 mus masculu
144	2	18.2	10	11	Q8Q370	Q8Q370 mus masculu	18.2	1	Q8Q370	Q8Q370 mus masculu
145	2	18.2	10	11	Q8Q350	Q8Q350 ratius nery	18.2	1	Q8Q350	Q8Q350 ratius nery
146	2	18.2	10	12	Q8Q3K9	Q8Q3K9 polyomaviru	18.2	1	Q8Q3K9	Q8Q3K9 polyomaviru
147	2	18.2	10	12	Q8J170	Q8J170 polyomaviru	18.2	1	Q8J170	Q8J170 polyomaviru
148	2	18.2	10	12	Q8Q0W1	Q8Q0W1 polyomaviru	18.2	1	Q8Q0W1	Q8Q0W1 polyomaviru
149	2	18.2	10	12	Q8J168	Q8J168 polyomaviru	18.2	1	Q8J168	Q8J168 polyomaviru
150	2	18.2	10	12	Q8Q0V9	Q8Q0V9 polyomaviru	18.2	1	Q8Q0V9	Q8Q0V9 polyomaviru
151	2	18.2	10	12	Q8J184	Q8J184 polyomaviru	18.2	1	Q8J184	Q8J184 polyomaviru
152	2	18.2	10	12	Q8Q0W7	Q8Q0W7 polyomaviru	18.2	1	Q8Q0W7	Q8Q0W7 polyomaviru
153	2	18.2	10	12	Q8J166	Q8J166 polyomaviru	18.2	1	Q8J166	Q8J166 polyomaviru
154	2	18.2	10	12	Q8Q0V7	Q8Q0V7 polyomaviru	18.2	1	Q8Q0V7	Q8Q0V7 polyomaviru
155	2	18.2	10	12	Q8J182	Q8J182 polyomaviru	18.2	1	Q8J182	Q8J182 polyomaviru
156	2	18.2	10	12	Q8J265	Q8J265 infectious	18.2	1	Q8J265	Q8J265 infectious
157	2	18.2	10	12	Q8J176	Q8J176 polyomaviru	18.2	1	Q8J176	Q8J176 polyomaviru
158	2	18.2	10	12	Q8J174	Q8J174 polyomaviru	18.2	1	Q8J174	Q8J174 polyomaviru
159	2	18.2	10	12	Q8J178	Q8J178 inf. uenavir	18.2	1	Q8J178	Q8J178 inf. uenavir
160	2	18.2	10	12	Q8Q0X7	Q8Q0X7 polyomaviru	18.2	1	Q8Q0X7	Q8Q0X7 polyomaviru
161	2	18.2	10	12	Q8J178	Q8J178 polyomaviru	18.2	1	Q8J178	Q8J178 polyomaviru
162	2	18.2	10	12	Q8Q0W5	Q8Q0W5 polyomaviru	18.2	1	Q8Q0W5	Q8Q0W5 polyomaviru

236	2	18.2	12	2	Q8KH47	Q8KH47 enterococci	409	2	18.2	12	6	Q8K512	Q8K512 sylvaticus
237	2	18.2	12	2	Q8R5F7	Q8R5f7 helicobacte	410	2	18.2	12	6	Q8K524	Q8K524 canis fami
238	2	18.2	12	2	Q8A08	Q8A08 tniobacilli	411	2	18.2	12	6	Q8K534	Q8K534 bos taurus
239	2	18.2	12	2	Q8R5F5	Q8R5f5 helicobacte	412	2	18.2	12	6	Q8K544	Q8K544 helicobact
240	2	18.2	12	2	Q8KH5	Q8KH5 campylobact	413	2	18.2	12	6	Q8K554	Q8K554 amelia aris
241	2	18.2	12	2	Q8K5F5	Q8K5f5 campylobact	414	2	18.2	12	6	Q8K564	Q8K564 helicobact
242	2	18.2	12	2	Q8L4W9	Q8L4W9 escherichia	415	2	18.2	12	6	Q8K574	Q8K574 helicobact
243	2	18.2	12	2	Q8R3B3	Q8R3B3 streptococ	416	2	18.2	12	6	Q8K584	Q8K584 helicobact
244	2	18.2	12	2	Q8R3B3	Q8R3B3 helicobacte	417	2	18.2	12	6	Q8K594	Q8K594 helicobact
245	2	18.2	12	4	Q8UMR0	Q8UMR0 homo sapien	418	2	18.2	12	6	Q8K604	Q8K604 helicobact
246	2	18.2	12	4	Q8U4F4	Q8U4F4 homo sapien	419	2	18.2	12	6	Q8K614	Q8K614 helicobact
247	2	18.2	12	4	Q8UC37	Q8UC37 homo sapien	420	2	18.2	12	6	Q8K624	Q8K624 helicobact
248	2	18.2	12	4	Q8YV9	Q8YV9 homo sapien	421	2	18.2	12	6	Q8K634	Q8K634 helicobact
249	2	18.2	12	4	Q8PK0	Q8PK0 homo sapien	422	2	18.2	12	6	Q8K644	Q8K644 helicobact
250	2	18.2	12	4	Q8UMZ8	Q8UMZ8 homo sapien	423	2	18.2	12	6	Q8K654	Q8K654 helicobact
251	2	18.2	12	4	Q8NTR7	Q8NTR7 homo sapien	424	2	18.2	12	6	Q8K664	Q8K664 helicobact
252	2	18.2	12	5	Q8MUN4	Q8MUN4 helicobact	425	2	18.2	12	6	Q8K674	Q8K674 helicobact
253	2	18.2	12	5	Q8MY01	Q8MY01 drosophila	426	2	18.2	12	6	Q8K684	Q8K684 helicobact
254	2	18.2	12	5	Q8TY79	Q8TY79 paruliculus i	427	2	18.2	12	6	Q8K694	Q8K694 helicobact
255	2	18.2	12	5	Q8MUN9	Q8MUN9 helicobact	428	2	18.2	12	6	Q8K704	Q8K704 helicobact
256	2	18.2	12	5	Q8L574	Q8L574 osteriaqia	429	2	18.2	12	6	Q8K714	Q8K714 helicobact
257	2	18.2	12	6	Q8BFT6	Q8BFT6 ateles fusc	430	2	18.2	12	6	Q8K724	Q8K724 helicobact
258	2	18.2	12	6	Q8BFT6	Q8BFT6 ciactopirac	431	2	18.2	12	6	Q8K734	Q8K734 helicobact
259	2	18.2	12	6	Q8BFT6	Q8BFT6 canis famil	432	2	18.2	12	6	Q8K744	Q8K744 helicobact
260	2	18.2	12	6	Q8BFS3	Q8BFS3 okapia john	433	2	18.2	12	6	Q8K754	Q8K754 helicobact
261	2	18.2	12	6	Q8BFT1	Q8BFT1 condylura c	434	2	18.2	12	6	Q8K764	Q8K764 helicobact
262	2	18.2	12	6	Q8BFT1	Q8BFT1 tarsius ban	435	2	18.2	12	6	Q8K774	Q8K774 helicobact
263	2	18.2	12	6	Q8BFR4	Q8BFR4 manis penta	436	2	18.2	12	6	Q8K784	Q8K784 helicobact
264	2	18.2	12	6	Q8BFT9	Q8BFT9 tupia mino	437	2	18.2	12	6	Q8K794	Q8K794 helicobact
265	2	18.2	12	6	Q8BFS9	Q8BFS9 megaloptera c	438	2	18.2	12	6	Q8K804	Q8K804 helicobact
266	2	18.2	12	6	Q8BFS3	Q8BFS3 erinaceus c	439	2	18.2	12	6	Q8K814	Q8K814 helicobact
267	2	18.2	12	6	Q8BFS5	Q8BFS5 tamandua te	440	2	18.2	12	6	Q8K824	Q8K824 helicobact
268	2	18.2	12	6	Q8BFS5	Q8BFS5 tragelaphus	441	2	18.2	12	6	Q8K834	Q8K834 helicobact
269	2	18.2	12	6	Q8T31	Q8T31 callithrix	442	2	18.2	12	6	Q8K844	Q8K844 helicobact
270	2	18.2	12	6	Q8BFS2	Q8BFS2 equus cabal	443	2	18.2	12	6	Q8K854	Q8K854 helicobact
271	2	18.2	12	6	Q8TQW3	Q8TQW3 bos taurus	444	2	18.2	12	6	Q8K864	Q8K864 helicobact
272	2	18.2	12	6	Q8BFS3	Q8BFS3 orycteropus	445	2	18.2	12	6	Q8K874	Q8K874 helicobact
273	2	18.2	12	6	Q8BFS0	Q8BFS0 sorex arane	446	2	18.2	12	6	Q8K884	Q8K884 helicobact
274	2	18.2	12	6	Q8BFS5	Q8BFS5 ursus arcto	447	2	18.2	12	6	Q8K894	Q8K894 helicobact
275	2	18.2	12	6	Q8BFS7	Q8BFS7 hippopotamu	448	2	18.2	12	6	Q8K904	Q8K904 helicobact
276	2	18.2	12	6	Q8BFT3	Q8BFT3 artibeus ia	449	2	18.2	12	6	Q8K914	Q8K914 helicobact
277	2	18.2	12	6	Q8BFT2	Q8BFT2 talpa alta	450	2	18.2	12	6	Q8K924	Q8K924 helicobact
278	2	18.2	12	6	Q8X31	Q8X31 sus scrofa	451	2	18.2	12	6	Q8K934	Q8K934 helicobact
279	2	18.2	12	6	Q8BFT1	Q8BFT1 roussetus l	452	2	18.2	12	6	Q8K944	Q8K944 helicobact
280	2	18.2	12	6	Q8BFT0	Q8BFT0 macropus eu	453	2	18.2	12	6	Q8K954	Q8K954 helicobact
281	2	18.2	12	6	Q8BFT0	Q8BFT0 trichectus	454	2	18.2	12	6	Q8K964	Q8K964 helicobact
282	2	18.2	12	6	Q8BFT0	Q8BFT0 nycterus th	455	2	18.2	12	6	Q8K974	Q8K974 helicobact
283	2	18.2	12	6	Q8BFT4	Q8BFT4 callimico q	456	2	18.2	12	6	Q8K984	Q8K984 helicobact
284	2	18.2	12	6	Q8BFT7	Q8BFT7 procavia qa	457	2	18.2	12	6	Q8K994	Q8K994 helicobact
285	2	18.2	12	6	Q8BFT2	Q8BFT2 pteropus ci	458	2	18.2	12	6	Q8L004	Q8L004 helicobact
286	2	18.2	12	6	Q8BFT8	Q8BFT8 choleopus d	459	2	18.2	12	6	Q8L014	Q8L014 helicobact
287	2	18.2	12	6	Q8TRU2	Q8TRU2 bos taurus	460	2	18.2	12	6	Q8L024	Q8L024 helicobact
288	2	18.2	12	6	Q8BFT1	Q8BFT1 ochotona hy	461	2	18.2	12	6	Q8L034	Q8L034 helicobact
289	2	18.2	12	6	Q8BFT4	Q8BFT4 myimicophag	462	2	18.2	12	6	Q8L044	Q8L044 helicobact
290	2	18.2	12	6	Q8BFS8	Q8BFS8 tarsius tr	463	2	18.2	12	6	Q8L054	Q8L054 helicobact
291	2	18.2	12	6	Q8BFT7	Q8BFT7 euphractus	464	2	18.2	12	6	Q8L064	Q8L064 helicobact
292	2	18.2	12	6	Q8BFS1	Q8BFS1 ceratotheri	465	2	18.2	12	6	Q8L074	Q8L074 helicobact
293	2	18.2	12	6	Q8BFS6	Q8BFS6 lama glama	466	2	18.2	12	6	Q8L084	Q8L084 helicobact
294	2	18.2	12	6	Q8BFS6	Q8BFS6 felis silve	467	2	18.2	12	6	Q8L094	Q8L094 helicobact
295	2	18.2	12	6	Q8BFT8	Q8BFT8 lemur calta	468	2	18.2	12	6	Q8L104	Q8L104 helicobact
296	2	18.2	12	6	Q8BFT9	Q8BFT9 echinops te	469	2	18.2	12	6	Q8L114	Q8L114 helicobact
297	2	18.2	12	6	Q8BFS0	Q8BFS0 tapirus ind	470	2	18.2	12	6	Q8L124	Q8L124 helicobact
298	2	18.2	12	6	Q8BFT9	Q8BFT9 choleopus h	471	2	18.2	12	6	Q8L134	Q8L134 helicobact
299	2	18.2	12	6	Q8M93	Q8M93 equus cabal	472	2	18.2	12	6	Q8L144	Q8L144 helicobact
300	2	18.2	12	6	Q8BFT5	Q8BFT5 macroscelid	473	2	18.2	12	6	Q8L154	Q8L154 helicobact
301	2	18.2	12	6	Q8BFT7	Q8BFT7 panthera on	474	2	18.2	12	6	Q8L164	Q8L164 helicobact
302	2	18.2	12	6	Q8BFT0	Q8BFT0 cynocephalu	475	2	18.2	12	6	Q8L174	Q8L174 helicobact
303	2	18.2	12	6	Q8BFR8	Q8BFR8 leopardus p	476	2	18.2	12	6	Q8L184	Q8L184 helicobact
304	2	18.2	12	6	Q8BFT6	Q8BFT6 loxodonta a	477	2	18.2	12	6	Q8L194	Q8L194 helicobact
305	2	18.2	12	6	Q8BFT5	Q8BFT5 macaca mula	478	2	18.2	12	6	Q8L204	Q8L204 helicobact
306	2	18.2	12	6	Q8BFS4	Q8BFS4 sus scrofa	479	2	18.2	12	6	Q8L214	Q8L214 helicobact
307	2	18.2	12	6	Q8T29	Q8T29 saguinus oe	480	2	18.2	12	6	Q8L224	Q8L224 helicobact
308	2	18.2	12	6	Q8BFT4	Q8BFT4 elephanthulu	481	2	18.2	12	6	Q8L234	Q8L234 helicobact

Q8K162	sylvaticus	12	6	Q8K512	Q8K512 sylvaticus
Q8K524	canis fami	12	6	Q8K524	Q8K524 canis fami
Q8K534	bos taurus	12	6	Q8K534	Q8K534 bos taurus
Q8K544	helicobact	12	6	Q8K544	Q8K544 helicobact
Q8K554	amelia aris	12	6	Q8K554	Q8K554 amelia aris
Q8K564	helicobact	12	6	Q8K564	Q8K564 helicobact
Q8K574	helicobact	12	6	Q8K574	Q8K574 helicobact
Q8K584	helicobact	12	6	Q8K584	Q8K584 helicobact
Q8K594	helicobact	12	6	Q8K594	Q8K594 helicobact
Q8K604	helicobact	12	6	Q8K604	Q8K604 helicobact
Q8K614	helicobact	12	6	Q8K614	Q8K614 helicobact
Q8K624	helicobact	12	6	Q8K624	Q8K624 helicobact
Q8K634	helicobact	12	6	Q8K634	Q8K634 helicobact
Q8K644	helicobact	12	6	Q8K644	Q8K644 helicobact
Q8K654	helicobact	12	6	Q8K654	Q8K654 helicobact
Q8K664	helicobact	12	6	Q8K664	Q8K664 helicobact
Q8K674	helicobact	12	6	Q8K674	Q8K674 helicobact
Q8K684	helicobact	12	6	Q8K684	Q8K684 helicobact
Q8K694	helicobact	12	6	Q8K694	Q8K694 helicobact
Q8K704	helicobact	12	6	Q8K704	Q8K704 helicobact
Q8K714	helicobact	12	6	Q8K714	Q8K714 helicobact
Q8K724	helicobact	12	6	Q8K724	Q8K724 helicobact
Q8K734	helicobact	12	6	Q8K734	Q8K734 helicobact
Q8K744	helicobact	12	6	Q8K744	Q8K744 helicobact
Q8K754	helicobact	12	6	Q8K754	Q8K754 helicobact
Q8K764	helicobact	12	6	Q8K764	Q8K764 helicobact
Q8K774	helicobact	12	6	Q8K774	Q8K774 helicobact
Q8K784	helicobact	12	6	Q8K784	Q8K784 helicobact
Q8K794	helicobact	12	6	Q8K794	Q8K794 helicobact
Q8K804	helicobact	12	6	Q8K804	Q8K804 helicobact
Q8K814	helicobact	12	6	Q8K814	Q8K814 helicobact
Q8K824	helicobact	12	6	Q8K824	Q8K824 helicobact
Q8K834	helicobact	12	6	Q8K834	Q8K834 helicobact
Q8K844	helicobact	12	6	Q8K844	Q8K844 helicobact
Q8K854	helicobact	12	6	Q8K854	Q8K854 helicobact
Q8K864	helicobact	12	6	Q8K864	Q8K864 helicobact
Q8K874	helicobact	12	6	Q8K874	Q8K874 helicobact
Q8K884	helicobact	12	6	Q8K884	Q8K884 helicobact
Q8K894	helicobact	12	6	Q8K894	Q8K894 helicobact
Q8K904	helicobact	12	6	Q8K904	Q8K904 helicobact
Q8K914	helicobact	12	6	Q8K914	Q8K914 helicobact
Q8K924	helicobact	12	6	Q8K924	Q8K924 helicobact
Q8K934	helicobact	12	6	Q8K934	Q8K934 helicobact
Q8K944	helicobact	12	6	Q8K944	Q8K944 helicobact
Q8K954	helicobact	12	6	Q8K954	Q8K954 helicobact
Q8K964	helicobact	12	6	Q8K964	Q8K964 helicobact
Q8K974	helicobact	12	6	Q8K974	Q8K974 helicobact
Q8K984	helicobact	12	6	Q8K984	Q8K984 helicobact
Q8K994	helicobact	12	6	Q8K994	Q8K994 helicobact



Best Local Similarity 100.0%; Pred. No. 9,1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
Db 2 AKKK 5

## RESULT 2

Q9SQ16 PRELIMINARY; PRT: 15 AA.  
AC Q9SQ16  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)  
DE Translation elongation factor (Fraumeni).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzoideae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li Z.-Y., Chen S.-Y.;  
RT "Inducible expression of translation elongation factor 1A gene in rice seedlings in response to environmental stresses.";  
RL Acta Bot. Sin. 41:800-806(1999).  
DR EMBL: AF067195; AAC79991.1; -;  
DR Gramene: Q9SQ16; -;  
KW Elongation factor.  
FT NON\_TER  
SQ SEQUENCE 15 AA: 1514 MW: 95E5C46F069C9775 CRC64:

Query Match 36.4%; Score 4; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9,1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AKKK 4  
Db 12 AKKK 15

## RESULT 3

Q99MG3 PRELIMINARY; PRT: 5 AA.  
AC Q99MG3  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE NCAM protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA More M.I., Kirsch F.P., Rathjen F.G.;  
RT "Targeted ablation of Nrcam and ankyrin-8 results in disorganized lens fibres leading to cataract formation.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF346472; AAK25814.1; -;  
FT NON\_TER  
SQ SEQUENCE 9 AA: 1039 MW: 32FCB721E3333327 CRC64:

Query Match 27.3%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8,3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4  
Db 3 KKK 5

## RESULT 4

C9H4H5 PRELIMINARY; PRT: 11 AA.  
AC C9H4H5  
DT 01-MAR-2001 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE domain containing a zinc finger (domain).  
OS Homo sapiens (Homo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Skolnik D.;  
KL Submitted (01-MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF067195; AAC79991.1; -;  
FT NON\_TER  
SQ SEQUENCE 11 AA: 111 MW: 11272 MW: 662A4E29E5B4813 CRC64:

## Query Match

Best Local Similarity 100.0%; Pred. No. 9,1e+03; Length 11;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 6  
Db 7 KKK 9

## RESULT 5

C9V1XB PRELIMINARY; PRT: 12 AA.  
AC C9V1XB  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)  
DE LYSYL-PNA synthetase (fragment).  
OS Thermus thermophilus.  
OC Bacteria; Firmicutes; Thermoterrae; Thermococcales; Thermococcaceae; Thermococcus.  
OX NCBI\_TaxID=2244;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Spada S.;  
KL "Cloning and characterization of the gene for total cation-activated protein from T. thermophilus.";  
KL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF067195; AAC79991.1; -;  
FT NON\_TER  
SQ SEQUENCE 12 AA: 121 MW: 662A4E29E5B4813 CRC64:

## Query Match

Best Local Similarity 100.0%; Pred. No. 8,3e+03; Length 12;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 6  
Db 4 KKK 6

## RESULT 6

C25179 PRELIMINARY; PRT: 12 AA.  
AC C25179  
DT 01-JAN-1998 (TRENBLrel. 05, Created)  
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)

DE Hypothetical protein HP0429.  
GN HP0429.  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=26695 / ATCC 700392;  
RX MESLINE=97394467; PubMed=9252185;  
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.B.,  
RA Fleischmann R.D., Ketchum K.A., Kleck H.P., Gill S., Dougherty R.A.,  
RA Loftus B., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,  
RA Lioris H., Richardson D., Dodson R., Khalak H.G., Glodek A.,  
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Beckey E.K.,  
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,  
RA Colton M.D., Weidman J.M., Fujii C., Bowman C., Wattey L., Wallin F.,  
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,  
RA Venter J.C.;  
RT "The complete genome sequence of the gastric pathogen Helicobacter  
RT pylori.";  
RL Nature 388:539-547(1997).  
DR EMBL: AE000559; AA007512.1; .  
DR TIGR: HP0429; .  
KW Hypothetical protein: Complete proteome.  
SQ SEQUENCE 12 AA: 1375 MW: 20959AB4E21333B CRC64:

Query Match 27.38; Score 3; DB 16; Length 12;  
Best Local Similarity 100.0%; Pred. No. H. 0.03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKE 5  
DB III  
6 KKE 8

RESULT 7  
Q50117  
ID Q50117 PRELIMINARY; PRT: 13 AA.  
AC Q50117;  
DT 01-NOV-1996 (TrEMBLrel. 0); Created)  
DT 01-NOV-1996 (TrEMBLrel. 0); Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23; last annotation update)  
DE U650W.  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Smith D.R.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Robinson K.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U15184; AAA63055.1; .  
SQ SEQUENCE 13 AA: 1503 MW: CAARF1429DEP5412 CRC64:

Query Match 27.38; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. H. 0.03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RNA 11  
DB III  
7 RNA 9

RESULT 8  
Q9H4C1  
ID Q9H4C1 PRELIMINARY; PRT: 13 AA.  
AC Q9H4C1;  
DT 01-MAR-2001 (TrEMBLrel. 16; Created)

DE 01-MAR-2001 (TrEMBLrel. 16; last sequence update)  
DE 01-MAR-2001 (TrEMBLrel. 16; last annotation update)  
LE Androgen-binding protein  
OS ANGIOGENIN-2B  
GN HOMO SAPIENS  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Hominidae; Hominidae; Homo  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC METLINE=214444; PubMed=111111;  
RX Mezzapita R., Mezzapita R., Mezzapita R., Mezzapita R.,  
RA Villalpando X., Mezzapita R., Mezzapita R., Mezzapita R.,  
RT "Genomic structure and function of the gene encoding chicken androgen-  
RT binding protein.";  
RL Biochem. Biophys. Res. Commun. 214: 40-45(2000).  
DR EMBL: AL444444; .  
FT NON-REF  
SQ SEQUENCE 14 AA: 1066 MW: 15664.000000000000 CRC64:

Query Match 27.38; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. H. 0.03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKE 4  
DB III  
6 KKE 4

RESULT 9  
Q50117  
ID Q50117 PRELIMINARY; PRT: 13 AA.  
AC Q50117;  
DT 01-MAY-2000 (TrEMBLrel. 15; last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 15; last annotation update)  
DE 01-MAR-2003 (TrEMBLrel. 23; last annotation update)  
DE 01-MAR-2003 (TrEMBLrel. 23; last annotation update)  
OS 2003-03-03 (MAY-2000)  
OX Mycobacterium leprae  
OC Mycobacterium leprae  
OC Eukaryota; Vertebrata; Chordata; Vertebrata; Euteleostomi; Tardigrada;  
OC Spermatozoa; Mollusca; Mollusca; Mollusca; Mollusca; Mollusca;  
OC PAVAB; Chordata; Mollusca; Mollusca; Mollusca; Mollusca;  
OX NCBI\_TaxID=1769;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE: Skin  
RA TISSUE: Skin  
RT "Transcription of the 2' 3' 5' triphosphate plasmid.";  
RL Plant Mol Biol 10: 255-260(1987)  
DR EMBL: M16997; AAA63055.1; .  
KW Mitochondrion  
FT NON-REF  
SQ SEQUENCE 14 AA: 1066 MW: 15664.000000000000 CRC64:

Query Match 27.38; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. H. 0.03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKE 3  
DB III  
6 KKE 3

RESULT 10  
Q9H4C1  
ID Q9H4C1 PRELIMINARY; PRT: 13 AA.  
AC Q9H4C1;  
DT 01-MAR-2002 (TrEMBLrel. 23; last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 23; last annotation update)  
DE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
GN 75884  
OS Escherichia coli O157:H7

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=0157:H7 / EDL933 / ATCC 700927;  
 RA MEDLINE=21074935; PubMed=11206551;  
 RA Petra N.T., Plunkett G. III, Burland V., Mau R., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor C., Kirkpatrick B.A.,  
 RA Postai G., Hackett J., Klink S., Boutin A., Stao V., Miller S.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocitis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RL \*Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.\*;  
 RL Nature 409:529-533(2001).  
 DR EMBL: AE005659; AAG59469.1;  
 KW Hypothetical protein; Complete proteome.  
 SW SEQUENCE: 13 AA; 1520 MW; 4145922/44041877 bp44;

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKK 3  
 |||  
 DB 8 AKK 10

## RESULT 11

Q9UWM2 PRELIMINARY; PRI: 14 AA.  
 AC Q9UWM2;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DE L-glutamate:NAD(P)+ oxidoreductase (EC 1.4.1.4) (Fragment).  
 OS Pyrococcus furiosus.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=2261;  
 RN [1]  
 RC SEQUENCE.  
 RP MEDLINE=92247806; PubMed=1576153;  
 RA Robb F.T., Park J.B., Adams M.W.;  
 RT \*Characterization of an extremely thermostable glutamate  
 RT dehydrogenase; a key enzyme in the primary metabolism of the  
 RT hyperthermophilic archaeobacterium, Pyrococcus furiosus.\*;  
 RL Biochim. Biophys. Acta 1120:267-272(1992).  
 SW SEQUENCE: 14 AA; 1684 MW; 1E8F0506R25550B CR664;

Query Match 27.3% Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KEQ 5  
 |||  
 DB 2 KEQ 4

## RESULT 12

Q56750 PRELIMINARY; PRI: 14 AA.  
 AC Q56750;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 01, Last annotation update)  
 DE Ribosomal protein S19 (Fragment).  
 OS Western x phytoplasmatales.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Phytoplasma.  
 OX NCBI\_TaxID=37704;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=4308747; PubMed=1101100;  
 RA Gundersen L.F., Davis K.E., Kinsbury R.E.;  
 RT \*Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for  
 RT their classification.\*;  
 RL J. Bacteriol. 174:1144-1149(1992).  
 DR EMBL: L22013; AAA55114;  
 SW SEQUENCE: 14 AA; 177 MW; 133181F41E1FA3 CR664;  
 Query Match 27.3% Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKK 3  
 |||  
 DB 8 AKK 10

## RESULT 13

Q56750 PRELIMINARY; PRI: 14 AA.  
 AC Q56750;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DE L-glutamate:NAD(P)+ oxidoreductase (EC 1.4.1.4) (Fragment).  
 OS Pyrococcus furiosus.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
 OC Pyrococcus.  
 OX NCBI\_TaxID=2261;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RP MEDLINE=92247806; PubMed=1576153;  
 RA Gundersen L.F., Davis K.E., Kinsbury R.E.;  
 RT \*Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for  
 RT their classification.\*;  
 RL J. Bacteriol. 174:1144-1149(1992).  
 DR EMBL: L22013; AAA55114;  
 SW SEQUENCE: 14 AA; 177 MW; 133181F41E1FA3 CR664;  
 Query Match 27.3% Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8; E=0.0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKK 3  
 |||  
 DB 8 AKK 10

## RESULT 14

Q56750 PRELIMINARY; PRI: 14 AA.  
 AC Q56750;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 01, Last annotation update)  
 DE Mitochondrial cytochrome c oxidase (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eucarya; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=2142915; PubMed=1140044;  
 RA Komachi N., Sano T., Yoshida M., Matsui M., Kaida M., Higa S.,  
 RA Katanabe K., Tanaka T.;  
 RT \*The human mitochondrial ribosomal protein genes: Mapping of 14 genes  
 RT to the chromosomes and implications for human disorders.\*;  
 RL Genes 27:157-163(1991).  
 DR EMBL: AB01623; BAB5195.1;  
 KW Ribosomal Protein.



Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQ 6  
DB 13 KEQ 15

## RESULT 19

Q9UCN2 PRELIMINARY: PRT; 15 AA.  
AC Q9UCN2; 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)  
DE Fructose-1,6-bisphosphate aldolase A (EC 4.1.2.13) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92353128; PubMed=1353685;  
RA Lee K.N., Maxwell M.D., Patterson M.K.Jr., Birckbichler P.J., Conway E.;  
RT "Identification of transglutaminase substrates in HT29 colon cancer cells: use of 5-(biotinamido)pentylamine as a transglutaminase-specific probe."  
RL Biochim. Biophys. Acta 1135:12-16(1992).  
DR HSSP: P04075; 2ALD.  
SQ SEQUENCE 15 AA; 1805 MW; 8D07536D1FC03F61 CRC64;

Query Match 27.38; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKE 5  
DB 12 KKE 14

## RESULT 20

Q81Z00 PRELIMINARY: PRT; 15 AA.  
AC Q81Z00; 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Protein kinase A catalytic subunit beta (Fragment).  
GN PKACR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wu K.-J., Mattioli M., Morse H.C., Galla-Ravera R.;  
RT "c-MYC activates protein kinase A (PKA) by direct transcriptional activation of the PKA catalytic subunit beta (PAA- $\beta$ ) gene."  
RL Oncogene 0:0-0(2002).  
DR EMBL: AF538872; AAN16454.1; .  
KW Kinase.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1480 MW; 52FE5695C19R70A CRC64;

Query Match 27.38; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
DB 7 AKK 9

## RESULT 21

Q9TW34 PRELIMINARY: PRT; 15 AA.  
AC Q9TW34; 01-MAY-2000 (TRENBLrel. 14, Created)  
DT 01-MAY-2000 (TRENBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE KINA-binding protein (Fragment).  
OS Crithidia fasciculata.  
OC Eukaryota; Excavaria; Kinetoplastida; Trypanosomatidae; Crithidia.  
OX NCBI\_TaxID=5656;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93249912; PubMed=852495;  
RA Tiliawalla I.;  
RT "Identification of cDNA encoding proteins in the parasitic protozoan Crithidia fasciculata and evidence for their association with the mitochondrial genome."  
RL Exp. Cell. Res. 200:145-151(1999).  
DR EXP. CELL. RES. 200:145-151(1999).  
SQ SEQUENCE 15 AA; 1453 MW; 3D93552569B27D CRC64;

Query Match 27.14; Score 3; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3  
DB 14 AKK 15

## RESULT 22

P42207 PRELIMINARY: PRT; 15 AA.  
AC P42207; 01-SEP-2001 (TRENBLrel. 14, Created)  
DT 01-SEP-2001 (TRENBLrel. 14, Last sequence update)  
DT 01-SEP-2001 (TRENBLrel. 14, Last annotation update)  
DE Unknown protein from sheep (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuidae;  
OX NCBI\_TaxID=7943;  
RN [1]  
RP SEQUENCE.  
RX STRAIN XINGANG X KEMING; TISSUE Body wall, and Fat body;  
RX MEDLINE=3117483; PubMed=11280904;  
RA Zhouo B.X.;  
RT "Protein database for several tissues derived from five instar of silkworm."  
RL J. Mol. Biol. 306:227-228(2001).  
DR NLS TER 15  
SQ SEQUENCE 15 AA; 1623 MW; 58F6B4766A75C CRC64;

Query Match 27.06; Score 3; DB 5; Length 15;

Best Local Similarity 100.0%; Pred. No. 9, Re+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QKQ 8  
DB 3 QKQ 9

## RESULT 23

Q9TR45 PRELIMINARY: PRT; 15 AA.  
AC Q9TR45; 01-MAY-2000 (TRENBLrel. 14, Created)  
DT 01-MAY-2000 (TRENBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE Amphoterin (Amphotericin).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96029671; PubMed=7592757;
RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
RA Nagashima M., Lundh E.R., Vijay S., Niecek D.,
RT "The receptor for advanced glycation end products (RAGE) is a cellular
RT binding site for amphoterin. Mediation of neurite outgrowth and co-
RT expression of rage and amphoterin in the developing nervous system.";
RL J. Biol. Chem. 270:25752-25761(1995).
SQ SEQUENCE 15 AA; 1757 MW; 390B9679501CE020 CRC64;

Query Match 27.38; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
DB 11 KKK 13

RESULT 24
Q9S8F1 PRELIMINARY; PRT; 15 AA.
ID 01-JUN-2000 (TrEMBLrel. 13, Created)
AC Q9S8F1;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Glutathione S-transferase isoform II (EC 2.5.1.16) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RX MEDLINE=95322859; PubMed=7599527;
RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,
RA Greenland A.J.;
RT "Characterization of the safener-induced glutathione S-transferase
RT isoform II from maize.";
RL Planta 196:295-302(1995).
SQ SEQUENCE 15 AA; 1530 MW; 2F105C48F7D3A56 CRC64;

Query Match 27.38; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQ 6
DB 13 KEQ 15

RESULT 25
P82431 PRELIMINARY; PRT; 15 AA.
ID P82431;
AC P82431;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 100 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Holwell G.P.;

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```

RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco cultured.";
RL Planta 199:1(2000).
OX NCBI_TaxID=9913;
RN [1]
RP SUBCELLULAR LOCATION: CELL WALL.
OC 01-TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON-TER 15
SQ SEQUENCE 15 AA; 1530 MW; 54-00-25-4E-14-76-26 CRC64;

Query Match 27.38; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
DB 4 KKK 4

RESULT 26
P82431 PRELIMINARY; PRT; 15 AA.
ID P82431;
AC P82431;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 100 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Holwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco cultured.";
RL Planta 199:1(2000).
OX NCBI_TaxID=9913;
RN [1]
RP SUBCELLULAR LOCATION: CELL WALL.
OC 01-TISSUE SPECIFICITY: XYLEM.
KW Cell wall; Hydroxylation.
FT NON-TER 15
SQ SEQUENCE 15 AA; 1530 MW; 54-00-25-4E-14-76-26 CRC64;

Query Match 27.38; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 4
DB 11 KKK 13

RESULT 27
Q9R712 PRELIMINARY; PRT; 15 AA.
ID Q9R712;
AC Q9R712;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 100 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97361202; PubMed=8936242;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Hirao A.,

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RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kawai K., Koshimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.,
RT "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT to the 12.7-28.0 min Region on the Linkage Map."
RL DNA Res. 3:137-155(1996).
DR EMBL: D90705; BAA3510.1;
DR KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 8 AA; 964 MW; DF133B1F0045476A CR664;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KE 5
DB 7 KE 8

RESULT 28
Q9AGP4
ID Q9AGP4 PRELIMINARY; PRT; 8 AA.
AC Q9AGP4
DT 01-JUN-2001 (TREMHLrel. 17, Created)
DT 01-JUN-2001 (TREMHLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMHLrel. 20, Last annotation update)
DE Serine hydroxymethyltransferase (Fragment).
GN GLYA.
OS
OC Arthrobacter sp. LIN.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Arthrobacteraceae.
OX NCBI_TaxID=153502;
RN [1]
RC STRAIN=LIN.
RA Meskys R., Harris R.J., Casalte V., Hassan J., Scrutton N.S.
RT "Genetic organization of the genes involved in dimethylglycine and
RT sarcosine degradation in Arthrobacter spp.: implications for glycine
RT betaine catabolism."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF329478; AAK16486.1;
DR KW Methyltransferase; Transferase.
FT NON_TER
SQ SEQUENCE 8 AA; 898 MW; 5B1870533372457 CR664;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 4 KE 5

RESULT 24
Q93SR0
ID Q93SR0 PRELIMINARY; PRT; 8 AA.
AC Q93SR0
DT 01-DEC-2001 (TREMHLrel. 19, Created)
DT 01-DEC-2001 (TREMHLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMHLrel. 19, Last annotation update)
DE Beta-lactamase repressor Blal (Fragment).
GN BLAI.
OS Staphylococcus epidermidis.
OG Plasmid pST6.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RC STRAIN=6;

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RA Slime M.S., Best L., Scrutton N.S., Scrutton N.S., Scrutton N.S.,
RA "Genetic Linkage Map of the Genetically Defined Food Spoilage
RA Resistant Strain of Escherichia coli O157:H7."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF262729; AAK04472;
DR KW Endonuclease.
FT NON_TER
SQ SEQUENCE 8 AA; 4564 MW; 4F66766A54472B CR664;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 4
DB 7 KE 8

RESULT 40
Q9XK1
ID Q9XK1 PRELIMINARY; PRT; 8 AA.
AC Q9XK1
DT 01-NOV-2001 (TREMHLrel. 12, Created)
DT 01-NOV-2001 (TREMHLrel. 12, Last sequence update)
DT 01-NOV-2001 (TREMHLrel. 12, Last annotation update)
DE Proteobacterium sp. (Sequence)
GN PFT5.
OS
OC Proteobacteria; Sphingobacteriales; Sphingobacteriaceae;
OC Proteobacteria; Sphingobacteriales; Sphingobacteriaceae.
OX NCBI_TaxID=1223;
RN [1]
RC STRAIN=FROM N.A.
RA Scrutton N.S., Scrutton N.S., Scrutton N.S., Scrutton N.S.,
RT "Genetic diversity in Proteobacteria: Proteobacteria: Proteobacteria:
RT sorted from the Sphingobacteriales: Sphingobacteriales:
RL Local Similarity 100.0%; Pred. No. 8.3e-05;
DR EMBL: AF262729; AAK04472;
FT NON_TER
SQ SEQUENCE 8 AA; 100 MW; 1000000000000000 CR664;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KE 8
DB 1 KE 2

RESULT 31
Q56429
ID Q56429 PRELIMINARY; PRT; 8 AA.
AC Q56429
DT 01-NOV-1996 (TREMHLrel. 4, Created)
DT 01-NOV-1996 (TREMHLrel. 4, Last sequence update)
DT 01-DEC-2001 (TREMHLrel. 19, Last annotation update)
DE SAOR (Fragment)
OS
OC Bacteria; Proteobacteria; Sphingobacteriales; Sphingobacteriaceae;
OX NCBI_TaxID=1223;
RN [1]
RC STRAIN=FROM N.A.
RA Scrutton N.S., Scrutton N.S., Scrutton N.S., Scrutton N.S.,
RT "Genetic diversity in Proteobacteria: Proteobacteria: Proteobacteria:
RL Local Similarity 100.0%; Pred. No. 8.3e-05;
DR EMBL: AF262729; AAK04472;
FT NON_TER
SQ SEQUENCE 8 AA; 100 MW; 1000000000000000 CR664;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KE 8
DB 1 KE 2

RESULT 31
Q56429
ID Q56429 PRELIMINARY; PRT; 8 AA.
AC Q56429
DT 01-NOV-1996 (TREMHLrel. 4, Created)
DT 01-NOV-1996 (TREMHLrel. 4, Last sequence update)
DT 01-DEC-2001 (TREMHLrel. 19, Last annotation update)
DE SAOR (Fragment)
OS
OC Bacteria; Proteobacteria; Sphingobacteriales; Sphingobacteriaceae;
OX NCBI_TaxID=1223;
RN [1]
RC STRAIN=FROM N.A.
RA Scrutton N.S., Scrutton N.S., Scrutton N.S., Scrutton N.S.,
RT "Genetic diversity in Proteobacteria: Proteobacteria: Proteobacteria:
RL Local Similarity 100.0%; Pred. No. 8.3e-05;
DR EMBL: AF262729; AAK04472;
FT NON_TER
SQ SEQUENCE 8 AA; 100 MW; 1000000000000000 CR664;

```

Query Match 18.2% Score 2: DB 2: Length 8:  
Best Local Similarity 100.0%: Pred. No. 8.4e-05:  
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KK 3  
DB 5 KK 6

## RESULT 32

Q9R9E0 ID Q9R9E0 PRELIMINARY: PRT: 8 AA.  
AC Q9R9E0:  
DT 01-MAY-2000 (TREMREL: 13, Created)  
DT 01-MAY-2000 (TREMREL: 13, Last sequence update)  
DT 01-MAY-2000 (TREMREL: 13, Last annotation update)  
DE Stage V sporulation protein E (Fragment)  
GN SPOVE.  
OS Bacillus subtilis.  
OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus  
CX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=93003529; PubMed=1391053;  
RA Henriques A.O., de Lencastre H., Pignot F.J.,  
RT "A Bacillus subtilis morphogenic cluster that includes *spoVE* is  
RT homologous to the *mra* region of *Escherichia coli*."  
RL Biochimie 74:735-748(1992).  
DR EMBL: X64258; CAA45556.1;  
FT NON\_TER 8  
SQ SEQUENCE 8 AA: 893 MW: 8755AIAAAG121HIAE (P064)

Query Match 18.2% Score 2: DB 2: Length 8:  
Best Local Similarity 100.0%: Pred. No. 8.4e-05:  
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KK 3  
DB 4 KK 5

## RESULT 33

Q9R5R0 ID Q9R5R0 PRELIMINARY: PRT: 8 AA.  
AC Q9R5R0:  
DT 01-MAY-2000 (TREMREL: 13, Created)  
DT 01-MAY-2000 (TREMREL: 13, Last sequence update)  
DT 01-JUN-2002 (TREMREL: 21, Last annotation update)  
DE 11,500 DA product of ORF4 (Fragment).  
OS Shigella dysenteriae.  
OC Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;  
CX NCBI\_TaxID=622;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92085268; PubMed=1660923;  
RA Polard P., Prere M.F., Chandler M., Fayat G.  
RT "Programmed translational frameshifting and tailoring of an *Adi* codes  
RT in gene expression of bacterial insertion sequence IS1111."  
RL J. Mol. Biol. 222:465-477(1991).  
FT NON\_TER 8  
SQ SEQUENCE 8 AA: 935 MW: 9405B9C45A5A5446 (P064)

Query Match 18.2% Score 2: DB 2: Length 8:  
Best Local Similarity 100.0%: Pred. No. 8.4e-05:  
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KK 3  
DB 2 KK 3

## RESULT 34

Q94S4 ID Q94S4 PRELIMINARY: PRT: 8 AA.  
AC Q94S4:  
DT 01-DEC-2001 (TREMREL: 13, Created)  
DT 01-DEC-2001 (TREMREL: 13, Last sequence update)  
DT 01-DEC-2001 (TREMREL: 13, Last annotation update)  
LE Word protein (Fragment)  
GN MPEO.  
OS *Thiobacillus* *ferrooxidans*  
OC Bacteria: Acidithiobacterales; Acidithiobacteriales;  
CX NCBI\_TaxID=92;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=93003529; PubMed=1391053;  
RA Henriques A.O., de Lencastre H., Pignot F.J.,  
RT "A Bacillus subtilis morphogenic cluster that includes *spoVE* is  
RT homologous to the *mra* region of *Escherichia coli*."  
RL Biochimie 74:735-748(1992).  
DR EMBL: X64258; CAA45556.1;  
FT NON\_TER 8  
SQ SEQUENCE 8 AA: 893 MW: 8755AIAAAG121HIAE (P064)

Query Match 18.2% Score 2: DB 2: Length 8:  
Best Local Similarity 100.0%: Pred. No. 8.4e-05:  
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KK 3  
DB 2 KK 3

## RESULT 35

Q9154 ID Q9154 PRELIMINARY: PRT: 8 AA.  
AC Q9154:  
DT 01-NOV-1996 (TREMREL: 13, Created)  
DT 01-NOV-1996 (TREMREL: 13, Last sequence update)  
DT 01-DEC-2001 (TREMREL: 13, Last annotation update)  
DE Copper protein (Fragment)  
OS *Escherichia coli*  
CX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=93003529; PubMed=1391053;  
RA Henriques A.O., de Lencastre H., Pignot F.J.,  
RT "A Bacillus subtilis morphogenic cluster that includes *spoVE* is  
RT homologous to the *mra* region of *Escherichia coli*."  
RL Biochimie 74:735-748(1992).  
DR EMBL: X64258; CAA45556.1;  
FT NON\_TER 8  
SQ SEQUENCE 8 AA: 893 MW: 8755AIAAAG121HIAE (P064)

Query Match 18.2% Score 2: DB 2: Length 8:  
Best Local Similarity 100.0%: Pred. No. 8.4e-05:  
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KK 3  
DB 2 KK 3

## RESULT 36

Q94R8 ID Q94R8 PRELIMINARY: PRT: 8 AA.  
AC Q94R8:  
DT 01-MAY-2000 (TREMREL: 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Aminopectidase B (Fragment).  
 OS Eukaryotes cerevisiae (Baker's Yeast).  
 OC Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92088139; PubMed=1750699;  
 RA Kassel D.B., Williams K.P., Musselman B.D., Smith J.A.;  
 RT "Optimization of the fragmentation in a frit-fast atom bombardment ion  
 source for the sequencing of peptides at the picomole level".  
 RL Anal. Chem. 63:1978-1983(1991).  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 8  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 772 MW; 783DDAADC2C732C8 CRC64;

Query Match 18.2%; Score 2; DR 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2  
 DB 7 AK 8

## RESULT 17

Q16468  
 ID Q16468 PRELIMINARY; PRT: 8 AA.  
 AC Q16468;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE DNA for cosmid cCl3-1134 PCR primer 1 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96435920; PubMed=8638806;  
 RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,  
 RA Anand R.;  
 RT "Walking, cloning and mapping with YACs in 3p27. Localisation of 5  
 ESTs including 3 members of the Cystatin gene family and  
 RT identification of CpG islands.";  
 RL Genomics 32:425-430(1996).  
 DR EMBL: X88976; CAA61407.1;  
 FT NON\_TER 8  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 925 MW; FD5411A7376871E6 CRC64;

Query Match 18.2%; Score 2; DR 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RN 10  
 DB 7 RN 8

## RESULT 38

Q9UCN4  
 ID Q9UCN4 PRELIMINARY; PRT: 8 AA.  
 AC Q9UCN4;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE Cell-surface heparin/HEPARANSULFATE-binding protein peptide 3  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92291766; PubMed=11118623  
 RA Hubbard N.J., Lim E., Huber R., Carson D.D.  
 RT "Identification of a surface heparin/heparan sulfate-binding  
 RI protein of a viral glycoprotein cell line (RG-95)."  
 RL J. Biol. Chem. 267:11595-11597(1992).  
 SQ SEQUENCE 5 AA; 140 MW; 50E334C140E87D CRC64;

Query Match 16.2%; Score 2; DR 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2  
 DB 1  
 DB 1 AK 4

## RESULT 49

Q8404  
 ID Q8404 PRELIMINARY; PRT: 8 AA.  
 AC Q8404;  
 DT 01-MAR-2001 (Tremblrel. 10, Created)  
 DT 01-MAR-2001 (Tremblrel. 10, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 10, Last annotation update)  
 DE LIM domain only; Protease (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE:Blood;  
 RA Bruckner T., Wirtz-Pepper A., Hunkeler T., Schmidt F., Zebeli A.H.;  
 RT "Human PAC clone 8017448029 (p11 781K3), sequenced in BACP project  
 RT (Comparative Sequencing of 4.1 Mb Region in Man (Chromosome 3p11) and  
 RT Mouse (Chromosome 7))."  
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ277611; CAA34474.1;  
 FT NON\_TER 8  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 961 MW; F4A134AA7420596 CRC64;

Query Match 16.2%; Score 2; DR 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 4  
 DB 1 AK 7

## RESULT 40

Q81VK3  
 ID Q81VK3 Peptide; Metazoa; 1 AA; 8 AA.  
 AC Q81VK3;  
 DT 01-MAR-2001 (Tremblrel. 25, Created)  
 DT 01-MAR-2001 (Tremblrel. 25, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 25, Last annotation update)  
 DE Steeplez (Fragment).  
 GN STEEPLZ.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Peeters P., Verhasselt P., Moelsters D.W., Luyten W.H.M.;  
 RA Geysen J.C.G.H.;  
 RT "Sensor neural detects in vivo hypomorphia for a mammalian homolog of  
 RT unc-53.";  
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ488208; CAD32561.1; -  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;

Query Match 18.2% Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 RN 10  
 II  
 DB 5 RN 5

## RESULT 41

Q8MUN6 PRELIMINARY: PRT; 8 AA.  
 AC Q8MUN6  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN MPI.  
 OS Heliconius melpomene melpomene.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius  
 OX NCBI\_TaxID=171917;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=STRI-B-441-Mpi-2;  
 RA Bull V., Beltran M., Birmingham E., Jiggins C., McMillan C.,  
 RA Mallet J.;  
 RT "Molecular evidence for gene flow between species of Heliconius";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF516247; AAM61933.1; -  
 KW Isomerase.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 977 MW; 16E736DB100:EAA3 CRC64;

Query Match 18.2% Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 RN 6  
 II  
 DB 5 RN 6

## RESULT 42

Q9N6M5 PRELIMINARY: PRT; 8 AA.  
 AC Q9N6M5  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Dihydrofolate reductase thymidylate synthase (Fragment).  
 GN POLI.  
 OS Toxoplasma gondii.  
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;  
 OC Toxoplasma  
 OX NCBI\_TaxID=5811;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RH, COUGAR TC751034, SEA OTTER TC82801, and HEVEXLEY;  
 RA Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;  
 RT "Strain Typing of Toxoplasma gondii: Comparison of Antigen-Coding and  
 RT Housekeeping Genes";  
 RL J. Parasitol. 0:0-0(2000).  
 DR EMBL: AF249695; AAF79153.1; -  
 DR EMBL: AF249692; AAF79150.1; -  
 DR EMBL: AF249693; AAF79151.1; -  
 DR EMBL: AF249694; AAF79152.1; -

FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 1030 MW; 4CAAAA50131644 CRC64;

Query Match 14.2% Score 2; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RN 5  
 II  
 DB 4 RN 4

## RESULT 43

Q1885A PRELIMINARY: PRT; 8 AA.  
 AC Q1885A  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Eukaryotic Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OS Canis familiaris (dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteleostomi; Carnivora; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC "A human PCR/PCR product of the canine T cell antigen gene";  
 RE Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF044717; AAF04471.1; -  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 862 MW; 20CAAAHPT125A7 CRC64;

Query Match 14.2% Score 2; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RN 5  
 II  
 DB 4 RN 4

## RESULT 44

Q45M23 PRELIMINARY: PRT; 8 AA.  
 AC Q45M23  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Na+/K+ ATPase alpha subunit (EF 4.6.1.37) (Fragment).  
 GN ATPAL.  
 OS Sus scrofa (pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteleostomi; Artiodactyla; Suidae; Sus.  
 OX NCBI\_TaxID=4823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PIR123;  
 RA Blazkova P., Stratil A., Beebe M., Van Poucke M., Reiner G.,  
 RA Geldermann H., Kopecky M.;  
 RT "PH mapping of the porcine ATPAL, ATPAL1, V-ATPase, IVL genes and  
 RT linkage assignments of ATPAL and IVL to chromosome 4";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ344138; GAF5422.1; -  
 KW Hydrolase  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 1137 MW; 664H41AR133R02D3 CRC64;

Query Match 14.2% Score 2; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KE 5  
II  
DB 4 KE 5

## RESULT 45

O19957 PRELIMINARY; PRT; 8 AA.  
AC O19957;  
DT 01-JAN-1998 (TRENBLrel. 05, Created)  
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE Ribosomal protein L16 (fragment).  
GN RPL16.  
OS Gossypium hirsutum (Upland cotton).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
OX NCBI\_TaxID=3635;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.:  
RT "The tortoise and the hare: choosing between noncoding plastome and  
RT nuclear Adh sequences for phylogeny reconstruction in a recently  
RT diverged plant group."  
RL Am. J. Bot. 85:1301-1315(1998).  
DR EMBL: AF031452; AAC63546.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 971 MW; 71B5B73404540327 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 9 RN 10  
II  
DB 3 RN 4

## RESULT 46

Q36898 PRELIMINARY; PRT; 8 AA.  
AC Q36898;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)  
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)  
DE RPS19' protein (fragment).  
GN RPS19'.  
OS Nicotiana glauca, and  
OS Nicotiana glauca (Bigelov's tobacco).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=49453, 4088;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.:  
RL Mol. Gen. Genet. 0:0-0(1996).  
DR EMBL: Z71234; CAA94933.1; -.  
DR EMBL: Z71225; CAA94921.1; -.  
KW Chloroplast.  
FT NON\_TER 8 8  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 977 MW; FD43333735A411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 2 KK 5  
II  
DB 6 KK 7

## RESULT 47

O41002 PRELIMINARY; PRT; 8 AA.  
AC O41002;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
DE Cytochrome c oxidase subunit 1 (fragment).  
OS Terranatos dolichopterus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neoptera; Teleostei; Euteleostei; Neopteleostei;  
OC Actinopterygii; Atherinomorpha; Atherinomorpha; Atherinomorpha;  
OC Cyprinodontiformes; Aplocheilichthys; Aplocheilichthys;  
OX NCBI\_TaxID=61800;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Urbek T., Larsen A.  
RT "The evolution of diapause in the killifish family Rivulidae  
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and  
RT biogeographic perspective."  
RL Evolution 53:229-233(1999).  
DR EMBL: AF024242; AAC00411.1; -.  
KW Mitochondrion.  
FT NON\_TER 8 8  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 1062 MW; F009040B944056 CRC64;

Query Match 14.2%; Score 2; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 15 NA 11  
DB 4 NA 4

## RESULT 48

Q37854 PRELIMINARY; PRT; 8 AA.  
AC Q37854;  
DT 01-MAY-1996 (TRENBLrel. 01, Created)  
DT 01-MAY-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 17, Last annotation update)  
DE Coliphage genome of unknown function, 5' end (fragment).  
OS Bacteriophage P1.  
OX Viruses; SSENA positive-stranded DNA virus, no DNA stage; Leviviridae;  
OX Levivirus.  
OX NCBI\_TaxID=12426;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 7324673; PubMed 456723.  
RA Bonding R.F.E.  
RT "A sequence of genomic DNA nucleotides from the Coliphage P1  
RT genome."  
RL Houghton J., Bonding R.F.E. (1973).  
DR EMBL: M24826; AAA22765.1; -.  
FT NON\_TER 8 8  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 967 MW; EM4541233E72726 CRC64;

Query Match 18.2%; Score 2; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 9 RN 10  
II  
DB 6 RN 7

Wed Oct 1 09:04:40 2003

## RESULT 49

Q99NX9  
ID Q99NX9 PRELIMINARY; PRT: 8 AA.  
AC Q99NX9;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Amyloid beta protein (fragment).  
GN APP.  
OS Hydrochoerus hydrochaeris (Capybara) (Carpinche).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Hydrochaeridae;  
OC Hydrochaeris.  
OX NCBI\_TaxID=10149;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21082082; PubMed=11214319;  
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
O'Brien S.J.;  
RT "Molecular phylogenetics and the origins of proboscideans";  
RL Nature 409:614-618(2001).  
DR FMBL; AY011342; AAG47377.1;  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 1071 MW; 13560686DB19C9C3 26064;

Query Match 18.2%; Score 2; DB 11; Length 8;  
Best local Similarity 100.0%; Pred. No. 8, 3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EQ 6  
DB 4 EQ 5

## RESULT 50

Q62721  
ID Q62721 PRELIMINARY; PRT: 8 AA.  
AC Q62721;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Prohibitin (fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Fisher;  
RX MEDLINE=95331633; PubMed=7607556;  
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.L., Friedman V.,  
Henderson T., Owens G.A., Danner D.H., Jupp E.B., DelGioco R.T.,  
McClung J.K.;  
RT "Regions of evolutionary conservation between the rat and human  
prohibitin-encoding genes.";  
RL Gene 158:291-294(1995).  
DR FMBL; U17178; AAA86692.1;  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1150 MW; EFD3237805A41376 38064;

Query Match 18.2%; Score 2; DB 11; Length 8;  
Best local Similarity 100.0%; Pred. No. 6, 3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KQ 8  
DB 7 KQ 8

Search completed: September 30, 2003, 17:24:05  
Job time : 110 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 17:21:07 : Search time 28 seconds  
(without alignments)  
16,622 Million cell updates/sec

Title: US-09-787-443-20  
Perfect score: 11  
Sequence: 1 AKKEOKQRNA 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext: 50.0

Searched: 328717 seqs, 4210853 residues

Word size: 0

Total number of hits satisfying chosen parameters: 38154

Minimum DH seq length: 8  
Maximum DH seq length: 15

Post-processing: Listing first 500 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 2: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 3: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 4: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 5: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*
- 6: /cgn2\_6/protdata/1/iaa/IA\_OMP pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	4	36.4	8	US-08-160-604.7	Sequence 7, Appl
2	4	36.4	8	US-08-160-604.8	Sequence 8, Appl
3	4	36.4	8	US-08-160-604.9	Sequence 9, Appl
4	4	36.4	8	US-08-160-604.10	Sequence 10, Appl
5	4	36.4	8	US-08-160-604.11	Sequence 11, Appl
6	4	36.4	8	US-08-160-604.12	Sequence 12, Appl
7	4	36.4	8	US-08-160-604.13	Sequence 13, Appl
8	4	36.4	8	US-08-160-604.14	Sequence 14, Appl
9	4	36.4	8	US-08-160-604.15	Sequence 15, Appl
10	4	36.4	8	US-08-160-604.16	Sequence 16, Appl
11	4	36.4	8	US-08-160-604.17	Sequence 17, Appl
12	4	36.4	8	US-08-160-604.18	Sequence 18, Appl
13	4	36.4	8	US-08-160-604.19	Sequence 19, Appl
14	4	36.4	10	US-08-213-897A.18	Sequence 20, Appl
15	4	36.4	10	US-08-213-897A.19	Sequence 21, Appl
16	4	36.4	10	US-08-213-897A.20	Sequence 22, Appl
17	4	36.4	10	US-08-213-897A.21	Sequence 23, Appl
18	4	36.4	10	US-08-213-897A.22	Sequence 24, Appl
19	4	36.4	11	US-08-213-897A.23	Sequence 25, Appl
20	4	36.4	11	US-08-213-897A.24	Sequence 26, Appl
21	4	36.4	11	US-08-213-897A.25	Sequence 27, Appl
22	4	36.4	12	US-08-369-643.88	Sequence 28, Appl
23	4	36.4	12	US-08-369-643.89	Sequence 29, Appl
24	4	36.4	12	US-08-369-643.90	Sequence 30, Appl
25	4	36.4	12	US-08-369-643.91	Sequence 31, Appl
26	4	36.4	12	US-08-369-643.92	Sequence 32, Appl
27	4	36.4	12	US-08-369-643.93	Sequence 33, Appl









1 APPLICATION NUMBER: US 07/472,947  
2 FILING DATE: 31-JAN-1990  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Pabst, Patrea L.  
5 REGISTRATION NUMBER: 31,284  
6 REFERENCE/DOCKET NUMBER: OMRP114CIP(3)  
7 TELEPHONE: (404)-815-6508  
8 TELEFAX: (404)-815-6555  
9 INFORMATION FOR SEQ ID NO: 7:  
10 SEQUENCE CHARACTERISTICS:  
11 LENGTH: 8 amino acids  
12 TYPE: amino acid  
13 STRANDEDNESS: single  
14 TOPOLOGY: linear  
15 MOLECULE TYPE: peptide  
16 HYPOTHETICAL: NO  
17 ANTI-SENSE: NO  
18 FRAGMENT TYPE: N-terminal  
19 US-08-160-604-7

Query Match: 36.4%, Score 4, 165 G, Length 8:  
Best Local Similarity 100.0%, Pred. No. 2, 564, 45:  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEQK 7  
111  
Db 5 KEQK 8

RESULT 2  
US-08-160-604-8  
1 Sequence 8, Application US/08160604  
2 Patent No. 5232522  
3 GENERAL INFORMATION:  
4 APPLICANT: Harley, John  
5 APPLICANT: James, Judith A.  
6 APPLICANT: Scofield, R. H.  
7 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
8 NUMBER OF SEQUENCES: 127  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: Patrea L. Pabst  
11 STREET: 1100 Peachtree Street, Suite 2830  
12 CITY: Atlanta  
13 STATE: Georgia  
14 COUNTRY: USA  
15 ZIP: 30309-4530  
16 COMPUTER READABLE FORM:  
17 MEDIUM TYPE: Floppy disk  
18 COMPUTER: IBM PC Compatible  
19 OPERATING SYSTEM: PC-DOS/MS-DOS  
20 SOFTWARE: PatentIn Release #1.0, Version #1.25  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/08/160,604  
23 FILING DATE: 30-NOV-1993  
24 CLASSIFICATION: 424  
25 PRIOR APPLICATION DATA:  
26 APPLICATION NUMBER: US 07/867,819  
27 FILING DATE: 13-APR-1992  
28 PRIOR APPLICATION DATA:  
29 APPLICATION NUMBER: US 07/648,205  
30 FILING DATE: 31-JAN-1991  
31 PRIOR APPLICATION DATA:  
32 APPLICATION NUMBER: US 07/472,947  
33 FILING DATE: 31-JAN-1990  
34 ATTORNEY/AGENT INFORMATION:  
35 NAME: Pabst, Patrea L.  
36 REGISTRATION NUMBER: 31,284  
37 REFERENCE/DOCKET NUMBER: OMRP114CIP(3)  
38 TELECOMMUNICATION INFORMATION:  
39 TELEPHONE: (404)-815-6508  
40 TELEFAX: (404)-815-6555  
41 INFORMATION FOR SEQ ID NO: 8:

1 SEQUENCE CHARACTERISTICS  
2 LENGTH: 8 amino acids  
3 TYPE: amino acid  
4 STRANDEDNESS: single  
5 TOPOLOGY: linear  
6 MOLECULE TYPE: peptide  
7 HYPOTHETICAL: NO  
8 ANTI-SENSE: NO  
9 FRAGMENT TYPE: N-terminal  
10 US-08-160-604-8  
11 Query Match: 36.4%, Score 4, 165 G, Length 8:  
12 Best Local Similarity 100.0%, Pred. No. 2, 564, 45:  
13 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
14 QY 4 KEQK 7  
15 111  
16 Db 4 KEQK 8  
17 RESULT 3  
18 US-08-160-604-9  
19 Sequence 9, Application US/08160604  
20 Patent No. 5232522  
21 GENERAL INFORMATION:  
22 APPLICANT: Harley, John  
23 APPLICANT: James, Judith A.  
24 APPLICANT: Scofield, R. H.  
25 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
26 NUMBER OF SEQUENCES: 127  
27 CORRESPONDENCE ADDRESS:  
28 ADDRESSEE: Patrea L. Pabst  
29 STREET: 1100 Peachtree Street, Suite 2830  
30 CITY: Atlanta  
31 STATE: Georgia  
32 COUNTRY: USA  
33 ZIP: 30309-4530  
34 COMPUTER READABLE FORM:  
35 MEDIUM TYPE: Floppy disk  
36 COMPUTER: IBM PC Compatible  
37 OPERATING SYSTEM: PC-DOS/MS-DOS  
38 SOFTWARE: PatentIn Release #1.0, Version #1.25  
39 CURRENT APPLICATION DATA:  
40 APPLICATION NUMBER: US/08/160,604  
41 FILING DATE: 30-NOV-1993  
42 CLASSIFICATION: 424  
43 PRIOR APPLICATION DATA:  
44 APPLICATION NUMBER: US 07/867,819  
45 FILING DATE: 13-APR-1992  
46 PRIOR APPLICATION DATA:  
47 APPLICATION NUMBER: US 07/648,205  
48 FILING DATE: 31-JAN-1991  
49 PRIOR APPLICATION DATA:  
50 APPLICATION NUMBER: US 07/472,947  
51 FILING DATE: 31-JAN-1990  
52 ATTORNEY/AGENT INFORMATION:  
53 NAME: Pabst, Patrea L.  
54 REGISTRATION NUMBER: 31,284  
55 REFERENCE/DOCKET NUMBER: OMRP114CIP(3)  
56 TELECOMMUNICATION INFORMATION:  
57 TELEPHONE: (404)-815-6508  
58 TELEFAX: (404)-815-6555  
59 INFORMATION FOR SEQ ID NO: 9:

Query Match 36.48; Score 4; IP 4; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2, 5, 6, 7;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEOK 7  
 1111  
 DB 3 KEOK 5

RESULT 4  
 US-08-160-604-10  
 : Sequence 10, Application US/08:604-10  
 : Patent No. 6242522  
 : GENERAL INFORMATION:  
 : APPLICANT: James, John  
 : APPLICANT: James, Judith A.  
 : APPLICANT: Scofield, R. H.  
 : TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOLYMPHATIC CLONAL SIMILARITY  
 : NUMBER OF SEQUENCES: 127  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Patricia L. Paest  
 : STREET: 1100 Peachtree Street, Suite 2800  
 : CITY: Atlanta  
 : STATE: Georgia  
 : COUNTRY: USA  
 : ZIP: 30309-4530  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/160,604  
 : FILING DATE: 30-NOV-1993  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/667,819  
 : FILING DATE: 13-APR-1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/668,205  
 : FILING DATE: 31-JAN-1991  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/472,947  
 : FILING DATE: 31-JAN-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Padst, Palrea L.  
 : REGISTRATION NUMBER: 31,284  
 : REFERENCE/DOCKET NUMBER: OMRF114CIP(3)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (404)-815-6508  
 : TELEFAX: (404)-815-6555  
 : INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : HYPOTHEetical: NO  
 : ANTI-SENSE: NO  
 : FRAGMENT TYPE: N-terminal  
 : US-08-160-604-10

Query Match 36.48; Score 4; IP 4; Length 8;  
 Best local Similarity 100.0%; Pred. No. 2, 5, 6, 7;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEOK 7  
 1111  
 DB 2 KEOK 5

RESULT 4  
 US-08-160-604-10  
 : Sequence 10, Application US/08:604-10  
 : Patent No. 6242522  
 : GENERAL INFORMATION:  
 : APPLICANT: James, John  
 : APPLICANT: James, Judith A.  
 : APPLICANT: Scofield, R. H.  
 : TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOLYMPHATIC CLONAL SIMILARITY  
 : NUMBER OF SEQUENCES: 127  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Patricia L. Paest  
 : STREET: 1100 Peachtree Street, Suite 2800  
 : CITY: Atlanta  
 : STATE: Georgia  
 : COUNTRY: USA  
 : ZIP: 30309-4530  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/160,604  
 : FILING DATE: 30-NOV-1993  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/667,819  
 : FILING DATE: 13-APR-1992  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/668,205  
 : FILING DATE: 31-JAN-1991  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/472,947  
 : FILING DATE: 31-JAN-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Padst, Palrea L.  
 : REGISTRATION NUMBER: 31,284  
 : REFERENCE/DOCKET NUMBER: OMRF114CIP(3)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (404)-815-6508  
 : TELEFAX: (404)-815-6555  
 : INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : HYPOTHEtical: NO  
 : ANTI-SENSE: NO  
 : FRAGMENT TYPE: N-terminal  
 : US-08-160-604-10  
 : Query Match 36.48; Score 4; IP 4; Length 8;  
 : Best local Similarity 100.0%; Pred. No. 2, 5, 6, 7;  
 : Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 : QY 4 KEOK 7  
 : 1111  
 : DB 3 KEOK 5  
 : RESULT 4  
 : US-08-160-604-10  
 : Sequence 10, Application US/08:604-10  
 : Patent No. 6242522  
 : GENERAL INFORMATION:  
 : APPLICANT: James, John  
 : APPLICANT: James, Judith A.  
 : APPLICANT: Scofield, R. H.  
 : TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOLYMPHATIC CLONAL SIMILARITY  
 : NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/160,604  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,619  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/948,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMRF114-P{f}  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)-815-6568  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 40:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-160-604-40

Query Match 36.4%, Score 4, Lk 3, Length 8:  
 Best Local Similarity 100.0%, Pct. No. 2, Lk 0.05:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 4 KORN 7

RESULT 7  
 US-08-160-604-41  
 Sequence 41, Application US/08160604  
 Patent No. 6232522  
 GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: James, Judith A.  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCERS OF AUTOIMMUNITY: CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09-787-443-20  
 FILING DATE: 01-01-2003  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/948,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMRF114-P{f}  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)-815-6568  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 41:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-160-604-41

Query Match 36.4%, Score 4, Lk 3, Length 8:  
 Best Local Similarity 100.0%, Pct. No. 2, Lk 0.05:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 4 KORN 7

RESULT 8  
 US-08-160-604-42  
 Sequence 42, Application US/08160604  
 Patent No. 6232522  
 GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: James, Judith A.  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCERS OF AUTOIMMUNITY: CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

QY 7 KORN 10  
 DB 4 KORN 7

RESULT 9  
 US-08-160-604-43  
 Sequence 43, Application US/08160604  
 Patent No. 6232522  
 GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: James, Judith A.  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCERS OF AUTOIMMUNITY: CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30309-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,547  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Babst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)-815-6508  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 42:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-08-160-604-42

Query Match 36.4% Score 43 TB 43 Length 8:  
 Best Local Similarity 100.0% Prod. No. 2,60-05:  
 Matches 4: Conservative 9: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 2 KORN 5

## RESULT 9

US-08-160-604-43  
 Sequence 43, Application US/08160604  
 Patent No. 6232522

GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Patrea L. Babst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30109-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/160,604  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,619  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Babst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 815-6508  
 TELEFAX: (404) 815-6555  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 US-09-787-443-20

Query Match 100.0% Score 43 TB 43 Length 8:  
 Best Local Similarity 100.0% Prod. No. 2,60-05:  
 Matches 4: Conservative 9: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 2 KORN 5

## RESULT 10

US-09-787-443-20  
 Sequence 43, Application US/09787443A  
 Patent No. 6415550

GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Patrea L. Babst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30109-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/787,443A  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,619  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Babst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:

US-09-787-443-20

Query Match 100.0% Score 43 TB 43 Length 8:  
 Best Local Similarity 100.0% Prod. No. 2,60-05:  
 Matches 4: Conservative 9: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 2 KORN 5

## RESULT 11

US-09-787-443-20  
 Sequence 43, Application US/09787443A  
 Patent No. 6415550  
 GENERAL INFORMATION:  
 APPLICANT: Harley, John  
 APPLICANT: Scofield, R. H.  
 TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
 NUMBER OF SEQUENCES: 127  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Patrea L. Babst  
 STREET: 1100 Peachtree Street, Suite 2800  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30109-4530  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/787,443A  
 FILING DATE: 30-NOV-1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/867,619  
 FILING DATE: 13-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/648,205  
 FILING DATE: 31-JAN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Babst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMR114CIP(3)  
 TELECOMMUNICATION INFORMATION:

Query Match 100.0% Score 43 TB 43 Length 8:  
 Best Local Similarity 100.0% Prod. No. 2,60-05:  
 Matches 4: Conservative 9: Mismatches 0: Indels 0: Gaps 0:

QY 7 KORN 10  
 DB 2 KORN 5

```

RESULT 12
US-09-100-930A-24
: Sequence 24, Application US/09100930A
: Patent No. 6248549
: GENERAL INFORMATION:
: APPLICANT: Van Eyk, Jennifer E.
: APPLICANT: Ma, Alan S.
: APPLICANT: Cote, Graham P.
: TITLE OF INVENTION: Methods of Modulating Muscle Contraction
: CURRENT APPLICATION NUMBER: US/09/100,930A
: CURRENT FILING DATE: 1998-06-22
: PRIOR APPLICATION NUMBER: 60/050,478
: PRIOR FILING DATE: 1997-06-23
: PRIOR APPLICATION NUMBER: 60/089,505
: PRIOR FILING DATE: 1998-06-16
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 24
: LENGTH: 9
: TYPE: PPT
: ORGANISM: Unknown
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (1)..(9)
: OTHER INFORMATION: Residues 25 to 38 of Inl
: LOCATION: (9)
: OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-100-930A-24

Query Match          36.48; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4
DB 1111 5 AKKK 8

RESULT 13
US-09-445-615-4
: Sequence 4, Application US/09445615
: Patent No. 6350452
: GENERAL INFORMATION:
: APPLICANT: Riss, Terry
: TITLE OF INVENTION: APOPTOSIS MARKER ANTIBODIES AND METHODS OF USE
: FILE REFERENCE: 16026,9033
: CURRENT APPLICATION NUMBER: US/09/445,615
: CURRENT FILING DATE: 1999-12-08
: PRIOR APPLICATION NUMBER: 60/101,920
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 9
: TYPE: PPT
: ORGANISM: Homo sapiens
US-09-445-615-4

Query Match          36.48; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4
DB 1111 6 AKKK 9

RESULT 14
US-08-213-897A-18

```

```

: Sequence 18, Application US/0821897A
: Patent No. 5618730
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Anticase Modulated Drug Delivery System
: NUMBER OF SEQUENCES: 18
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30 (RPR)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/213,897A
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/43,867
: FILING DATE: 1997-11-06
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/43,867
: FILING DATE: 1997-11-06
: INFORMATION FOR SEQUENCES:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: MOLECULE TYPE: polypep
US-08-213-897A-18

Query Match          46.48; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4
DB 1111 6 AKKK 5

RESULT 15
US-08-082-2840-3
: Sequence 3, Application US/08-422693
: Patent No. 677127
: GENERAL INFORMATION:
: APPLICANT: Kohn, Michael
: APPLICANT: Bock, Thomas
: APPLICANT: Aull, Thomas
: TITLE OF INVENTION: Polystyrene-Cellulose Conjugates
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bionet, Inc., Inc., Inc.
: STREET: 4849 Elwood Avenue
: CITY: Elwood
: STATE: Ohio
: COUNTRY: USA
: ZIP: 43022-9444
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: PatentIn Ver. 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/082,269
: FILING DATE: 2000-03-01
: CLASSIFICATION: I35
: ALTERNATE/OTHER INFORMATION:
: NAME: Bionet, Inc., Alton, AL
: REGISTRATION NUMBER: 44,429
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (502)465-8400
: TELEFAX: (502)344-6024
: INFORMATION FOR SEQUENCES:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 AMINO ACIDS
: TYPE: Amino Acid

```



; TOPOLOGY: Linear  
 ; MOLECULE TYPE: Peptide  
 ; HYPOTHETICAL: no  
 ; FRAGMENT TYPE:  
 ; FEATURE:  
 ; OTHER INFORMATION: Xaa at position 3 is the modified amino acid ornithine.  
 ; PUBLICATION INFORMATION:  
 ; AUTHORS: Chelsky, Daniel, Ralph, Rebecca and Jonak, Gerald  
 ; TITLE: Sequence Requirements for Synthetic Peptide Mediated Translocation to the  
 ; Patent No. 5773227  
 ; JOURNAL: Molecular and Cellular Biology  
 ; VOLUME: 9  
 ; ISSUE: 6  
 ; PAGES: 2487-2492  
 ; DATE: 1989  
 ; US-08-082-269D-3

Query Match 36.4%; Score 4; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKKK 4  
 DB 4 AKKK 7

RESULT 15  
 US-08-986-234-3  
 ; Sequence 3, Application US/08986234  
 ; Patent No. 5981706  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wallen, et al.  
 ; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes  
 ; FILE REFERENCE: UNNE-0008-1  
 ; CURRENT APPLICATION NUMBER: US/08/986.234  
 ; CURRENT FILING DATE: 1997-12-05  
 ; NUMBER OF SEQ ID NOS: 114  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Feline immunodeficiency virus  
 US-08-986-234-3

Query Match 36.4%; Score 4; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KORN 10  
 DB 7 KORN 10

RESULT 17  
 US-08-986-234-4  
 ; Sequence 4, Application US/08986234  
 ; Patent No. 5981706  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wallen, et al.  
 ; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes  
 ; FILE REFERENCE: UNNE-0008-1  
 ; CURRENT APPLICATION NUMBER: US/08/986.234  
 ; CURRENT FILING DATE: 1997-12-05  
 ; NUMBER OF SEQ ID NOS: 114  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Feline immunodeficiency virus  
 US-08-986-234-4

Query Match 36.4%; Score 4; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 QY 7 KORN 10  
 DB 7 KORN 10

RESULT 18  
 US-09-434-476A-1  
 ; Sequence 3, Application US/0943476A  
 ; Patent No. 6445108  
 ; GENERAL INFORMATION:  
 ; APPLICANT: van Nieuwenhuijzen, et al.  
 ; APPLICANT: Bioprocess International  
 ; TITLE OF INVENTION: Methods for Identifying Potent Sequences of Peptides  
 ; FILE REFERENCE: US/09-434-476A  
 ; CURRENT APPLICATION NUMBER: US/09-434-476A  
 ; CURRENT FILING DATE: 2000-01-03  
 ; PRIOR APPLICATION NUMBER: US/09-434-476A  
 ; PRIOR FILING DATE: 2000-01-03  
 ; PRIOR APPLICATION NUMBER: US/09-434-476A  
 ; PRIOR FILING DATE: 2000-01-03  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-09-434-476A-1

Query Match 36.4%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKKK 4  
 DB 6 AKKK 9

RESULT 19  
 US-08-160-604-2  
 ; Sequence 6, Application US/081604-2  
 ; Patent No. 6296422  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hoffmann, et al.  
 ; APPLICANT: Hoffmann, et al.  
 ; TITLE OF INVENTION: METHOD FOR THE DETECTION OF AUTOREGULATORY CLINICAL SYMPTOMS  
 ; NUMBER OF SEQ ID NOS: 114  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; ADDRESS: Hoffmann, et al.  
 ; STREET: Hoffmann, et al.  
 ; CITY: Atlanta  
 ; STATE: Georgia  
 ; COUNTRY: USA  
 ; ZIP: 30309-4500  
 ; COMPUTER PROGRAM NAME:  
 ; MEDIUM TYPE: CD-ROM  
 ; OPERATING SYSTEM: WINDOWS 95  
 ; SOFTWARE: Patent In Ver. 2.0, Version 2.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08-160-604  
 ; FILING DATE: 2000-01-03  
 ; CLASSIFICATION: 4-2  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07-967,819  
 ; FILING DATE: 1997-10-02  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07-967,819  
 ; FILING DATE: 1997-10-02

PRIORITY DATA: 07/472,947  
 FILING DATE: 31-JAN-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: 048F1421P(3)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)-815-6508  
 TELEFAX: (404)-815-6555  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N terminal  
 US-08-162-604 6

Qy 4 KEQK 7  
 IIII  
 Db 5 KEQK 8

## RESULT 20

```

US-09-025-596-34
  : Sequence 34, Application US/09035596
  : Patent No. 6340463
  : GENERAL INFORMATION:
  : APPLICANT: Mitchell, William M.
  : APPLICANT: Stratton, Charles W.
  : TITLE OF INVENTION: IDENTIFICATION OF ANT
  : TITLE OF INVENTION: SEQUENCES
  : FILE REFERENCE: VDB98-01
  : CURRENT APPLICATION NUMBER: US/09/025,596
  : CURRENT FILING DATE: 1998-02-18
  : EARLIER APPLICATION NUMBER: 09/911,593
  : EARLIER FILING DATE: 1997-08-14
  : EARLIER APPLICATION NUMBER: 62/023,921
  : EARLIER FILING DATE: 1996-08-14
  : NUMBER OF SEQ ID NOS: 118
  : SOFTWARE: FASTSEQ for Windows Version 3.0
  : SEQ ID NO 34
  : LENGTH: 11
  : TYPE: PRT
  : ORGANISM: Chlamydia pneumoniae
US-09-025-596-34

```

Qy 1 AKKK 4  
1111  
Db 3 AKKK 6

## RESULT 21

RESOLUTION 21  
US-09-579-664R-33

: Sequence 33, Application US/09579664H  
: Patent No. 6514719  
: GENERAL INFORMATION:  
: APPLICANT: ImmuneX Corporation  
: APPLICANT: Bird, Timothy A.  
: APPLICANT: Virca, C. Duke  
: APPLICANT: Martin, Unia

```

1 LENGTH: 12
2 TYPE: PRT
3 ORGANISM: Artificial Sequence
4 FEATURE:
5 OTHER INFORMATION: Description of Artificial Sequence: Optimized
6 OTHER INFORMATION: substrate for Abl
7 US-09-480-993-13

Query Match          36.4%  Score 4: 05 4: Length 12:
Best Local Similarity 100.0%  Pred. No. 2,200-2:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4
DB 9 AKKK 12

RESULT 24
US-09-167-065A-13
1 Sequence 18, Application US/09367065A
2 Patent No. 6390821
3 GENERAL INFORMATION:
4 APPLICANT: Shokat, Kevan M.
5 TITLE OF INVENTION: Engineered Protein Kinases which can Utilize Modified
6 TITLE OF INVENTION: Nucleotide Triphosphate Substrates
7 FILE REFERENCE: 51538-5002-US
8 CURRENT APPLICATION NUMBER: US/06/167,065A
9 CURRENT FILING DATE: 1999-11-17
10 PRIOR APPLICATION NUMBER: US 06/797,522
11 PRIOR FILING DATE: 1997-02-07
12 PRIOR APPLICATION NUMBER: US 60/046,727
13 PRIOR FILING DATE: 1997-05-16
14 PRIOR APPLICATION NUMBER: PCT/US98/32522
15 PRIOR FILING DATE: 1998-02-05
16 NUMBER OF SEQ ID NOS: 20
17 SOFTWARE: PatentIn Ver. 2.1
18 SEQ ID NO 18
19 LENGTH: 12
20 TYPE: PRT
21 ORGANISM: Artificial Sequence
22 FEATURE:
23 OTHER INFORMATION: Description of Artificial Sequence: Optimized
24 OTHER INFORMATION: enzyme inhibitor for Abl
25 US-09-367-065A-18

Query Match          36.4%  Score 4: 05 4: Length 12:
Best Local Similarity 100.0%  Pred. No. 2,200-2:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4
DB 9 AKKK 12

RESULT 25
US-09-579-664B-35
1 Sequence 35, Application US/09579664B
2 Patent No. 6514719
3 GENERAL INFORMATION:
4 APPLICANT: Immunex Corporation
5 APPLICANT: Bird, Timothy A.
6 APPLICANT: Virca, G. Duke
7 APPLICANT: Martin, Unja
8 APPLICANT: Anderson, Dirk M.
9 TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
10 FILE REFERENCE: 2923-A
11 CURRENT APPLICATION NUMBER: US/09/579,664B
12 CURRENT FILING DATE: 2000-05-26
13 NUMBER OF SEQ ID NOS: 36
14 SOFTWARE: PatentIn version 3.1
15 SEQ ID NO 35
16 LENGTH: 12
17 TYPE: PRT

```

```

1 ORGANISM: Artificial Sequence
2 FEATURE:
3 OTHER INFORMATION: Description of Artificial Sequence: Optimized
4 OTHER INFORMATION: substrate for Abl
5 US-09-579-664B-35

Query Match          36.4%  Score 4: 05 4: Length 12:
Best Local Similarity 100.0%  Pred. No. 2,200-2:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKK 4
DB 9 AKKK 12

RESULT 26
US-09-579-664B-35
1 Sequence 35, Application US/09579664B
2 Patent No. 6514719
3 GENERAL INFORMATION:
4 APPLICANT: Immunex Corporation
5 APPLICANT: Bird, Timothy A.
6 APPLICANT: Virca, G. Duke
7 APPLICANT: Martin, Unja
8 APPLICANT: Anderson, Dirk M.
9 TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
10 FILE REFERENCE: 2923-A
11 CURRENT APPLICATION NUMBER: US/09/579,664B
12 CURRENT FILING DATE: 2000-05-26
13 NUMBER OF SEQ ID NOS: 36
14 SOFTWARE: PatentIn version 3.1
15 SEQ ID NO 35
16 LENGTH: 12
17 TYPE: PRT

```

```

1 APPLICATION NUMBER: PCT/US95/00147
2 FILING DATE:
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 08/178,570
5 FILING DATE: JANUARY 7, 1994
6 ATTORNEY/AGENT INFORMATION:
7 NAME: DeConti, Giulio A., Jr.
8 REGISTRATION NUMBER: 31,503
9 REFERENCE/DOCKET NUMBER: BBI-0042PRC
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (617) 227-7400
12 TELEFAX: (617) 227-5941
13 INFORMATION FOR SEQ ID NO: 88:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 12 amino acids
16 TYPE: amino acid
17 TOPOLOGY: linear
18 MOLECULE TYPE: peptide
19 FRAGMENT TYPE: internal
20 PCT-US95-00147-88

```

```

Query Match 36.4% Score 4: (8 5) Length 12:
Best Local Similarity 100.0% Pred. No. 2,49-02:
Matches 4: Conservative 0; Mismatches 0; Gaps 0;

```

```

Qy 1 AKKK 4
    IIII
Db 9 AKKK 12

```

```

RESULT 28
US-08-342-101-2
1 Sequence 2, Application US/08342101
2 Patent No. 5756882
3 GENERAL INFORMATION:
4 APPLICANT: Wicks, Richard W.
5 APPLICANT: Zartman, Leslie O.
6 APPLICANT: Vardas, Annette M.
7 APPLICANT: Tortelli, Stacy A.
8 TITLE OF INVENTION: ASSAY FOR CARDIAC TROPONIN I
9 NUMBER OF SEQUENCES: 3
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: LAHIVE & COCKFIELD
12 STREET: 60 State Street, suite 510
13 CITY: Boston
14 STATE: Massachusetts
15 COUNTRY: U.S.
16 ZIP: 02109
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: ASCII
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/142,101
24 FILING DATE: 18-NOV-1994
25 CLASSIFICATION: 530
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US/08/063,166
28 FILING DATE: 17-MAY-1993
29 ATTORNEY/AGENT INFORMATION:
30 NAME: DeConti, Giulio A.
31 REGISTRATION NUMBER: 31,503
32 REFERENCE/DOCKET NUMBER: BBI-003
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (617) 227-7400
35 TELEFAX: (617) 227-5941
36 INFORMATION FOR SEQ ID NO: 2:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 13 amino acids
39 TYPE: amino acid
40 TOPOLOGY: linear
41 MOLECULE TYPE: peptide

```

```

1 FRAGMENT TYPE: internal
2 US-08-342-101-2
3 Query Match 36.4% Score 4: (8 5) Length 12:
4 Best Local Similarity 100.0% Pred. No. 2,49-02:
5 Matches 4: Conservative 0; Mismatches 0; Gaps 0;
6
7 Qy 1 AKKK 4
8    IIII
9 Db 9 AKKK 12
10
11 RESULT 28
12 US-08-342-101-2
13 Sequence 2, Application US/08342101
14 Patent No. 5756882
15 GENERAL INFORMATION:
16 APPLICANT: Wicks, Richard W.
17 APPLICANT: Zartman, Leslie O.
18 APPLICANT: Vardas, Annette M.
19 APPLICANT: Tortelli, Stacy A.
20 TITLE OF INVENTION: ASSAY FOR CARDIAC TROPONIN I
21 NUMBER OF SEQUENCES: 3
22 CORRESPONDENCE ADDRESS:
23 ADDRESSEE: LAHIVE & COCKFIELD
24 STREET: 60 State Street, suite 510
25 CITY: Boston
26 STATE: Massachusetts
27 COUNTRY: U.S.
28 ZIP: 02109
29 COMPUTER READABLE FORM:
30 MEDIUM TYPE: Floppy disk
31 COMPUTER: IBM PC compatible
32 OPERATING SYSTEM: PC-DOS/MS-DOS
33 SOFTWARE: ASCII
34 CURRENT APPLICATION DATA:
35 APPLICATION NUMBER: US/08/142,101
36 FILING DATE: 18-NOV-1994
37 CLASSIFICATION: 530
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US/08/063,166
40 FILING DATE: 17-MAY-1993
41 ATTORNEY/AGENT INFORMATION:
42 NAME: DeConti, Giulio A.
43 REGISTRATION NUMBER: 31,503
44 REFERENCE/DOCKET NUMBER: BBI-003
45 TELECOMMUNICATION INFORMATION:
46 TELEPHONE: (617) 227-7400
47 TELEFAX: (617) 227-5941
48 INFORMATION FOR SEQ ID NO: 2:
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 13 amino acids
51 TYPE: amino acid
52 TOPOLOGY: linear
53 MOLECULE TYPE: peptide

```

```

RESULT 28
US-08-342-101-2
Sequence 2, Application US/08342101
Patent No. 5756882
GENERAL INFORMATION:
APPLICANT: Wicks, Richard W.
APPLICANT: Zartman, Leslie O.
APPLICANT: Vardas, Annette M.
APPLICANT: Tortelli, Stacy A.
TITLE OF INVENTION: ASSAY FOR CARDIAC TROPONIN I
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,101
FILING DATE: 18-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/063,166
FILING DATE: 17-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

```

OTHER INFORMATION

RESULT 34  
US CR 2-2-46-A 4  
SEQUENCE 4: AFFIDAVIT OF DISCOVERY  
PATENT NO. 70898  
GENERAL DESCRIPTION  
APPLICANT: BUSHNELL, LEONARD  
TITLE OF INVENTION: TELETYPE  
TITLE OF INVENTION METHODS AND COMPOSITIONS FOR  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:

```

: ADDRESSEE: ARNOLD, WHITE & DURKEE
: STREET: P.O. BOX 4433
: CITY: HOUSTON
: STATE: TX
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,453A
: FILING DATE: APRIL 22, 1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/748,319
: FILING DATE: AUGUST 21, 1991
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: PARKER, DAVID L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: US/08/253/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-232-453A-4
:
: Query Match 36.4%, Score 4, DB 1, Length 14:
: Best Local Similarity 100.0%, Pred. No. 2,40-02:
: Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 AKKK 4
: DB 10 AKKK 13
:
: RESULT 34
: US-08-453-862-3
: Sequence 3, Application US/08453862
: Patent No. 5738999
: GENERAL INFORMATION:
: APPLICANT: Segerson, Thomas P.
: APPLICANT: Kinzie, J. Mark
: APPLICANT: Mulvihill, Eileen R.
: APPLICANT: Saugstad, Julie A.
: APPLICANT: Westbrook, Gary L.
: TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/453,862
: FILING DATE: 30-MAY-1995
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/176,401

```

```

: FILING DATE: 30-MAY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Parkerson, Steven W.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: US/08/253/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-453-862-3
:
: Query Match 36.4%, Score 4, DB 1, Length 14:
: Best Local Similarity 100.0%, Pred. No. 2,40-02:
: Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 AKKK 4
: DB 10 AKKK 13
:
: RESULT 35
: US-08-452-734A-4
: Sequence 3, Application US/08452734A
: Patent No. 5641042
: GENERAL INFORMATION:
: APPLICANT: Segerson, Thomas P.
: APPLICANT: Kinzie, J. Mark
: APPLICANT: Mulvihill, Eileen R.
: APPLICANT: Saugstad, Julie A.
: APPLICANT: Westbrook, Gary L.
: TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/452,734A
: FILING DATE: 30-MAY-1995
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/176,401
: FILING DATE: 30-MAY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Parkerson, Steven W.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: US/08/253/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-452-734A-4

```

Query Match 36.4% Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 8 AKKK 11

RESULT 36  
US-08-505-250-14  
Sequence 14, Application US/08505250  
Patent No. 6183983  
GENERAL INFORMATION:  
APPLICANT: Sato, Haruya  
APPLICANT: Yamamoto, Keiji  
APPLICANT: Suzuki, Kokichi  
APPLICANT: Ikeda, Masahiro  
APPLICANT: Sakagami, Masahiro  
APPLICANT: Taniguchi, Makoto  
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD  
FILE REFERENCE: 110-511  
CURRENT APPLICATION NUMBER: US/08/505,250  
CURRENT FILING DATE: 1995-11-29  
EARLIER APPLICATION NUMBER: PCT/JP95/03208  
EARLIER FILING DATE: 1995-02-27  
EARLIER APPLICATION NUMBER: JP 198187/94  
EARLIER FILING DATE: 1994-08-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 14  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-08-505-250-14

Query Match 36.4% Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 1 AKKK 4

RESULT 37  
US-09-100-930A-7  
Sequence 7, Application US/09100930A  
Patent No. 6248549  
GENERAL INFORMATION:  
APPLICANT: Van Eyk, Jennifer E.  
APPLICANT: Mak, Alan S.  
APPLICANT: Cote, Graham P.  
TITLE OF INVENTION: Methods of Modulating Macrot Degradation  
FILE REFERENCE: 1997-021-0305  
CURRENT APPLICATION NUMBER: US/09/100,930A  
CURRENT FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/050,478  
PRIOR FILING DATE: 1997-06-23  
PRIOR APPLICATION NUMBER: 60/089,505  
PRIOR FILING DATE: 1998-06-16  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 7  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(14)

OTHER INFORMATION: Description of Cardiac Tissue  
NAME/KEY: PEPTIDE  
LOCATION: (1)  
OTHER INFORMATION: Description of Cardiac Tissue  
US-09-100-930A-7

Query Match 36.4% Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 10 AKKK 11

RESULT 38  
US-09-176-403B-4  
Sequence 3, Application US/09176403B  
Patent No. 6248549  
GENERAL INFORMATION:  
APPLICANT: Sato, Haruya  
APPLICANT: Yamamoto, Keiji  
APPLICANT: Suzuki, Kokichi  
APPLICANT: Ikeda, Masahiro  
APPLICANT: Sakagami, Masahiro  
APPLICANT: Taniguchi, Makoto  
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD  
FILE REFERENCE: 110-511  
CURRENT APPLICATION NUMBER: US/09/176,403B  
CURRENT FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/050,478  
PRIOR FILING DATE: 1997-06-23  
PRIOR APPLICATION NUMBER: 60/089,505  
PRIOR FILING DATE: 1998-06-16  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 4  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(14)

Query Match 36.4% Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 10 AKKK 11

RESULT 39  
US-08-505-250-14  
Sequence 14, Application US/08505250  
Patent No. 6183983  
GENERAL INFORMATION:

```

: APPLICANT: Sato, Haruya
: APPLICANT: Yamamoto, Keiji
: APPLICANT: Suzuki, Kokiichi
: APPLICANT: Ikeda, Masahiro
: APPLICANT: Taniguchi, Makoto
: TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
: FILE REFERENCE: 110-511
: CURRENT APPLICATION NUMBER: US/08/505,250
: PRIOR FILING DATE: 1995-11-29
: PRIOR APPLICATION NUMBER: PCT/JP95/00294
: PRIOR FILING DATE: 1995-02-27
: PRIOR APPLICATION NUMBER: JP 198187/94
: PRIOR FILING DATE: 1994-08-23
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn ver. 2.0
: SEQ ID NO 14
: LENGTH: 14
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificially Sequenced Synthesis
: OTHER INFORMATION: peptide
US-08-505-250-14

```

```

Query Match 36.4% Score 4: IP 4: Length 14:
Best Local Similarity 100.0% Pred. No. 2,400/21
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

Qy 1 AKKK 4
Db 1 AKKK 4

```

```

RESULT 40
US-09-025-596-17
: Sequence 17, Application US/9025546
: Patent No. 6340463
: GENERAL INFORMATION:
: APPLICANT: Mitchell, William M.
: APPLICANT: Stratton, Charles W.
: TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
: FILE REFERENCE: VDB98-01
: CURRENT APPLICATION NUMBER: US/09/025,596
: CURRENT FILING DATE: 1998-02-18
: EARLIER APPLICATION NUMBER: 08/911,593
: EARLIER FILING DATE: 1997-08-14
: EARLIER APPLICATION NUMBER: 60/023,921
: EARLIER FILING DATE: 1996-08-14
: NUMBER OF SEQ ID NOS: 118
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 17
: LENGTH: 14
: TYPE: PRT
: ORGANISM: Chlamydia pneumoniae
US-09-025-596-17

```

```

Query Match 36.4% Score 4: IP 4: Length 14:
Best Local Similarity 100.0% Pred. No. 2,400/21
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

Qy 4 KEQK 7
Db 7 KEQK 10

```

```

RESULT 41
US-09-171-425-8
: Sequence 8, Application US/09171425A
: Patent No. 6465438
: GENERAL INFORMATION:
: APPLICANT: Schorr, Joachim

```

```

: APPLICANT: Baker, David E.
: APPLICANT: Smith, Barbara J.
: TITLE OF INVENTION: METHOD AND VACCINATION FOR PARVOVIRAL INFECTIONS
: FILE REFERENCE: 08/000000
: CURRENT APPLICATION NUMBER: US/07/11,425A
: CURRENT FILING DATE: 2000-01-14
: EARLIER APPLICATION NUMBER: PCT/US97/01470
: EARLIER FILING DATE: 1997-04-14
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FASTSEQ for Windows Version 1.0
: SEQ ID NO 1
: LENGTH: 14
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Sequences 1-10 generated oligonucleotides
US-09-171-425-8

```

```

Query Match 36.4% Score 4: IP 4: Length 14:
Best Local Similarity 100.0% Pred. No. 2,400/21
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

Qy 1 AKKK 1
Db 8 AKKK 1

```

```

RESULT 42
US-09-171-425-8
: Sequence 1, Application US/0711425A
: Patent No. 6465438
: GENERAL INFORMATION:
: APPLICANT: Baker, David E.
: APPLICANT: Smith, Barbara J.
: TITLE OF INVENTION: METHOD AND VACCINATION FOR PARVOVIRAL INFECTIONS
: FILE REFERENCE: 08/000000
: CURRENT APPLICATION NUMBER: US/07/11,425A
: CURRENT FILING DATE: 2000-01-14
: EARLIER APPLICATION NUMBER: PCT/US97/01470
: EARLIER FILING DATE: 1997-04-14
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FASTSEQ for Windows Version 1.0
: SEQ ID NO 1
: LENGTH: 14
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Sequences 1-10 generated oligonucleotides
US-09-171-425-8

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Query Match 36.4% Score 4: IP 4: Length 14:
Best Local Similarity 100.0% Pred. No. 2,400/21
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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Qy 1 AKKK 1
Db 8 AKKK 1

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RESULT 43
US-09-171-425-8

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; Sequence 3, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RRI-064
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3-6
; OTHER INFORMATION: /note= "Xaa is any amino acid"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note "Xaa is Ser, Thr or Tyr"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8-11
; OTHER INFORMATION: /note= "Xaa is any amino acid"
US-08-178-570-3

Query Match          36.48; Score 4; DB 1; Length 15;
Best Local Similarity 100.08; Pred. No. 2,666,21;
Matches 4; Conserved 0; Mismatches 0; Gaps 0;

QY      1 AKKK 4
DB      1111
       12 AKKK 15

RESULT: 44
US-08-178-570-76
; Sequence 76, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
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; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RRI-064
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3-6
; OTHER INFORMATION: /note= "Xaa is any amino acid"
US-08-178-570-3

Query Match          36.48; Score 4; DB 1; Length 15;
Best Local Similarity 100.08; Pred. No. 2,666,21;
Matches 4; Conserved 0; Mismatches 0; Gaps 0;

QY      1 AKKK 4
DB      1111
       12 AKKK 15

RESULT: 45
US-08-178-570-77
; Sequence 77, Application US/08/178,570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RRI-064
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3-6
; OTHER INFORMATION: /note= "Xaa is any amino acid"
US-08-178-570-4

Query Match          36.48; Score 4; DB 1; Length 15;
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Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 12 AKKK 15

## RESULT 46

US-08-369-643-76  
Sequence 76, Application US/08369643A  
Patent No. 6004757  
GENERAL INFORMATION:  
APPLICANT: Cantley, Lewis C.  
TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
FILE REFERENCE: CNS-001CP  
CURRENT APPLICATION NUMBER: US/08/369,643A  
CURRENT FILING DATE: 1995-01-06  
EARLIER APPLICATION NUMBER: US 08/178,576  
EARLIER FILING DATE: 1994-01-07  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 76  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: peptide  
OTHER INFORMATION: Synthesized as a substrate for src tyrosine  
US-08-369-643-76

Query Match 36.4%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 11 AKKK 14

## RESULT 47

US-08-461-384B-10  
Sequence 10, Application US/08461384B  
Patent No. 6025473  
GENERAL INFORMATION:  
APPLICANT: Cole, Susan P.C.  
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS  
STREET: Queen's University at Kingston  
CITY: Kingston  
STATE: Ontario  
COUNTRY: CANADA  
ZIP: K7L 3N6  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,384B  
FILING DATE: 05-JUN-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/966,923  
FILING DATE: 27-OCT-1992  
APPLICATION NUMBER: 08/029,340  
FILING DATE: 8-MAR-1993  
APPLICATION NUMBER: 08/141,893  
FILING DATE: 26-OCT-1993

APPLICATION NUMBER: US/08/461,384B  
FILING DATE: 05-JUN-95  
ATTORNEY/AGENT INFORMATION:  
NAME: Stuart, Robert M.  
REGISTRATION NUMBER: 09,349  
TELEPHONE: (613) 546-2447  
TELEFAX: (613) 546-2447  
INFORMATION FOR SEQUENCING:  
SEQUENCE MARKER POSITIONS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
MOLECULE TYPE: polypep  
US-08-407-207A-1

Query Match 36.4%; Score 4; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 48

US-08-407-207A-1  
Sequence 7, Application US/08407207A  
Patent No. 6004757  
GENERAL INFORMATION:  
APPLICANT: Cole, Susan P.C.  
TITLE OF INVENTION: ARTICLES OF A MULTIDRUG RESISTANCE PROTEIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS  
STREET: Queen's University at Kingston  
CITY: Kingston  
STATE: Ontario  
COUNTRY: CANADA  
ZIP: K7L 3N6  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/407,207A  
FILING DATE: 20-MAR-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/966,923  
FILING DATE: 27-OCT-1992  
APPLICATION NUMBER: 08/029,340  
FILING DATE: 8-MAR-1993  
APPLICATION NUMBER: 08/141,893  
FILING DATE: 26-OCT-1993

Query Match 36.4%; Score 4; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OKOR 9  
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 Db 8 OKOR 11

## RESULT 49

PCT-US95-00147-3  
 ; Sequence 3, Application PC/TUS9500147  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 STATE STREET, suite 510  
 ; CITY: BOSTON  
 ; STATE: MASSACHUSETTS  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/00147  
 ; FILING DATE:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/178,570  
 ; FILING DATE: JANUARY 7, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeConiti, Giulio A., Jr.  
 ; REGISTRATION NUMBER: 31,503  
 ; REFERENCE/DOCKET NUMBER: BJI-00407PC  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 3-6  
 ; OTHER INFORMATION: /note= "Xaa is any amino acid"  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 7  
 ; OTHER INFORMATION: /note= "Xaa is Ser, Thr or Tyr"  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 8-11  
 ; OTHER INFORMATION: /note= "Xaa is any amino acid"  
 ; PCT-US95-00147-3

Query Match 36.4%; Score 4; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
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 Db 12 AKKK 15

## RESULT 50

PCT-US95-00147-76

; Sequence 76, Application PC/TUS9500147  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: Substrate Specificity of Protein Kinases  
 ; NUMBER OF SEQUENCES: 88  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 60 STATE STREET, suite 510  
 ; CITY: BOSTON  
 ; STATE: MASSACHUSETTS  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: ASCII text  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/00147  
 ; FILING DATE:  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/178,570  
 ; FILING DATE: JANUARY 7, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeConiti, Giulio A., Jr.  
 ; REGISTRATION NUMBER: 31,503  
 ; REFERENCE/DOCKET NUMBER: BJI-00407PC  
 ; TELEPHONE: (617) 227-7400  
 ; TELEFAX: (617) 227-5941  
 ; INFORMATION FOR SEQ ID NO: 76:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 3-6  
 ; OTHER INFORMATION: /note= "Xaa is any amino acid"  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 7  
 ; OTHER INFORMATION: /note= "Xaa is Ser, Thr or Tyr"  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 8-11  
 ; OTHER INFORMATION: /note= "Xaa is any amino acid"  
 ; PCT-US95-00147-76

Query Match 36.4%; Score 4; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 ||  
 Db 11 AKKK 14

Search completed. Sequence no. 203, 175, 125, 12  
 Job time: 141 sec

GenCore version 5.1.5  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: September 30, 2003, 17:21:47 : Search time 26 Seconds

(without alignments)  
64.015 Million cell updates/sec

Title: US-09-787-443-20

Perfect score: 11

Sequence: 1 AKKXEQKQRNA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 566894 seqs, 151107093 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6466

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : Published\_Applications\_AA:

- 1: /cqn2\_6/ptodata/2/pubpa/US07\_PUBCOMB.pep.\*
- 2: /cqn2\_6/ptodata/2/pubpa/PCT\_NK\_PUB.pep.\*
- 3: /cqn2\_6/ptodata/2/pubpa/US06\_NEW\_PUB.pep.\*
- 4: /cqn2\_6/ptodata/2/pubpa/US06\_PUBCOMB.pep.\*
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- 6: /cqn2\_6/ptodata/2/pubpa/PCTCS\_PUBCOMB.pep.\*
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- 13: /cqn2\_6/ptodata/2/pubpa/US10\_PUBCOMB.pep.\*
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- 18: /cqn2\_6/ptodata/2/pubpa/US06\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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10	4	36.4	9	10	US-09-916-201-17
11	4	36.4	9	12	US-10-291-250-13
12	4	36.4	9	12	US-10-077-106-13
13	4	36.4	9	12	US-10-077-106-15
14	4	36.4	9	12	US-10-304-443-102
15	4	36.4	9	14	US-10-011-321-4

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Sequence 19, Appl	19	4	36.4	11	US-09-813-653-5
Sequence 20, Appl	20	4	36.4	11	US-09-813-653-5
Sequence 21, Appl	21	4	36.4	11	US-09-813-653-5
Sequence 22, Appl	22	4	36.4	11	US-09-813-653-5
Sequence 23, Appl	23	4	36.4	11	US-09-813-653-5
Sequence 24, Appl	24	4	36.4	11	US-09-813-653-5
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Sequence 26, Appl	26	4	36.4	11	US-09-813-653-5
Sequence 27, Appl	27	4	36.4	11	US-09-813-653-5
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Sequence 31, Appl	31	4	36.4	11	US-09-813-653-5
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Sequence 33, Appl	33	4	36.4	11	US-09-813-653-5
Sequence 34, Appl	34	4	36.4	11	US-09-813-653-5
Sequence 35, Appl	35	4	36.4	11	US-09-813-653-5
Sequence 36, Appl	36	4	36.4	11	US-09-813-653-5
Sequence 37, Appl	37	4	36.4	11	US-09-813-653-5
Sequence 38, Appl	38	4	36.4	11	US-09-813-653-5
Sequence 39, Appl	39	4	36.4	11	US-09-813-653-5
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Sequence 42, Appl	42	4	36.4	11	US-09-813-653-5
Sequence 43, Appl	43	4	36.4	11	US-09-813-653-5
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Sequence 46, Appl	46	4	36.4	11	US-09-813-653-5
Sequence 47, Appl	47	4	36.4	11	US-09-813-653-5
Sequence 48, Appl	48	4	36.4	11	US-09-813-653-5
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Sequence 81, Appl	81	4	36.4	11	US-09-813-653-5
Sequence 82, Appl	82	4	36.4	11	US-09-813-653-5
Sequence 83, Appl	83	4	36.4	11	US-09-813-653-5
Sequence 84, Appl	84	4	36.4	11	US-09-813-653-5
Sequence 85, Appl	85	4	36.4	11	US-09-813-653-5
Sequence 86, Appl	86	4	36.4	11	US-09-813-653-5
Sequence 87, Appl	87	4	36.4	11	US-09-813-653-5
Sequence 88, Appl	88	4	36.4	11	US-09-813-653-5



[illegible]

381 10 9 US-09-010-714-4 Sequence 4, Appl 1 451  
382 10 9 US-09-819-308-19 Sequence 19, Appl 1 456  
383 10 9 US-09-150-947B-1 Sequence 3, Appl 1 456  
384 10 9 US-09-150-947B-4 Sequence 4, Appl 1 457  
385 10 9 US-09-124-280A-1 Sequence 12, Appl 1 458  
386 10 9 US-09-124-280A-12 Sequence 12, Appl 1 459  
387 10 9 US-09-124-280A-19 Sequence 19, Appl 1 460  
388 10 9 US-09-124-280A-42 Sequence 42, Appl 1 461  
389 10 9 US-09-694-427A-1 Sequence 1, Appl 1 462  
390 10 9 US-09-873-459A-47 Sequence 47, Appl 1 463  
391 10 9 US-09-845-667-18 Sequence 18, Appl 1 464  
392 10 9 US-09-845-667-26 Sequence 26, Appl 1 465  
393 10 9 US-09-780-662A-1 Sequence 1, Appl 1 466  
394 10 9 US-09-881-450-179 Sequence 179, Appl 1 467  
395 10 9 US-09-881-450-180 Sequence 180, Appl 1 468  
396 10 9 US-09-801-968-16 Sequence 16, Appl 1 469  
397 10 9 US-09-798-743A-25 Sequence 26, Appl 1 470  
398 10 10 US-09-780-053-287 Sequence 287, Appl 1 471  
399 10 10 US-09-780-053-284 Sequence 284, Appl 1 472  
400 10 10 US-09-780-053-376 Sequence 375, Appl 1 473  
401 10 10 US-09-780-053-479 Sequence 379, Appl 1 474  
402 10 10 US-09-950-692-4 Sequence 4, Appl 1 475  
403 10 10 US-09-984-056-86 Sequence 85, Appl 1 476  
404 10 10 US-09-984-056-91 Sequence 91, Appl 1 477  
405 10 10 US-09-764-176-18 Sequence 18, Appl 1 478  
406 10 10 US-09-780-133-19 Sequence 19, Appl 1 479  
407 10 10 US-04-973-145-5 Sequence 5, Appl 1 480  
408 10 10 US-09-824-568-5 Sequence 5, Appl 1 481  
409 10 10 US-09-962-172-129 Sequence 109, Appl 1 482  
410 10 10 US-09-952-432A-13 Sequence 13, Appl 1 483  
411 10 10 US-09-779-308-119 Sequence 119, Appl 1 484  
412 10 10 US-09-779-308-147 Sequence 147, Appl 1 485  
413 10 10 US-09-779-308-150 Sequence 150, Appl 1 486  
414 10 10 US-09-779-308-329 Sequence 329, Appl 1 487  
415 10 10 US-09-779-308-356 Sequence 356, Appl 1 488  
416 10 10 US-09-779-308-426 Sequence 426, Appl 1 489  
417 10 10 US-09-779-308-434 Sequence 434, Appl 1 490  
418 10 10 US-09-984-057-85 Sequence 85, Appl 1 491  
419 10 10 US-09-871-638-41 Sequence 41, Appl 1 492  
420 10 10 US-09-824-787B-16 Sequence 136, Appl 1 493  
421 10 10 US-09-824-787B-198 Sequence 188, Appl 1 494  
422 10 10 US-09-824-787B-345 Sequence 145, Appl 1 495  
423 10 10 US-09-554-050-55 Sequence 55, Appl 1 496  
424 10 10 US-09-805-101-4 Sequence 4, Appl 1 497  
425 10 10 US-09-805-101-42 Sequence 42, Appl 1 498  
426 10 10 US-09-805-101-44 Sequence 44, Appl 1 499  
427 10 10 US-09-995-847-2 Sequence 98, Appl 1 500  
428 10 10 US-09-770-102A-2 Sequence 2, Appl 1 501  
429 10 11 US-09-814-604-7 Sequence 7, Appl 1 502  
430 10 11 US-09-959-845-8 Sequence 8, Appl 1 503  
431 10 11 US-09-882-774-12 Sequence 12, Appl 1 504  
432 10 11 US-09-876-235-2 Sequence 2, Appl 1 505  
433 10 11 US-09-978-917A-48 Sequence 46, Appl 1 506  
434 10 11 US-09-799-250-298 Sequence 295, Appl 1 507  
435 10 11 US-09-799-250-343 Sequence 381, Appl 1 508  
436 10 11 US-09-154-793-3 Sequence 3, Appl 1 509  
437 10 11 US-09-882-291-65 Sequence 65, Appl 1 510  
438 10 11 US-09-882-291-66 Sequence 66, Appl 1 511  
439 10 11 US-09-882-291-71 Sequence 71, Appl 1 512  
440 10 11 US-09-775-052-45 Sequence 45, Appl 1 513  
441 10 11 US-09-880-748-3100 Sequence 3100, Appl 1 514  
442 10 11 US-09-876-904A-22 Sequence 22, Appl 1 515  
443 10 11 US-09-876-904A-152 Sequence 152, Appl 1 516  
444 10 11 US-09-876-904A-245 Sequence 245, Appl 1 517  
445 10 11 US-09-876-904A-274 Sequence 274, Appl 1 518  
446 10 11 US-09-876-904A-274 Sequence 274, Appl 1 519  
447 10 11 US-09-876-904A-440 Sequence 440, Appl 1 520  
448 10 11 US-09-876-904A-440 Sequence 440, Appl 1 521  
449 10 11 US-09-876-904A-546 Sequence 546, Appl 1 522  
450 10 11 US-09-876-904A-572 Sequence 572, Appl 1 523  
451 10 11 US-09-876-904A-598 Sequence 598, Appl 1 524  
452 10 11 US-09-922-226-41 Sequence 41, Appl 1 525  
453 10 11 US-09-572-404B-79 Sequence 79, Appl 1 526  
454 10 11 US-09-572-404B-447 Sequence 447, Appl 1 527

## APPENDIX

## RESULT 1

US-09-814-604-7  
1 Sequence 7, Appl 1  
2 Patent No. US-7,930,429 B2  
3 GENERAL INFORMATION  
4 APPLICANT: BEST, JAMES B  
5 APPLICANT: WITHDRAWN  
6 APPLICANT: NEW, BRYAN D  
7 APPLICANT: LAW, BRYAN D  
8 TITLE OF INVENTION: METHOD OF IDENTIFYING BINDING COMPONENTS  
9 FILE REFERENCE: US 2003/0000000  
10 CURRENT APPLICANT: US-7,930,429 B2  
11 PRIOR APPLICANT: US-7,930,429 B2  
12 PRIOR APPLICANT: US-7,930,429 B2  
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14 PRIOR APPLICANT: US-7,930,429 B2  
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17 PRIOR APPLICANT: US-7,930,429 B2  
18 PRIOR APPLICANT: US-7,930,429 B2  
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84 PRIOR APPLICANT: US-7,930,429 B2  
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87 PRIOR APPLICANT: US-7,930,429 B2  
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92 PRIOR APPLICANT: US-7,930,429 B2  
93 PRIOR APPLICANT: US-7,930,429 B2  
94 PRIOR APPLICANT: US-7,930,429 B2  
95 PRIOR APPLICANT: US-7,930,429 B2  
96 PRIOR APPLICANT: US-7,930,429 B2  
97 PRIOR APPLICANT: US-7,930,429 B2  
98 PRIOR APPLICANT: US-7,930,429 B2  
99 PRIOR APPLICANT: US-7,930,429 B2  
100 PRIOR APPLICANT: US-7,930,429 B2

SEQ ID NO 5  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: preferred peptide for pdz binding domain  
US-09-813-653-5

Query Match 36.4% Score 4; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 2 KKKE 5

RESULT 2  
US-09-813-448-2  
Sequence 2, Application US/09813448  
Patent No. US20020142346A1  
GENERAL INFORMATION:  
APPLICANT: Nestor, John  
TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds  
FILE REFERENCE: CNS-006  
CURRENT APPLICATION NUMBER: US/09/813.448  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: US 60/190,946  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/190,996  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/191,299  
PRIOR FILING DATE: 2000-03-21  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: preferred amino acids for PDZ binding domain  
US-09-813-448-2

Query Match 36.4% Score 4; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 2 KKKE 5

RESULT 3  
US-09-876-904A-352  
Sequence 352, Application US/99876904A  
Publication No. US2003007294A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMODIAL DNA (LIP GENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/POSITIVE PEPTIDE  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876.904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 352  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens

FEATURE:  
OTHER INFORMATION: Human ATR11.1, basic region/leucine zipper  
US-09-876-904A-352

Query Match 66.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 5 KKKE 5

RESULT 4  
US-09-876-904A-394  
Sequence 394, Application US/99876904A  
Publication No. US2003007294A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMODIAL DNA (LIP GENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/POSITIVE PEPTIDE  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876.904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 394  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: from 11 to 199 (related to 398/416)  
US-09-876-904A-394

Query Match 66.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 5 KKKE 5

RESULT 5  
US-09-876-904A-394  
Sequence 394, Application US/99876904A  
Publication No. US2003007294A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMODIAL DNA (LIP GENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/POSITIVE PEPTIDE  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876.904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 394  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: from 11 to 199 (related to 398/416)  
US-09-876-904A-394

Query Match 66.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKE 5  
DB 5 KKKE 5



QY 2 KKKE 5  
IIII  
Db 5 KKKE 8

## RESULT 6

US-10-014-322A-62  
; Sequence 62, Application US/10014322A  
; Publication No. US20030167129A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, Jr., John  
; APPLICANT: Wilson, Carol  
; APPLICANT: Tan Hehir, Christina  
; APPLICANT: Kates, Steven  
; APPLICANT: Krstenansky, John  
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds  
; FILE REFERENCE: CNS-008  
; CURRENT APPLICATION NUMBER: US/10/014.322A  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: US 60/243,587  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 09/813,651  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 09/813,653  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 09/813,448  
; PRIOR FILING DATE: 2001-03-20  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 62  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred peptide for p32 binding domain  
US-10-014-322A-62

Query Match 36.4%, Score 4, DB 12, Length 8;  
Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 2 KKKE 5  
IIII  
Db 2 KKKE 5

## RESULT 7

US-10-024-935-19  
; Sequence 19, Application US/10024935  
; Publication No. US20020142966A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth Walter Bair  
; APPLICANT: YingNan Fan Chen  
; APPLICANT: Timothy Michael Ramsey  
; APPLICANT: Michael Lloyd Sabio  
; APPLICANT: Sushill Kumar Sharma  
; TITLE OF INVENTION: Inhibitors of the F2R1/tyrosin  
; FILE REFERENCE: 4-31664P1/Procy Interaction for Cancer Therapy  
; CURRENT APPLICATION NUMBER: US/10/024,935  
; CURRENT FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic protein  
US-10-024-935-19

Query Match 36.4%, Score 4, DB 14, Length 8;

Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AKKK 4  
III  
Db 2 AKKK 5

## RESULT 8

US-10-040-572-8  
; Sequence 8, Application US/10040572  
; Publication No. US2003057190A1  
; GENERAL INFORMATION:  
; APPLICANT: Sky Robotics  
; APPLICANT: Bathurst, David  
; APPLICANT: Pecher, Matthew  
; TITLE OF INVENTION: Artificial ANTI-AP-PTIC COMPOSITIONS  
; FILE REFERENCE: 414,231  
; CURRENT APPLICATION NUMBER: US/10/040,572  
; CURRENT FILING DATE: 2002-07-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
US-10-040-572-8

Query Match 66.4%, Score 4, DB 14, Length 8;  
Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AKKK 4  
I  
Db 4 AKKK 7

## RESULT 9

US-09-879-936-24  
; Sequence 24, Application US/0909879936  
; Patent No. US2003040044A1  
; GENERAL INFORMATION:  
; APPLICANT: VBI Pharmaceuticals  
; APPLICANT: Mark A. Jones  
; APPLICANT: Walter, Robert J  
; TITLE OF INVENTION: Islet Water-soluble Muscle Contraction  
; FILE REFERENCE: 1997-23,048  
; CURRENT APPLICATION NUMBER: US/09/879,936  
; CURRENT FILING DATE: 2001-07-14  
; PRIOR APPLICATION NUMBER: 09/564,478  
; PRIOR FILING DATE: 1997-06-24  
; PRIOR APPLICATION NUMBER: 09/564,478  
; PRIOR FILING DATE: 1997-06-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: PEP-IDE  
; LOCATION: (1) (3)  
; OTHER INFORMATION: Postlines 26, to 38 of 107  
; NAME/KEY: PEP-IDE  
; LOCATION: (9)  
; OTHER INFORMATION: Islet-soluble serine-phospho-amino acid  
US-09-879-936-24

Query Match 66.4%, Score 4, DB 9, Length 9;

Best Local Similarity 100.0%, Pred. No. 5e-05;  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 AKKK 4

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DB          5 AKKK 8
RESULT 10
US-09-916-201-17
; Sequence 17, Application US/09916201
; Patent No. US20020131976A1
; GENERAL INFORMATION:
; APPLICANT: KALVANI, Ajit
; APPLICANT: LALVANI, Ajit
; APPLICANT: PATHANI, Anwar A.
; TITLE OF INVENTION: TUBERCULOSIS VACCINE
; FILE REFERENCE: 117-359
; CURRENT APPLICATION NUMBER: US/09/916,201
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/467,895
; PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: M.tuberculosis
US-09-916-201-17
Query Match          36.4%  Score 4: 16 10: Length 9:
Best Local Similarity 100.0%  Pred. No. 65009
Matches 4:  Conservative 0:  Mismatches 0:  Labels 0:  Gaps 0:

QY          5 EQKQ 8
DB          1111
          1 EQKQ 4
RESULT 11
US-10-291-250-13
; Sequence 13, Application US/10291250
; Publication No. US20030133912A1
; GENERAL INFORMATION:
; APPLICANT: University of Iowa Research Foundation
; APPLICANT: Davidson, Beverly L.
; APPLICANT: Xia, Haibin
; APPLICANT: Law, Lane K.
; TITLE OF INVENTION: RECEPTOR-TARGETED ADENOVIRAL VECTORS
; FILE REFERENCE: 875.051051
; CURRENT APPLICATION NUMBER: US/10/291,250
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/139,242
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Adenovirus
US-10-291-250-13
Query Match          36.4%  Score 4: 16 12: Length 9:
Best Local Similarity 100.0%  Pred. No. 65009
Matches 4:  Conservative 0:  Mismatches 0:  Labels 0:  Gaps 0:

QY          1 AKKK 4
DB          1111
          3 AKKK 6
RESULT 12
US-10-077-106-13
; Sequence 13, Application US/10077106
; Publication No. US20030166531A1

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: CURRENT APPLICATION NUMBER: US/10/304.443  
 : CURRENT FILING DATE: 2002-11-26  
 : PRIOR APPLICATION NUMBER: US/09/698.936A  
 : PRIOR FILING DATE: 2001-02-20  
 : NUMBER OF SEQ ID NOS: 121  
 : SOFTWARE: FASTSEQ for Windows Version 3.0  
 : SEQ ID NO 102  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Human peptide sequence  
 US-10-304-443-102

Query Match 36.4% Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 50/65;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KORN 10  
 IIII  
 Db 2 KURN 5

RESULT 15  
 US-10-011-321-4  
 : Sequence 4, Application US/10/11321  
 : Publication No. US20020102268A1  
 : GENERAL INFORMATION:  
 : APPLICANT: KISS, Terry  
 : TITLE OF INVENTION: APOPTOSIS MAKER ANTIBODIES AND METHODS OF USE  
 : FILE REFERENCE: 16026-9033  
 : CURRENT APPLICATION NUMBER: US/10/011.42;  
 : CURRENT FILING DATE: 2001-12-03  
 : PRIOR APPLICATION NUMBER: 09/445,615  
 : PRIOR FILING DATE: 1999-12-08  
 : PRIOR APPLICATION NUMBER: 60/101,920  
 : PRIOR FILING DATE: 1998-09-24  
 : NUMBER OF SEQ ID NOS: 5  
 : SOFTWARE: Patent In Ver. 2.0  
 : SEQ ID NO: 4  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-011-321-4

Query Match 36.4% Score 4; DB 14; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 50/65;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 IIII  
 Db 5 AKKK 9

RESULT 16  
 US-10-211-207-13  
 : Sequence 14, Application US/10/211.207  
 : Publication No. US20030004113A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Collins, Mary  
 : APPLICANT: Madtenas, Joaquin  
 : APPLICANT: Carreno, Beatriz  
 : APPLICANT: Kuchroo, Vijay  
 : TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 : TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CD14 AND  
 : TITLE OF INVENTION: PP2A  
 : FILE REFERENCE: GNN-027  
 : CURRENT APPLICATION NUMBER: US/10/211.207  
 : CURRENT FILING DATE: 2002-09-02  
 : PRIOR APPLICATION NUMBER: US/10/077.106  
 : PRIOR FILING DATE: 2002-02-15  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 13  
 : LENGTH: 9

: TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-211-207-13

Query Match 36.4% Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 50/65;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKK 1  
 IIII  
 Db 5 AKKK 5

RESULT 17  
 US-10-211-207-13  
 : Sequence 15, Application US/10/211.207  
 : Publication No. US20030004113A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Collins, Mary  
 : APPLICANT: Madtenas, Joaquin  
 : APPLICANT: Carreno, Beatriz  
 : APPLICANT: Kuchroo, Vijay  
 : TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 : TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CD14 AND  
 : TITLE OF INVENTION: PP2A  
 : FILE REFERENCE: GNN-027  
 : CURRENT APPLICATION NUMBER: US/10/211.207  
 : CURRENT FILING DATE: 2002-09-02  
 : PRIOR APPLICATION NUMBER: US/10/077.106  
 : PRIOR FILING DATE: 2002-02-15  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 15  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-211-207-13

Query Match 36.4% Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 50/65;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKK 1  
 IIII  
 Db 5 AKKK 5

RESULT 18  
 US-10-211-207-13  
 : Sequence 15, Application US/10/211.207  
 : Publication No. US20030004113A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Collins, Mary  
 : APPLICANT: Madtenas, Joaquin  
 : APPLICANT: Carreno, Beatriz  
 : APPLICANT: Kuchroo, Vijay  
 : TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 : TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CD14 AND  
 : TITLE OF INVENTION: PP2A  
 : FILE REFERENCE: GNN-027  
 : CURRENT APPLICATION NUMBER: US/10/211.207  
 : CURRENT FILING DATE: 2002-09-02  
 : PRIOR APPLICATION NUMBER: US/10/077.106  
 : PRIOR FILING DATE: 2002-02-15  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 17  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : OTHER INFORMATION: FASTSEQ for Windows Version 4.0  
 : OTHER INFORMATION: FASTSEQ for Windows Version 4.0  
 US-10-211-207-13

Query Match 36.4% Score 4; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 5,30-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKKK 4  
DB 7 AKKK 10

RESULT 19

US-09-876-904A-90  
; Sequence 90, Application US/09876904A  
; Publication No. US2003007294A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMO DNA (LIPID-GENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/GENIC PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPIDOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/2210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 90  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Xenopus  
US-09-876-904A-90

Query Match 36.48; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,30-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKKK 4  
DB 4 AKKK 7

RESULT 20

US-09-572-404B-1694  
; Sequence 1694, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 1694  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Sequence located in LAMA2 OR LAMM at 1-10,14-25 and may interact  
; OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

Query Match 36.48; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,30-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKKE 5  
DB 1 KKKE 4

RESULT 21

US-09-572-404B-1694  
; Sequence 1694, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 1694  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Sequence located in LAMA2 OR LAMM at 1-10,14-25 and may interact  
; OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

Query Match 36.48; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,30-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKKE 5  
DB 1 KKKE 4

RESULT 22

US-09-572-404B-1694  
; Sequence 1694, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 1694  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Sequence located in CYP11 at 73-82 and may interact with Sec  
; OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

Query Match 36.48; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,30-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKKE 5  
DB 1 KKKE 4

RESULT 23

US-09-572-404B-1694  
; Sequence 1694, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 1694  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Sequence located in LAMA2 OR LAMM at 1-10,14-25 and may interact  
; OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

RESULT 24

US-09-572-404B-1694  
; Sequence 1694, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: Protpatent version 1.0  
; SEQ ID NO 1694  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Sequence located in LAMA2 OR LAMM at 1-10,14-25 and may interact  
; OTHER INFORMATION: Sequence 1694 in this patent  
US-09-572-404B-1694

TYPE: PRI  
ORGANISM: Arabidopsis Thaliana  
OTHER INFORMATION: Sequence located in AG, at 255-264 and may interact with  
US-09-572-270A-97

Query Match 36.4%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,40-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKEQ 6  
Db 1 KKEQ 4

RESULT 24

US-09-572-270A-99  
Sequence 99, Application US/09572270A  
Publication No. US20030148368A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Inter-complementary peptide listing  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/572.270A  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 1144  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 99  
LENGTH: 10  
TYPE: PRI  
ORGANISM: Arabidopsis Thaliana  
OTHER INFORMATION: Sequence located in AG, at 255-264 and may interact with  
US-09-572-270A-99

Query Match 36.4%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,40-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKEQ 6  
Db 1 KKEQ 4

RESULT 25

US-09-572-270A-318  
Sequence 318, Application US/09572270A  
Publication No. US20030148368A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Inter-complementary peptide listing  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/572.270A  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 1144  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 318  
LENGTH: 10  
TYPE: PRI  
ORGANISM: Arabidopsis Thaliana  
OTHER INFORMATION: Sequence located in PG2, at 1249-1258 and may interact with  
US-09-572-270A-318

Query Match 36.4%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,40-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
Db 1 AKKK 4

RESULT 26

US-09-572-270A-320  
Sequence 320, Application US/09572270A

Publication No. US20030148368A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Inter-complementary peptide listing  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/572.270A  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 1144  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 320  
LENGTH: 10  
TYPE: PRI  
ORGANISM: Arabidopsis Thaliana  
OTHER INFORMATION: Sequence located in PG2, at 1249-1258 and may interact with  
US-09-572-270A-320

Query Match 36.4%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5,40-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
Db 1 AKKK 4

RESULT 27

US-09-572-270A-439  
Sequence 439, Application US/09572270A  
Publication No. US20030148368A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Inter-complementary peptide listing  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/572.270A  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 1144  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 439  
LENGTH: 10  
TYPE: PRI  
ORGANISM: Arabidopsis Thaliana  
OTHER INFORMATION: Sequence located in PG2, at 1249-1258 and may interact with  
US-09-572-270A-439

QY 1 AKKK 4  
Db 1 AKKK 4

RESULT 28

US-09-572-270A-444  
Sequence 444, Application US/09572270A  
Publication No. US20030148368A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Inter-complementary peptide listing  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/572.270A  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 1144  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 444  
LENGTH: 10  
TYPE: PRI  
ORGANISM: Arabidopsis Thaliana  
OTHER INFORMATION: Sequence located in PG2, at 1249-1258 and may interact with  
US-09-572-270A-444

QY 1 AKKK 4  
Db 1 AKKK 4

RESULT 29

US-09-572-270A-445  
Sequence 445, Application US/09572270A

APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of  
FILE OF INVENTION: Cancer  
FILE REFERENCE: 51158-20062.01  
CURRENT APPLICATION NUMBER: US/10/062,109A  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 444  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-062-109A-444

Query Match 36.4%, Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5, 7e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KORN 10  
DB 6 KORN 9

RESULT 29  
US-09-876-904A-273  
Sequence 273, Application US/09/876,904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PTC-GENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPID-SOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 273  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Drosophila sp.  
FEATURE:  
OTHER INFORMATION: Recombination repair protein 1  
US-09-876-904A-273

Query Match 36.4%, Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5, 7e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 5  
DB 6 KKE 9

RESULT 40  
US-09-876-904A-354  
Sequence 354, Application US/09/876,904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PTC-GENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPID-SOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 354  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human AFP (the cystic region that binds DNA)  
US-09-876-904A-354

Query Match 36.4%, Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5, 7e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 5  
DB 6 KKE 9

RESULT 41  
US-10-062-109A-444  
Sequence 444, Application US/10/062,109A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: Jakobovits, Aya  
APPLICANT: VITRO, G. L. L.  
APPLICANT: MATTHEW, L. L.  
APPLICANT: AGENTSE, L. L. L.  
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTIC  
FILE REFERENCE: 2002.01  
CURRENT APPLICATION NUMBER: US/10/062,109A  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2002-01-31  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 444  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Human AFP (the cystic region that binds DNA)  
US-10-062-109A-444

Query Match 36.4%, Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5, 7e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 5  
DB 6 KKE 9

RESULT 42  
US-10-062-109A-444  
Sequence 444, Application US/10/062,109A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: Jakobovits, Aya  
APPLICANT: MATTHEW, L. L.  
APPLICANT: AGENTSE, L. L. L.  
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTIC  
FILE REFERENCE: 2002.01  
CURRENT APPLICATION NUMBER: US/10/062,109A  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2002-01-31  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 444  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-304-443-91

Query Match 36.48; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5,76+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KORN 10  
DB 3 KORN 6

RESULT 37

US-10-020-269-34  
Sequence 34, Application US/10020269  
Publication No. US20030175310A1  
GENERAL INFORMATION:  
APPLICANT: Mitchell, William M.  
APPLICANT: Stratton, Charles W.  
TITLE OF INVENTION: IDENTIFICATION OF ANTIHERPES PEPTIDE  
TITLE OF INVENTION: SEQUENCES  
FILE REFERENCE: VDE98-01  
CURRENT APPLICATION NUMBER: US/10/020,269  
CURRENT FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/020,196  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/024,921  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-14  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 34  
LENGTH: 11  
TYPE: PRI  
ORGANISM: Chlamydia pneumoniae  
US-10-020-269-34

Query Match 36.48; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5,76+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 3 AKKK 6

RESULT 34

US-09-985-157-11  
Sequence 11, Application US/09985157  
Patent No. US20020145797A1  
GENERAL INFORMATION:  
APPLICANT: SHOKAT, Kevan M.  
TITLE OF INVENTION: Engineered Protein Kinases Which Can Utilize Modified Nucleotides  
TITLE OF INVENTION: Triphosphate Substrates  
FILE REFERENCE: 51538-5002-05  
CURRENT APPLICATION NUMBER: US/09/985,157  
CURRENT FILING DATE: 2002-03-13  
PRIOR APPLICATION NUMBER: US 09/367,065  
PRIOR FILING DATE: 1999-11-17  
PRIOR APPLICATION NUMBER: PCT/US98/02522  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 60/046,727  
PRIOR FILING DATE: 1997-05-16  
PRIOR APPLICATION NUMBER: US 08/797,552  
PRIOR FILING DATE: 1997-02-07  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 12  
TYPE: PRI  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Optimized Abl substrate  
US-09-985-157-11

Query Match 36.48; Score 4; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,76+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 9 AKKK 7

RESULT 35

US-09-882-291-54  
Sequence 54, Application US/09882291  
Publication No. US20030175310A1  
GENERAL INFORMATION:  
APPLICANT: Zeng and Peckham  
TITLE OF INVENTION: Nucleoside Analogues, Peptide Analogues  
FILE REFERENCE: 51538-5002-05  
CURRENT APPLICATION NUMBER: US/09/882,291  
CURRENT FILING DATE: 2001-12-14  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 12  
TYPE: PRI  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Optimized Abl substrate  
US-09-882-291-54

Query Match 36.48; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,76+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
DB 2 AKKK 6

RESULT 36

US-09-876-904-78  
Sequence 78, Application US/09876904  
Publication No. US20030175310A1  
GENERAL INFORMATION:  
APPLICANT: POLIKAS, LEE  
TITLE OF INVENTION: ANALOGS OF FLASHP DNA (LIPID-SPONSORED) AND FLASHP-FLIP-  
TITLE OF INVENTION: ANALOGS WITH MODIFIED LOCALIZATION SIGNAL/FLASHP-FLIP-  
TITLE OF INVENTION: ANALOGS WITH MODIFIED LOCALIZATION SIGNAL/FLASHP-FLIP-  
FILE REFERENCE: 51538-5002-05  
CURRENT APPLICATION NUMBER: US/09/876,904  
CURRENT FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/021,925  
PRIOR FILING DATE: 1998-02-09  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 78  
LENGTH: 12  
TYPE: PRI  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Optimized Abl substrate  
US-09-876-904-78

Query Match 36.48; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,76+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKK 7  
DB 9 KKKK 12

RESULT 37

US-09-954-385-126  
 : Sequence 126, Application US/04954385  
 : Publication No. US20030100467A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Aehle, Wolfgang  
 : APPLICANT: Baldwin, Toby L.  
 : APPLICANT: Van Gastel, Franciscus J.G.  
 : APPLICANT: Janssen, Giselle G.  
 : APPLICANT: Murray, Christopher J.  
 : APPLICANT: Wang, Huaming  
 : APPLICANT: Winetzk, Deborah S.  
 : TITLE OF INVENTION: Binding Phenol oxidizing Enzyme-partic  
 : FILE REFERENCE: GC690  
 : CURRENT APPLICATION NUMBER: US/09/954,385  
 : NUMBER OF SEQ ID NOS: 12  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 126  
 : LENGTH: 12  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: binding peptide  
 US-09-954-385-126

Query Match 36.4% Score 45 PR 12 Length 12  
 Best Local Similarity 100.0% Pref No. 6, Length 12  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0

OY 6 OKOR 9  
 IIII  
 DB 8 OKOR 11

RESULT 18  
 US-10-293-086-75  
 : Sequence 75, Application US/1029386  
 : Publication No. US20030134310A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Cujec, Thomas P.  
 : TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors  
 : FILE REFERENCE: 50036/048002  
 : CURRENT APPLICATION NUMBER: US/10/293,086  
 : CURRENT FILING DATE: 2003-03-25  
 : PRIOR APPLICATION NUMBER: US 60/147,499  
 : PRIOR FILING DATE: 2001-11-14  
 : NUMBER OF SEQ ID NOS: 14  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 75  
 : LENGTH: 12  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Phenylalanine derivative  
 US-10-293-086-75

Query Match 36.4% Score 45 PR 12 Length 12  
 Best Local Similarity 100.0% Pref No. 6, Length 12  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0

OY 1 AKKK 4  
 IIII  
 DB 9 AKKK 12

RESULT 39  
 US-10-293-086-95  
 : Sequence 95, Application US/1029386  
 : Publication No. US20030134310A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Cujec, Thomas P.

: TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors  
 : FILE REFERENCE: 50036/048002  
 : CURRENT APPLICATION NUMBER: US/10/293,086  
 : CURRENT FILING DATE: 2003-03-25  
 : PRIOR APPLICATION NUMBER: US 60/147,499  
 : PRIOR FILING DATE: 2001-11-14  
 : NUMBER OF SEQ ID NOS: 14  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 95  
 : LENGTH: 12  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Phenylalanine derivative  
 US-10-293-086-95

Query Match 36.4% Score 45 PR 12 Length 12  
 Best Local Similarity 100.0% Pref No. 6, Length 12  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0

OY 1 AKKK 4  
 IIII  
 DB 9 AKKK 12

RESULT 40  
 US-10-293-086-111  
 : Sequence 111, Application US/1029386  
 : Publication No. US20030134310A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Cujec, Thomas P.  
 : TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors  
 : FILE REFERENCE: 50036/048002  
 : CURRENT APPLICATION NUMBER: US/10/293,086  
 : CURRENT FILING DATE: 2003-03-25  
 : PRIOR APPLICATION NUMBER: US 60/147,499  
 : PRIOR FILING DATE: 2001-11-14  
 : NUMBER OF SEQ ID NOS: 14  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 111  
 : LENGTH: 12  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Phenylalanine derivative  
 US-10-293-086-111

Query Match 36.4% Score 45 PR 12 Length 12  
 Best Local Similarity 100.0% Pref No. 6, Length 12  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0

OY 1 AKKK 4  
 IIII  
 DB 9 AKKK 12

RESULT 41  
 US-10-293-086-119  
 : Sequence 119, Application US/1029386  
 : Publication No. US20030134310A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Cujec, Thomas P.  
 : TITLE OF INVENTION: Cellular Kinase Targets and Inhibitors  
 : FILE REFERENCE: 50036/048002  
 : CURRENT APPLICATION NUMBER: US/10/293,086  
 : CURRENT FILING DATE: 2003-03-25  
 : PRIOR APPLICATION NUMBER: US 60/147,499  
 : PRIOR FILING DATE: 2001-11-14  
 : NUMBER OF SEQ ID NOS: 14  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO 119  
 : LENGTH: 12  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Phenylalanine derivative  
 US-10-293-086-119

Query Match 36.4% Score 45 PR 12 Length 12  
 Best Local Similarity 100.0% Pref No. 6, Length 12  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0

OY 1 AKKK 4  
 IIII  
 DB 9 AKKK 12



```

? PRIOR FILING DATE: 2000-05-26
? NUMBER OF SEQ ID NOS: 36
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 15
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: peptide
US-10-355-975-35

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Query Match 36.4%, Score 4, DB 12, Length 12,  
Best Local Similarity 100.0%, Pred. No. 6,100/2,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

```

QY 1 AKKK 4
    ||||
DB 9 AKKK 12

```

## RESULT 42

```

US-10-119-528-100
? Sequence 100, Application US/10119528
? Publication No. US20030175722A1
? GENERAL INFORMATION:
? APPLICANT: Mann, M.
? APPLICANT: Mortensen, P.
? TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING PHARMACOLOGICAL DATABASES
? FILE REFERENCE: MDSP-P01-004
? CURRENT APPLICATION NUMBER: US/10119528
? CURRENT FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/282,551
? PRIOR FILING DATE: 2001-04-09
? PRIOR APPLICATION NUMBER: 60/285,362
? PRIOR FILING DATE: 2001-04-20
? NUMBER OF SEQ ID NOS: 112
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 100
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Arabidopsis thaliana
US-10-119-528-100

```

Query Match 36.4%, Score 4, DB 12, Length 12,  
Best Local Similarity 100.0%, Pred. No. 6,100/2,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

```

QY 4 KEQK 7
    ||||
DB 8 KEQK 11

```

## RESULT 43

```

US-10-032-827A-7
? Sequence 7, Application US/10032827A
? Publication No. US20030049799A1
? GENERAL INFORMATION:
? APPLICANT: Schwartz, John J.
? APPLICANT: Jacobson, Joseph
? APPLICANT: Dasgupta, Ruchira
? TITLE OF INVENTION: Engineered Stimulus Responsive Switches
? FILE REFERENCE: EN2-004
? CURRENT APPLICATION NUMBER: US/10-23
? CURRENT FILING DATE: 2001-10-23
? PRIOR APPLICATION NUMBER: US 60/242,546
? PRIOR FILING DATE: 2000-10-23
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 7
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:

```

```

? OTHER INFORMATION:
US-10-032-827A-7

```

Query Match 36.4%, Score 4, DB 15, Length 12,  
Best Local Similarity 100.0%, Pred. No. 6,100/2,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

```

QY 1 AKKK 4
    |||
DB 9 AKKK 12

```

## RESULT 44

```

US-10-044-447-1
? Sequence 14, Application 100, Length 12,
? Publication No. US20030175722A1
? GENERAL INFORMATION:
? APPLICANT: Mann, M.
? APPLICANT: Mortensen, P.
? TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING PHARMACOLOGICAL DATABASES
? FILE REFERENCE: MDSP-P01-004
? CURRENT APPLICATION NUMBER: US/10119528
? CURRENT FILING DATE: 2002-04-09
? PRIOR APPLICATION NUMBER: 60/282,551
? PRIOR FILING DATE: 2001-04-09
? PRIOR APPLICATION NUMBER: 60/285,362
? PRIOR FILING DATE: 2001-04-20
? NUMBER OF SEQ ID NOS: 112
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 14
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Arabidopsis thaliana
? FEATURE:
? OTHER INFORMATION:
US-10-044-447-1

```

Query Match 36.4%, Score 4, DB 15, Length 12,  
Best Local Similarity 100.0%, Pred. No. 6,100/2,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

```

QY 1 AKKK 4
    |||
DB 9 AKKK 12

```

## RESULT 45

```

US-10-267-449-2
? Sequence 45, Application 100, Length 12,
? Publication No. US20030175722A1
? GENERAL INFORMATION:
? APPLICANT: Mann, M.
? APPLICANT: Mortensen, P.
? TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING PHARMACOLOGICAL DATABASES
? FILE REFERENCE: MDSP-P01-004
? CURRENT APPLICATION NUMBER: US/10-23
? CURRENT FILING DATE: 2001-10-23
? PRIOR APPLICATION NUMBER: US 60/242,546
? PRIOR FILING DATE: 2000-10-23
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 49
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
US-10-267-449-2

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Query Match 36.4%, Score 4, DB 15, Length 12,  
Best Local Similarity 100.0%, Pred. No. 6,100/2,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 AKKK 4  
 DB 6 AKKK 9

## RESULT 46

US-09-746-170-19  
 ; Sequence 19, Application US/09746170  
 ; Patent No. US20020127543A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Karn, Jonathan  
 ; APPLICANT: Walker, Stephen  
 ; TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules  
 ; FILE REFERENCE: 22620/1280  
 ; CURRENT APPLICATION NUMBER: US/09/746,170  
 ; CURRENT FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/71,804  
 ; PRIOR FILING DATE: 1999-12-22  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 19  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Hepatitis C virus  
 US-09-746-170-19

Query Match 36.4%; Score 4; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OKQR 9  
 DB 5 OKQR 8

## RESULT 47

US-09-876-904A-88  
 ; Sequence 88, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/USOCENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002-00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 88  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Xenopus  
 ; OTHER INFORMATION: nucleoplasmIn  
 US-09-876-904A-88

Query Match 36.4%; Score 4; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 DB 7 AKKK 10

## RESULT 48

US-09-876-904A-89  
 ; Sequence 89, Application US/09876904A

Publication No. US20030072794A1

GENERAL INFORMATION:  
 APPLICANT: BOULIKAS, TENI  
 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/USOCENIC PEPTIDE  
 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 FILE REFERENCE: TB-2002-00  
 CURRENT APPLICATION NUMBER: US/09/876,904A  
 CURRENT FILING DATE: 2001-06-08  
 PRIOR APPLICATION NUMBER: US 60/210,925  
 PRIOR FILING DATE: 2000-06-09  
 NUMBER OF SEQ ID NOS: 629  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 89  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Xenopus  
 OTHER INFORMATION: nucleoplasmIn  
 US-09-876-904A-89

Query Match 36.4%; Score 4; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 DB 7 AKKK 10

## RESULT 49

US-09-876-904A-92  
 ; Sequence 92, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/USOCENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002-00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 92  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Unknown Organism  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: XPC gene product  
 US-09-876-904A-92

Query Match 36.4%; Score 4; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKK 4  
 DB 7 AKKK 10

## RESULT 50

US-10-291-25-92  
 ; Sequence 92, Application US/1-29125-92  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Iowa Research Foundation  
 ; APPLICANT: Davidson, Beverly L.  
 ; APPLICANT: XIA, GUOLIN  
 ; APPLICANT: Gao, Lame K.

; TITLE OF INVENTION: RECEPTOR-TARGETED ADENOVIRAL VECTORS
; FILE REFERENCE: 875.051US1
; CURRENT APPLICATION NUMBER: US/10/291,250
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/339,282
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A protein motif.
US-10-291-250-32

Query Match 36.4% Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 6,40-02;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 AKKK 4
Db 4 AKKK 7

Search completed: September 30, 2003, 17:25:43
Job time : 28 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compucon Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 ; Search time 41.083 seconds  
(without alignments)  
42.495 Million cell updates/sec

Title: US-09-787-443-21

perfect score:

Sequence: 1 AKSRKGNSSLML

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of bits satisfying chosen parameters: 23,524

Minimum for sea level: 8

Minimum DB seq length:	6
Maximum DB seq length:	15

### post-processing: Listing first 500 summaries

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- 2: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1981.DAT \*
- 3: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1982.DAT \*
- 4: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1983.DAT \*
- 5: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1984.DAT \*
- 6: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1985.DAT \*
- 7: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1986.DAT \*
- 8: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1987.DAT \*
- 9: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1988.DAT \*
- 10: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1989.DAT \*
- 11: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1990.DAT \*
- 12: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1991.DAT \*
- 13: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1992.DAT \*
- 14: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA1993.DAT \*
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- 21: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA2000.DAT \*
- 22: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA2001.DAT \*
- 23: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA2002.DAT \*
- 24: /SIDSL/cqcdata/geneseq/geneseq-emb1/AA2003.DAT \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

Result No.	Query	%		DB	ID	Description
		Score	Match			
1	11	100.0	11	21	AAV88549	NCAM Iq1 binding p
2	11	100.0	11	23	ABG69349	Human neural cell
3	5	45.5	14	21	AAV87836	M. tuberculosis an
4	4	36.4	8	10	AAV91025	Bacter for prodn.
5	4	36.4	8	21	AAV82894	Antigenic peptide
6	4	36.4	8	21	AAV67468	NF79 peptide havin
7	4	36.4	8	22	ABP11995	HIV AG2 super moti
8	4	36.4	8	22	ABP14271	HIV A03 super moti
9	4	36.4	8	22	ABP19801	HIV AG3 motif env



229	3	27.3	8	22	ABP11534	HIV A21 super motif	334	27.3	4	22	AA060426	Human CD4 receptor
230	3	27.3	8	22	ABP11964	HIV A22 super motif	334	27.3	4	22	AA060427	Human CD4 receptor
231	3	27.3	8	22	ABP15172	HIV A24 super motif	334	27.3	4	22	AA060428	Human CD4 receptor
232	3	27.3	8	22	ABP15214	HIV A24 super motif	334	27.3	4	22	AA060429	Human CD4 receptor
233	3	27.3	8	22	ABP15925	HIV A24 super motif	334	27.3	4	22	AA060430	Human CD4 receptor
234	3	27.3	8	22	ABP17123	HIV B27 super motif	334	27.3	4	22	AA060431	Human CD4 receptor
235	3	27.3	8	22	ABP17614	HIV B58 super motif	334	27.3	4	22	AA060432	Human CD4 receptor
236	3	27.3	8	22	ABP18496	HIV B62 super motif	334	27.3	4	22	AA060433	Human CD4 receptor
237	3	27.3	8	22	ABP19840	HIV A23 motif env	334	27.3	4	22	AA060434	Human CD4 receptor
238	3	27.3	8	22	ABP22154	HIV A11 motif env	334	27.3	4	22	AA060435	Human CD4 receptor
239	3	27.3	8	22	ABP22465	HIV A11 motif env	334	27.3	4	22	AA060436	Human CD4 receptor
240	3	27.3	8	22	ABP24315	HIV A24 motif: hel	334	27.3	4	22	AA060437	Human CD4 receptor
241	3	27.3	8	22	AA009935	Systemic proteolytic	334	27.3	4	22	AA060438	Human CD4 receptor
242	3	27.3	8	22	AA065836	Type III mutant: B3	334	27.3	4	22	AA060439	Human CD4 receptor
243	3	27.3	8	22	AA098418	Human peptide: A15	334	27.3	4	22	AA060440	Human CD4 receptor
244	3	27.3	8	22	AA069074	Bacterial conserve	334	27.3	4	22	AA060441	Human CD4 receptor
245	3	27.3	8	22	AA069086	Bacterial conserve	334	27.3	4	22	AA060442	Human CD4 receptor
246	3	27.3	8	22	AA069109	Bacterial conserve	334	27.3	4	22	AA060443	Human CD4 receptor
247	3	27.3	8	22	AA051525	SV40 VP1 protein: B	334	27.3	4	22	AA060444	Human CD4 receptor
248	3	27.3	8	22	AA069789	Acidic acid sequence	334	27.3	4	22	AA060445	Human CD4 receptor
249	3	27.3	8	22	AA060936	KIX domain binding	334	27.3	4	22	AA060446	Human CD4 receptor
250	3	27.3	8	22	AA060520	Zinc finger protein	334	27.3	4	22	AA060447	Human CD4 receptor
251	3	27.3	9	22	AA006623	Zinc finger protein	334	27.3	4	22	AA060448	Human CD4 receptor
252	3	27.3	8	22	AA003444	Human: C100peptide	334	27.3	4	22	AA060449	Human CD4 receptor
253	3	27.3	8	22	AA004539	Nuclear: C102-peptide	334	27.3	4	22	AA060450	Human CD4 receptor
254	3	27.3	8	22	AA069558	153 epitope: A2 sup	334	27.3	4	22	AA060451	Human CD4 receptor
255	3	27.3	8	22	AA089559	153 epitope: A2 sup	334	27.3	4	22	AA060452	Human CD4 receptor
256	3	27.3	8	22	AA089559	153 epitope: A2 sup	334	27.3	4	22	AA060453	Human CD4 receptor
257	3	27.3	8	22	AA099001	SV40 VP1: nuclear: 1	334	27.3	4	22	AA060454	Human CD4 receptor
258	3	27.3	8	22	AA099108	Chenopodium album	334	27.3	4	22	AA060455	Human CD4 receptor
259	3	27.3	8	22	AA097513	Substituted phosph	334	27.3	4	22	AA060456	Human CD4 receptor
260	3	27.3	8	22	AA097563	Substituted phosph	334	27.3	4	22	AA060457	Human CD4 receptor
261	3	27.3	8	22	AA029462	Nuclear: localisat	334	27.3	4	22	AA060458	Human CD4 receptor
262	3	27.3	8	22	AA097220	Hepatitis B surface	334	27.3	4	22	AA060459	Human CD4 receptor
263	3	27.3	8	22	AA020268	Marine: Zif268: flnq	334	27.3	4	22	AA060460	Human CD4 receptor
264	3	27.3	8	22	AA020270	Marine: Zif268: flnq	334	27.3	4	22	AA060461	Human CD4 receptor
265	3	27.3	8	22	AA091752	Thymic peptide: SEQ	334	27.3	4	22	AA060462	Human CD4 receptor
266	3	27.3	8	22	AA010309	Hepatitis C virus	334	27.3	4	22	AA060463	Human CD4 receptor
267	3	27.3	8	22	AA030203	Hepatitis C virus	334	27.3	4	22	AA060464	Human CD4 receptor
268	3	27.3	8	22	AA067626	Peptide: derived fr	334	27.3	4	22	AA060465	Human CD4 receptor
269	3	27.3	8	22	AA070259	Peptide: #3: Unid	334	27.3	4	22	AA060466	Human CD4 receptor
270	3	27.3	8	22	AA061947	Human: h3-OSF: pept1	334	27.3	4	22	AA060467	Human CD4 receptor
271	3	27.3	8	22	AA078531	SV40 q4:1: enhancer	334	27.3	4	22	AA060468	Human CD4 receptor
272	3	27.3	8	22	AA078558	HIV 1 q4:1: enhanc	334	27.3	4	22	AA060469	Human CD4 receptor
273	3	27.3	8	22	AA083089	Peptide: which: sele	334	27.3	4	22	AA060470	Human CD4 receptor
274	3	27.3	8	22	AA075736	H2A class 1: bindin	334	27.3	4	22	AA060471	Human CD4 receptor
275	3	27.3	8	22	AA075741	H2A class 1: bindin	334	27.3	4	22	AA060472	Human CD4 receptor
276	3	27.3	8	22	AA059304	Hea1: binding: pept1	334	27.3	4	22	AA060473	Human CD4 receptor
277	3	27.3	8	22	AA055784	Hea1: motif: sequence	334	27.3	4	22	AA060474	Human CD4 receptor
278	3	27.3	8	22	AA057616	Glycoprotein: C: C-1	334	27.3	4	22	AA060475	Human CD4 receptor
279	3	27.3	8	22	AA058026	Glycoprotein: C: C-1	334	27.3	4	22	AA060476	Human CD4 receptor
280	3	27.3	8	22	ABP51944	VGF: C: 1: binding: pe	334	27.3	4	22	AA060477	Human CD4 receptor
281	3	27.3	8	23	ABG98137	Anti-neurosecretin: P	334	27.3	4	22	AA060478	Human CD4 receptor
282	3	27.3	8	23	ABG92997	Myristylation: org	334	27.3	4	22	AA060479	Human CD4 receptor
283	3	27.3	8	23	ABJ10442	Recombinase: domain	334	27.3	4	22	AA060480	Human CD4 receptor
284	3	27.3	8	23	ABJ10453	Recombinase: domain	334	27.3	4	22	AA060481	Human CD4 receptor
285	3	27.3	8	23	ABP53430	Actin: fundal: cyclic	334	27.3	4	22	AA060482	Human CD4 receptor
286	3	27.3	8	23	ABJ05282	T cell: surface: rec	334	27.3	4	22	AA060483	Human CD4 receptor
287	3	27.3	8	23	ABJ05892	Hepatitis B virus	334	27.3	4	22	AA060484	Human CD4 receptor
288	3	27.3	8	23	ABJ05538	Hepatitis B virus	334	27.3	4	22	AA060485	Human CD4 receptor
289	3	27.3	8	23	ABJ05065	Hepatitis B virus	334	27.3	4	22	AA060486	Human CD4 receptor
290	3	27.3	8	23	ABJ06457	Hepatitis B virus	334	27.3	4	22	AA060487	Human CD4 receptor
291	3	27.3	8	23	ABJ06359	Hepatitis B virus	334	27.3	4	22	AA060488	Human CD4 receptor
292	3	27.3	8	23	ABJ06441	Hepatitis B virus	334	27.3	4	22	AA060489	Human CD4 receptor
293	3	27.3	8	23	ABJ06842	Hepatitis B virus	334	27.3	4	22	AA060490	Human CD4 receptor
294	3	27.3	8	23	ABJ07164	Hepatitis B virus	334	27.3	4	22	AA060491	Human CD4 receptor
295	3	27.3	8	23	ABJ07174	Hepatitis B virus	334	27.3	4	22	AA060492	Human CD4 receptor
296	3	27.3	8	23	ABJ07484	Hepatitis B virus	334	27.3	4	22	AA060493	Human CD4 receptor
297	3	27.3	8	23	ABJ07497	Hepatitis B virus	334	27.3	4	22	AA060494	Human CD4 receptor
298	3	27.3	8	23	ABJ08061	Hepatitis B virus	334	27.3	4	22	AA060495	Human CD4 receptor
299	3	27.3	8	23	ABJ08095	Hepatitis B virus	334	27.3	4	22	AA060496	Human CD4 receptor
300	3	27.3	8	23	ABJ08128	Hepatitis B virus	334	27.3	4	22	AA060497	Human CD4 receptor
301	3	27.3	8	23	ABJ08247	Hepatitis B virus	334	27.3	4	22	AA060498	Human CD4 receptor



XX OS Synthetic.  
 XX PN WO200018801-A2.  
 XX PD 06-APR-2000.  
 XX PF 23-SEP-1999; 99WO-DK00500.  
 XX PR 29-SEP-1998; 98DK-0001232.  
 XX PR 29-APR-1999; 99DK-0000592.  
 XX (RONN/) RONN L C B.  
 PA (BOCK/) BOCK E.  
 PA (HOLM/) HOLM A.  
 PA (OLSE/) OLSEN M.  
 PA (OSTE/) OSTERGAARD S.  
 PA (JENS/) JENSEN P H.  
 PA (POUL/) POULSEN F H.  
 PA (SORO/) SOROKA V.  
 PA (RALE/) RALETS I.  
 PA (BERE/) BEREZIN V.  
 XX  
 PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
 PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
 XX  
 DR WPI: 2000-293111/25.  
 XX  
 PT Compositions that bind neural cell adhesion molecules useful for  
 PT treating disorders of the nervous system and muscles e.g. Alzheimer's  
 PT and Parkinson's diseases .  
 XX  
 PS Example 4: Page 25; 119pp; English.  
 XX  
 CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
 CC NCAM is found in three forms, two of which are transmembrane forms, while  
 CC the third is attached via a lipid anchor to the cell membrane. All three  
 CC NCAM forms have an extracellular structure consisting five immunoglobulin  
 CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the  
 CC N-terminal. The present sequence represents a peptide which binds to the  
 CC NCAM Ig1 domain. The peptide can be used in a compound which binds to  
 CC outgrowth from NCAM presenting cells, and is also capable of promoting  
 CC the proliferation of NCAM presenting cells. The compound may be used in  
 CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
 CC The compound may in particular be used to treat diseases of the central  
 CC and peripheral nervous systems such as post operative nerve damage,  
 CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
 CC dementias, sclerosis, nerve degeneration associated with diabetes  
 CC mellitus, disorders affecting the circadian clock or neuro-muscular  
 CC transmission and schizophrenia. Conditions affecting the muscles may also  
 CC be treated with the compound, such as conditions associated with impaired  
 CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
 CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
 CC liver and bowel may also be treated using the compound. The compound is  
 CC used in a prosthetic nerve guide, and also to stimulate the ability to  
 CC learn, and to stimulate the memory of a subject.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKSRKGNSSLM 11  
 |||||  
 DB 1 AKSRKGNSSLM 11  
 RESULT 2  
 ABG69349

ID ABG69349 Standard; Peptides 11 AA;  
 AC ABG69349;  
 XX  
 DI 21 OCT-2002 (first entry)  
 XX  
 DE Human neural cell adhesion molecule (NCAM) peptide #21.  
 XX  
 KW Human neural cell adhesion molecule; NCAM; heart muscle cell survival;  
 KW acute myocardial infarction; central nervous system disorder; stroke;  
 KW peripheral nerve system disorder; postoperative nerve damage;  
 KW traumatic nerve damage; spinal cord injury; nerve fiber; schizophrenia;  
 KW post-ischaemic disease; multifactorial dementia; multiple sclerosis;  
 KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease;  
 KW atrophic muscle disorder; a and degeneration; nephrosis;  
 XX  
 JS Bemo sapiens.  
 XX  
 PN WC200247719-A2.  
 XX  
 PD 29 JUN 2002.  
 XX  
 PF 12-DEC 2001; 2001WO-18306-22.  
 XX  
 PR 12-DEC 2001; 2001US-0001463.  
 XX  
 PA (ENKA-) ENKA PHARM AS.  
 XX  
 PI Bock E, Berezin V, Koller L;  
 XX  
 DR WPI: 2002-58437/e2.  
 XX  
 PT Use of a compound comprising a peptide of neural cell adhesion  
 PT molecule, in the preparation of treatment for preventing death of  
 PT cells presenting NCAM of NCAM ligand and treating central nervous  
 PT system diseases .  
 XX  
 PS Disclosure: Page 16; 57pp; English.  
 XX  
 CC The invention relates to use of a compound (1) comprising a peptide  
 CC which comprises at least 5 contiguous amino acid residues of a sequence  
 CC of the neural cell adhesion molecule (NCAM), its fragment, variant or its  
 CC mimic, for the preparation of a medicament for preventing death of cells  
 CC presenting the NCAM or an NCAM ligand (1) is useful in the preparation  
 CC of a medicament for preventing death of cells presenting the NCAM or an  
 CC NCAM ligand. The medicament is for the stimulation of the survival of  
 CC heart muscle cells, such as survival after acute myocardial infarction.  
 CC The medicament is for the treatment of diseases or conditions of the  
 CC central and peripheral nervous system, such as postoperative nerve  
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,  
 CC impaired myelination of nerve fibres, post-ischaemic damage, e.g.  
 CC resulting from a stroke, multifactorial dementia, multiple sclerosis, nerve  
 CC degeneration associated with diabetes mellitus, neuro-muscular  
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease  
 CC and Huntington's disease. The medicament is for the treatment of diseases  
 CC or conditions of the muscles, including conditions with impaired function  
 CC of neuromuscular connections, such as genetic or traumatic atrophic  
 CC muscle disorders, and for the treatment of diseases or conditions of  
 CC various organs, such as degenerative conditions of the gonads, pancreas  
 CC (e.g. diabetes mellitus types I and II) and kidney (e.g. nephrosis).  
 CC ABG69349 AbG69349 represents human NCAM peptides of the invention.  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 11; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKSRKGNSSLM 11  
 |||||  
 DB 1 AKSRKGNSSLM 11



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RESULT 3
AA87896
ID AAY87896 standard; Protein; 14 AA.
XX AC AAY87896:
XX DT 06-OCT-2000 (first entry)
XX DE M. tuberculosis antigen TB32 N-terminal fragment.
XX KW Tuberculosis; TB; antigen; vaccine; diagnosis; Somatic tuberculosis;
XX KW infection; interferon-gamma; IFN-gamma; protective immunity; therapy;
XX KW delayed type hypersensitivity response; TB32.
XX OS Mycobacterium tuberculosis.
XX PN WO200021983-A2.
XX PD 20-APR-2000.
XX PF 08-OCT-1999; 99WO-DK00548.
XX PR 08-OCT-1998; 98DK-0001281.
XX PR 21-JAN-1999; 99US-0116673.
XX PA (STAT-) STATENS SERUM INST.
XX PI Andersen P, Weldingh K, Hansen CV, Florio W, Chkots LMM;
XX PI Skjot RLV, Rosenkrands I;
XX WP: 2000-317931/27.
XX PT Novel polypeptide of somatic protein extract useful as vaccine against
XX PT virulent Mycobacterium infection, isolated from cell wall, cell
XX PT membrane and cytosol.
XX PS Example 4; Page 115; 126pp; English.
XX CC This invention describes a novel polypeptide (PP) of somatic proteins
XX CC extract (I) which have tuberculostatic activity. (I) or their subsequence
XX CC has at least one of the following properties: (a) the PP induces an in
XX CC vitro recall response, or an in vitro response, during primary infection
XX CC with virulent Mycobacterium, determined by a release of interferon
XX CC (IFN)-gamma, (b) PP induces a protective immunity, determined by
XX CC vaccinating an animal with PP and an adjuvant, three times at two weeks
XX CC intervals, (c) PP induces an in vitro response, or in vitro recall
XX CC response, determined by release of IFN-gamma of at least 1000 pg/ml, or
XX CC 500 pg/ml, respectively, from peripheral blood mononuclear cells (PBMC)
XX CC withdrawn from TB patients, or PP-positive individuals, 4 months after
XX CC diagnosis, (d) PP induces a specific antibody response in a TB patient,
XX CC as determined by enzyme linked immunosorbent assay (ELISA) technique or
XX CC a western blot, (e) PP induces a positive delayed type hypersensitivity
XX CC (DTH) response, determined by intradermal injection, (f) and (g) are
XX CC useful in preparing a prophylactic or therapeutic medicine as a vaccine
XX CC for induction of a protective or generation of an immune response in a
XX CC mammal against infection with a virulent Mycobacterium; (f) and (g) are
XX CC also useful as diagnostic reagent for the diagnosis of a virulent
XX CC Mycobacterium infection. The vaccine of the invention induces efficient
XX CC immunological memory, providing long term protection against TB. This
XX CC sequence represents a Microbacterium tuberculosis TB32 antigen.
XX CC N-terminal fragment described in the invention
XX SO Sequence 14 AA;
Query Match 45.5%; Score 5; DB 21; Length 14;
Best Local Similarity 100.0%; Pred No. 94;
Matches 5; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 6 GNSSL 10
DB 2 GNSSL 6

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RESULT 4
AAY87896
ID AAY87896 standard; Protein; 14 AA.
XX AC AAY87896:
XX DT 25 MAR 2000 (first entry)
XX DT 13 MAR 2000 (first entry)
XX DT 04 MAR 1999 (first entry)
XX DE E47896102 protein of Mycobacterium tuberculosis
XX KW Bacterial antibodies; antibodies
XX OS Synthesis
XX PN JF0124292-A1
XX PD 19 SEP 1999
XX PF 05 MAR 2000; 99WO-DK00548
XX PF 05 MAR 1999; 98DK-0001281
XX PA (STAT-) STATENS SERUM INST.
XX PR 08-OCT-1998; 98DK-0001281
XX PR 21-JAN-1999; 99US-0116673
XX PA (STAT-) STATENS SERUM INST.
XX PI Andersen P, Weldingh K, Hansen CV, Florio W, Chkots LMM;
XX PI Skjot RLV, Rosenkrands I;
XX WP: 2000-317931/27.
XX PT Novel polypeptide of somatic protein extract useful as vaccine against
XX PT virulent Mycobacterium infection, isolated from cell wall, cell
XX PT membrane and cytosol.
XX PS Example 4; Page 115; 126pp; English.
XX CC This peptide is an extract of the somatic peptide (PP) of somatic proteins
XX CC X as shown or subsequence of X as shown or subsequence of X as shown
XX CC or subsequence of X as shown or subsequence of X as shown or subsequence
XX CC revealed in the invention and its subsequence
XX CC (Updated on 25 MAR 2000; 99WO-DK00548)
XX CC (Updated on 25 MAR 2000; 99WO-DK00548)
XX SO Sequence 14 AA;
Query Match 45.5%; Score 5; DB 21; Length 14;
Best Local Similarity 100.0%; Pred No. 94;
Matches 5; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 6 GNSSL 10
DB 2 GNSSL 6

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RESULT 5
AAY87896
ID AAY87896 standard; Protein; 14 AA.
XX AC AAY87896:
XX DT 25 MAR 2000 (first entry)
XX DE E47896102 protein of Mycobacterium tuberculosis
XX KW Bacterial antibodies; antibodies
XX OS Synthesis
XX PN JF0124292-A1
XX PD 19 SEP 1999
XX PF 05 MAR 2000; 99WO-DK00548
XX PF 05 MAR 1999; 98DK-0001281
XX PA (STAT-) STATENS SERUM INST.
XX PR 08-OCT-1998; 98DK-0001281
XX PR 21-JAN-1999; 99US-0116673
XX PA (STAT-) STATENS SERUM INST.
XX PI Andersen P, Weldingh K, Hansen CV, Florio W, Chkots LMM;
XX PI Skjot RLV, Rosenkrands I;
XX WP: 2000-317931/27.
XX PT Novel polypeptide of somatic protein extract useful as vaccine against
XX PT virulent Mycobacterium infection, isolated from cell wall, cell
XX PT membrane and cytosol.
XX PS Example 4; Page 115; 126pp; English.
XX CC This peptide is an extract of the somatic peptide (PP) of somatic proteins
XX CC X as shown or subsequence of X as shown or subsequence of X as shown
XX CC or subsequence of X as shown or subsequence of X as shown or subsequence
XX CC revealed in the invention and its subsequence
XX CC (Updated on 25 MAR 2000; 99WO-DK00548)
XX CC (Updated on 25 MAR 2000; 99WO-DK00548)
XX SO Sequence 14 AA;
Query Match 45.5%; Score 5; DB 21; Length 14;
Best Local Similarity 100.0%; Pred No. 94;
Matches 5; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 6 GNSSL 10
DB 2 GNSSL 6

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RESULT 6
AAY87896
ID AAY87896 standard; Protein; 14 AA.
XX AC AAY87896:
XX DT 25 MAR 2000 (first entry)
XX DE E47896102 protein of Mycobacterium tuberculosis
XX KW Bacterial antibodies; antibodies
XX OS Synthesis
XX PN JF0124292-A1
XX PD 19 SEP 1999
XX PF 05 MAR 2000; 99WO-DK00548
XX PF 05 MAR 1999; 98DK-0001281
XX PA (STAT-) STATENS SERUM INST.
XX PR 08-OCT-1998; 98DK-0001281
XX PR 21-JAN-1999; 99US-0116673
XX PA (STAT-) STATENS SERUM INST.
XX PI Andersen P, Weldingh K, Hansen CV, Florio W, Chkots LMM;
XX PI Skjot RLV, Rosenkrands I;
XX WP: 2000-317931/27.
XX PT Novel polypeptide of somatic protein extract useful as vaccine against
XX PT virulent Mycobacterium infection, isolated from cell wall, cell
XX PT membrane and cytosol.
XX PS Example 4; Page 115; 126pp; English.
XX CC This peptide is an extract of the somatic peptide (PP) of somatic proteins
XX CC X as shown or subsequence of X as shown or subsequence of X as shown
XX CC or subsequence of X as shown or subsequence of X as shown or subsequence
XX CC revealed in the invention and its subsequence
XX CC (Updated on 25 MAR 2000; 99WO-DK00548)
XX CC (Updated on 25 MAR 2000; 99WO-DK00548)
XX SO Sequence 14 AA;
Query Match 45.5%; Score 5; DB 21; Length 14;
Best Local Similarity 100.0%; Pred No. 94;
Matches 5; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 6 GNSSL 10
DB 2 GNSSL 6

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CC The present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25397 to  
 CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP2542  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; (E 22; Length 4)

Best Local Similarity 100.0%; Prod. No. 9, 60,000;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

UY 6 GNSS 9

DB 3 GNSS 6

#### RESULT 8

ABP14271

ID ABP14271 standard; Peptide: 8 AA.

XX AC ABP14271;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A03 super motif env peptide #11.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;

XX KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;

XX KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX WC200124810-A1.

XX PD 12-APR 2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412864.

XX PA (EPIM-) EPIMUNE INC.

XX PI Scott A. Sidney J. Southwood S. Livingston, JR. George J. Ho.

XX PT Baker SM, Cellis E, Kubo RT, Gray RM.

XX DR WPI: 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)

XX PT peptide groups, useful for vaccinating against HIV 1.

XX PS Claim 32: Page 161: 448pp; English.

XX CC The present invention describes a composition (1) comprising a prepared

XX CC human immunodeficiency virus-1 (HIV 1) group comprising an amino acid

XX CC sequence selected from 51 defined amino acid sequences (ABP25397 to

XX ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
 XX may be used for immunising subjects against HIV-1 infections. The use of  
 XX group-based vaccines has several advantages over traditional vaccines,  
 XX particularly when compared to the use of whole antigens in vaccine  
 XX compositions. There is evidence that the immune response to whole  
 XX antigens is directed largely toward variable regions of the antigen,  
 XX allowing for immune escape due to mutations. The groups for inclusion in  
 XX an group-based vaccine may be selected from conserved regions of viral or  
 XX tumour-associated antigens, which therefore reduces the likelihood of  
 XX escape mutants. Furthermore, immunosuppressive groups that may be present  
 XX in whole antigens can be avoided with the use of group-based vaccines.  
 XX An additional advantage of an group-based vaccine approach is the ability  
 XX to combine selected groups (CTL and HTL), and further, to modify the  
 XX composition of the groups, achieving, for example, enhanced  
 XX immunogenicity. Accordingly, the immune response can be modulated, as  
 XX appropriate, for the target disease. Similar engineering of the response  
 XX is not possible with traditional approaches. ABP1501 to ABP2542  
 XX represent peptide sequences used in the exemplification of the present  
 XX invention.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; (E 22; Length 4)

Best Local Similarity 100.0%; Prod. No. 9, 60,000;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

XX 6 GNSS 9

XX 3 GNSS 6

#### RESULT 9

ABP14271

ID ABP14271 standard; Peptide: 8 AA.

XX AC ABP14271;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A03 super motif env peptide #11.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;

XX KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;

XX KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX WC200124810-A1.

XX PD 12-APR 2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412864.

XX PA (EPIM-) EPIMUNE INC.

XX PI Scott A. Sidney J. Southwood S. Livingston, JR. George J. Ho.

XX PT Baker SM, Cellis E, Kubo RT, Gray RM.

XX DR WPI: 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)

XX PT peptide groups, useful for vaccinating against HIV 1.

XX PS Claim 32: Page 161: 448pp; English.

XX CC The present invention describes a composition (1) comprising a prepared

XX CC human immunodeficiency virus-1 (HIV 1) group comprising an amino acid

XX CC sequence selected from 51 defined amino acid sequences (ABP25397 to

XX CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)

XX CC may be used for immunising subjects against HIV-1 infections. The use of

XX CC group-based vaccines has several advantages over traditional vaccines.

CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP1531 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

SO Sequence 8 AA;  
Query Match 36.4%; Score 4; ID 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9, 40-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
Db 4 GNSS 7

RESULT 19  
ABP19802  
ID ABP19802 standard; Peptide: 8 AA.  
XX  
AC ABP19802;  
XX  
DT 15-JUL 2002 (first entry)  
XX  
DE HIV A03 motif env peptide #6.  
XX  
KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
KW vif; tat; cytochrome T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; viricide  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US27766.  
XX  
PR 05-OCT-1999; 99US-0412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Gray HM;  
XX  
DR WPI: 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV 1  
XX  
PS Claim 32; Page 276; 448pp; English.

CC The present invention describes a composition (1) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABP25447 to  
CC ABP25337). (1) has virucide activity and can be used in vaccines. (1)  
CC may be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen.

CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP1531 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

SO Sequence 8 AA;  
Query Match 36.4%; Score 4; ID 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9, 40-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
Db 4 GNSS 7

RESULT 11  
ABP22440  
ID ABP22440 standard; Peptide: 8 AA.  
XX  
AC ABP22440;  
XX  
DT 15-JUL 2002 (first entry)  
XX  
DE HIV A11 motif env peptide #4.  
XX  
KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
KW vif; tat; cytochrome T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; viricide.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO200124810-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US27766.  
XX  
PR 05-OCT-1999; 99US-0412863.  
XX  
PA (EPIM-) EPIMMUNE INC.  
PI Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kubo RT, Gray HM;  
XX  
DR WPI: 2001-354887/37.  
XX  
PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV 1  
XX  
PS Claim 32; Page 276; 448pp; English.

CC The present invention describes a composition (1) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABP25447 to  
CC ABP25337). (1) has virucide activity and can be used in vaccines. (1)  
CC may be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CPI and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. AHP150, to AHP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.  
XX  
XX  
XX Sequence 8 AA:  
S0

```
Query Match      36.48; Score 4; DB 22; Length 8;
Best Local Similarity 100.00; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Pairs 0;
```

Query Match 36.48: Score 4; DB 22; Length 8;

Best local Similarity 100.08; Pred. No. 9.3e+05;

0y 6 :NSS 9

—  
—  
—  
—

## RESULT 12

AAG67710

ID	AAG67710	standard;	peptide; 8 AA.

XX

AC AAC567710;

XX

CC treating proliferative disorders, e.g. cancers and leukaemias. The  
 CC peptides are also for identifying substances which interfere with  
 CC protein-protein interactions involving cyclins (i.e. cyclin A, E or D),  
 CC especially CDK/cyclin interactions, and which are capable of inhibiting  
 CC CDK2 and/or CDK4 activity. P21 peptides other than p21(149-159)  
 CC competitively inhibit the binding of peptide p21(149-159) to cyclin and  
 CC may be used to identify substances that bind to, or inhibit peptide-  
 CC cyclin interactions. Substances for screening in the assays include  
 CC antibody products specific for p21 or cyclin binding regions.  
 CC combinatorial libraries and single compound collections. The present  
 CC sequence is a peptide derived from the C-terminus of p21.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 22; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 DB 2 AKSR 5

#### RESULT 14

ID AAR49852 standard; peptide; 9 AA.

XX AAR49852;

XX 25-MAR-2003 (updated)  
 DT 20-AUG-1994 (first entry)

XX Sequence of antigenic peptide based on non consensual sequences of  
 DE HIV-1 env protein.

XX Human immunodeficiency virus; HIV 1; env; AIDS.

XX Synthetic.

XX DE4228787-A1.

XX 03-MAR-1994.

XX 29-AUG-1992; 92DE-4228787.

XX 29-AUG-1992; 92DE-4228787.

XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.

XX Dietrich U, Grez M, Ruebsamen-waismann H, Van Briesen H;

XX WPI; 1994-075444/10.

XX New HIV-1 viral isolates - useful in the produ of a new HIV-1  
 PT vaccine

XX Claim 2; Page 4; 8pp; German.

XX HIV-1 D747, HIV-1 D757 and HIV-1 D760 are new viral isolates  
 CC deposited under ECACC V92082718, V92082719 and V92082720  
 CC respectively. The new isolates were isolated from patients in India  
 CC who did not yet show typical AIDS symptoms. Vaccines may be produced  
 CC using peptides which corresp. to regions of the env protein that  
 CC differ from the HIV-1 AA consensus sequences that are already  
 CC published. Such peptides are given in AAR49851-54.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KINS 8  
 DB 6 KINS 8

#### RESULT 15

ID AAW77371 standard; protein; 9 AA.

XX AAW77371;

XX 14-DEC-1993 (first entry)

XX mIL-10 (Vβ3) protein N terminus.

XX Gossackie virus (GV) viral vector (immune suppressor) of rat hepatoma  
 KW viral heart disease vector; heart transplant; inflammatory disease.

XX 21-DEC-1993

XX KAS sp.

XX Synthesis

XX Key

XX Key

XX Key

XX W0583424-A2

XX 11-SEP-1998

XX 15-MAR-1998

XX 05-MAR-1998

XX 05-MAR-1998

XX (CYBER) UNIV MERVASKA

XX Chapman NM, Koloski P, Pabon J, Tracy SM;

XX WPI; 1994-496442/42

XX N-PSIB; AAV-426.

XX New attenuated vaccinia virus vector - for delivery

XX of immunomodulatory and adjuvants to prevent or abate viral

XX heart disease and heart transplant rejection

XX Resubmission 44-6, 294p; analysis.

XX The full length of naturally occurring sequences located from a polymerase

XX site, was used in the production of a new viral vector including an

XX attenuated vaccinia virus, for the delivery of heterologous nucleic acid

XX to a target cell, tissue or organ. The engineered virus may be

XX administered to an individual as a vaccine or to suppress an immune

XX response. Specifically, uses include the prevention, amelioration or

XX ablation of infectious viral heart disease, and the reduction of

XX the ablation of heart rejection, particularly heart transplant rejection.

XX The attenuated viruses are also suitable as specific transfectants

XX delivery agents for treating inflammatory diseases and conditions of a

XX variety of tissues. Use of such a cardiotropic vector allows delivery of

XX genes encoding biologically active proteins including immunomodulators

XX and anti-inflammatory agents to the heart, so as to investigate the

XX effects of parenteral administration of such proteins.

Query Match 36.4%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KINS 9  
 DB 6 KINS 9



```

XX PD 12-APR-2001.
XX PF 05-OCT-2000: 2000WO-US27766.
XX PP 05 OCT-1999; 99US-0412861.
XX PR 05 OCT-1999; 99US-0412861.
XX PA (EPIMV) EPIMUNE INC.
XX PI Settle A. Sidney J. Southwood S. Livingston Rd. Chestnut R.
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)
XX PT peptide groups, useful for vaccinating against HIV 1
XX PS Claim 32; Page 118; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (A0135447 to
XX CC A025977). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines.
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be mediated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. A011501 to A025472
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 9 AA;
Query Match 36.4%; Score 4; Dn Z2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5, seqs 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 6 GNSS 9
Db 4 GNSS 7
RESULT 19
ABP12151
XX ID ABP12151 standard; Peptide: 9 AA.
XX AC ABP12151;
XX XX
XX DT 15 JUL-2002 (first entry)
XX DE HIV A02 super motif env peptide #208.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;
XX KW vif; tat; cytochrome P450; HIV infection; CTL immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX XX
XX PD 12-APR-2001.
XX PR 05-OCT-1999; 99US-0412861.

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XX PF 05-OCT-2001: 2001WO-US27766.
XX PR 05 OCT-1999; 99US-0412861.
XX PA (EPIMV) EPIMUNE INC.
XX PI Settle A. Sidney J. Southwood S. Livingston Rd. Chestnut R.
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)
XX PT peptide groups, useful for vaccinating against HIV 1
XX PS Claim 32; Page 118; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (A0135447 to
XX CC A025977). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines.
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be mediated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. A011501 to A025472
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 9 AA.
Query Match 36.4%; Score 4; Dn Z2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5, seqs 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 6 GNSS 9
Db 4 GNSS 7
RESULT 20
ABP12151
XX ID ABP12151 standard; Peptide: 9 AA.
XX AC ABP12151;
XX XX
XX DT 15 JUL-2002 (first entry)
XX DE HIV A02 super motif env peptide #208.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;
XX KW vif; tat; cytochrome P450; HIV infection; CTL immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX XX
XX PD 12-APR-2001.
XX PR 05-OCT-1999; 99US-0412861.

```



XX (EPIM-) EPIMUNE INC.  
XX  
XX  
PI Settle A., Sidney J., Southwood S., Livingstone RB., Chiesari R.  
PI Baker DM., Celis E., Kubo RT., Gray HM;  
XX WPI: 2001-354887/37.  
DR  
XX  
XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV 1  
PT  
XX Claim 32: Page 276; 448pp; English.  
XX  
XX The present invention describes a composition (1) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (AB125437 to  
CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
CC may be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. Appl156; to ABP254.2  
CC represent peptide sequences used in the exemplification of the present  
CC invention.  
XX  
XX SQ Sequence 9 AA;  
Query Match 36.4%; SCORE 4; DR 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 60.0%;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
Oy 6 GNSS 9  
Ob 1111  
4 GNSS 7  
RESULT 21  
ABP19810  
XX ABP19810 standard; Peptide: 9 AA.  
XX  
XX AC ABP19810;  
XX  
XX 15-JUL-2002 (first entry)  
XX  
XX DE HIV A03 motif env peptide #14.  
XX  
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;  
KW vif; tat; cytotoxic T lymphocyte; (1) immune response; (1) target  
KW antigen; vaccine; HIV infection; immunisation; virucide;  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX PN W0200124810-A1.  
XX  
XX PD 12-APR-2001.  
XX  
XX PF 05-OCT-2000; 2000WO-US27766.  
XX  
XX PR 05-OCT-1999; 99US-0412863.  
XX  
XX PA (EPIM-) EPIMUNE INC.  
XX

II Settle A., Sidney J., Southwood S., Livingstone RB., Chiesari R.  
II Baker DM., Celis E., Kubo RT., Gray HM;  
XX WPI: 2001-354887/37.  
XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV 1  
PT  
XX Claim 32: Page 276; 448pp; English.  
XX  
XX The present invention describes a composition (1) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (AB125437 to  
CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
CC may be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines.  
CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. Appl156; to ABP254.2  
CC represent peptide sequences used in the exemplification of the present  
CC invention.  
XX  
XX SQ Sequence 9 AA;  
Query Match 36.4%; SCORE 4; DR 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9; 60.0%;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
Oy 6 GNSS 9  
Ob 1111  
4 GNSS 7  
RESULT 22  
ABP19810  
XX ABP19810 standard; Peptide: 9 AA.  
XX  
XX AC ABP19810;  
XX  
XX 15-JUL-2002 (first entry)  
XX  
XX DE HIV A03 motif env peptide #14.  
XX  
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; rev;  
KW vif; tat; cytotoxic T lymphocyte; (1) immune response; (1) target  
KW antigen; vaccine; HIV infection; immunisation; virucide;  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX PN W0200124810-A1.  
XX  
XX PD 12-APR-2001.  
XX  
XX PF 05-OCT-2000; 2000WO-US27766.  
XX  
XX PR 05-OCT-1999; 99US-0412863.  
XX  
XX PA (EPIM-) EPIMUNE INC.  
XX

DR WPI: 2001-541537/60.  
 XX Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a  
 PT an epitope of the non-VNTR, non-leader region of a mucin  
 XX  
 PS Disclosure: Page 36; 84pp; English.  
 XX  
 CC The patent discloses peptide or polypeptides capable of eliciting  
 CC an immune response, comprising an amino acid sequence corresponding  
 CC to an epitope of the non-central portion of varying numbers of an  
 CC amino acid motif (VNTR), non-leader region of a mucin, the peptides  
 CC of the invention, fusion proteins comprising the peptide and conjugate  
 CC compounds with carbohydrate polymers are used to induce a cell mediated  
 CC immune response against mucin in the prevention or treatment of  
 CC carcinoma, preferably adenocarcinoma, most preferably breast cancer.  
 CC They are also used to pulse dendritic cell for in vivo transfer and  
 CC use as a vaccine. They are also used in gene therapy. The present  
 CC sequence is human mucin-1 (MUC-1) peptide which is an epitope for  
 CC cytotoxic T-lymphocytes (CTL).  
 XX  
 SQ Sequence 9 AA;  
 Query Match 36.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 7 NSSL 10  
 DB 1 NSSL 4  
 RESULT 23  
 AAB68480  
 ID AAB68480 standard; peptide: 9 AA.  
 AC AAB68480;  
 DT 23-JUL-2001 (first entry)  
 XX Peptide encoded by a unique region in exon 1 of dog motilin receptor.  
 XX  
 XX Motilin receptor; gastrointestinal disease; gastric motility disorder;  
 KW gastroparesis; irritable bowel syndrome; diarrhoea.  
 XX  
 OS Canis sp.  
 XX  
 XX W0200132710-A1.  
 XX  
 XX 10-MAY-2001.  
 XX  
 XX 25-OCT-2000; 2000WO-US29426.  
 XX  
 XX 29-OCT-1999; 99US-0162264.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Tan C, McKee K;  
 XX  
 XX WPI: 2001-343479/36.  
 XX  
 XX Novel polypeptides related to dog and rabbit motilin receptor  
 PT polypeptide, comprising unique regions from dog and rabbit receptor  
 PT amino acid sequence, useful for identifying compounds for treating  
 PT diarrhoea in humans  
 XX  
 XX Claim 3; Page 20; 42pp; English.  
 PS  
 CC AAB68480-84 represent peptides encoded by the unique region of exon 1  
 CC of a dog motilin receptor gene. The specification describes an unique  
 CC sequence present in exon 1 of the motilin receptor, which is not present  
 CC in human or Sphaeroides nephelus 75E7 motilin receptor sequences. The  
 CC unique nucleic acid sequence is useful for measuring the ability of a  
 CC compound to affect motilin receptor activity. Motilin receptor

CC Polypeptides and polypeptides are used to identify therapeutic  
 CC compounds such as used for treating gastrointestinal diseases and  
 CC bowel, syndrome, and diarrhoea.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 36.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 100%;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 NSSL 9  
 DB 3 NSSL 6  
 RESULT 24  
 AAE41377  
 ID AAE41377 standard; peptide: 9 AA  
 AC AAE41377;  
 DT 24-FEB-2003 (first entry)  
 XX Human MUC1 mutant peptide  
 XX  
 XX Human T-lymphocyte carcinoma viral infected cell gene therapy mutant;  
 KW mutant; mucin6.  
 XX  
 XX Homo Sapiens.  
 OS Synthesis  
 XX  
 XX Key: Location/positions  
 FT Mis-difference / site Wild Type Pro substituted with Leu  
 XX  
 XX W020027247-A2  
 XX  
 XX 16-SEP-2002.  
 XX  
 XX 11-MAR-2003; 2002WO-EP-2066.  
 XX  
 XX 03-MAR-2003; 2003US-24250P.  
 XX  
 XX 14-MAY-2003; 2003US-20055P.  
 XX  
 XX 14-MAY-2003; 2003US-20060P.  
 XX  
 XX (CA11)-2 (CA11)-2-GEN A;  
 XX  
 XX Wrote P, Warden P, Fether Mortons M, Fether M;  
 XX  
 XX WPI: 2002-7598-6/42  
 XX  
 XX Provisional identification of epitope peptides for and action cytotoxic  
 PT T-lymphocytes and for treating cancer, comprises selected epitopes  
 PT regions in antigen proteins and identifying CDR-T cell epitopes in  
 PT the protein  
 XX  
 XX Disclosure: Page 10; 34pp; English.  
 XX  
 XX The present invention relates to a method for providing, identifying and/or  
 CC optimising peptides which induce cytotoxic T-lymphocytes and to the  
 CC uses of the identified peptides for vaccination. The method is useful  
 CC for providing, identifying and/or optimising peptides that are useful  
 CC in manufacturing a pharmaceutical composition for the induction of  
 CC cytotoxic T-lymphocytes, and for the prevention, treatment or diagnosis  
 CC of cancer or viral infections. The invention is also used in gene  
 CC therapy. The present sequence is human MUC1 mutant peptide used to  
 CC illustrate the method of the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 36.4%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9, 100%;

	Matches	4: Conservative	0: Mismatches	0: Indels	0: Gaps	0:
QY	7	7 NSSL 10				
Db	3	3 NSSL 6				

RESULT 25

ABJ10457  
ID ABJ10457 standard; Peptide: 9 AA.

XX  
AC ABJ10457;

DT 28-NOV-2002 (first entry)

Recombinase domain-containing fusion protein-related NIS peptide 24  
XX  
DE

KW Fusion protein; recombinase domain; signal peptide domain; gene function;  
KW nuclear import; recombinase recognition sequence; transgenic organism;  
KW C31-int recombination system; site-specific integration; gene therapy;  
KW NLS; nuclear localisation signal.

OS Unidentified.

AA  
PN  
WO200238613-A2

16-MAY-2002

09-NRIV-2007-2001WO-FBI2975

XX  
PR 10-NOV-2000. 2000EP-0124629

PR 17-APR-2001; 2001EP-0309543  
PR 17-APR-2001; 2001EP-0124629

PR 13 AJG-2001; 2001US-311876P.  
PR 13 AJG-2001; 2001US-311876P.  
PR 13 AJG-2001; 2001US-311876P.

PA (ARTE-) ARTEMIS PHARM GMBH.

Kuehn R, Felder S, Schwenk F, Klueter-Juks R, Faust N.

WPI: 2002-519298/55.

Novel fusion protein useful for recombining DNA molecules in eukaryotic cells has recombinase protein which is linked to signal peptide domain which directs nuclear import of fusion protein in eukaryotic cells.

PS Claim 7: Page 75: 150pp: English

The invention comprises the amino acid and coding sequences of fusion proteins that contain a recombinase domain and a signal peptide domain which directs nuclear import of the fusion protein in eukaryotic cells. The fusion proteins of the invention are useful for recombining the DNA molecules of cells or organisms containing recombinase recognition sequences for the recombinase domain of the fusion proteins. The fusion proteins of the invention are useful for studying gene function at various developmental stages and for the creation of transgenic organisms. The C31-int recombination system of the invention can be used for the site-specific integration of foreign DNA into the genome of mammalian cells (e.g. for gene therapy). The present amino acid sequence represents an NLS (nuclear localisation signal) peptide that was used in the invention.

Sequence 9 AA:

Query Match 36.48. Score 4. DR 24. Length 9.

Query match	Score 4	Length 9
Best Local Similarity	38.4%	93.0%
Best Local Similarity	100.0%	93.0%

2025 Budget Summary	100.00%	Filed: NO. 4,300,000
Matches	4: Conservative	0: Mismatches
		100.00%

0v 2 KSRK 5

Qy	2	KSRK	5
Dh	3	KSRK	6

RESULTS

RESULT 2  
BAF17552

AAU75714  
 ID AAU75714 standard: Peptide; 9 AA.  
 AC AAU75714:  
 DT 23-APR-2002 (first entry)  
 XX  
 DE McCycDm antigenic peptide #68.  
 XX  
 KW D-cyclin; McCycDm; plant growth regulator; herbicide; transgenic plant;  
 KW plant regeneration; cell fate; plant development; plant morphology;  
 KW plant biochemistry; plant physiology; Cdc2-type kinase; fusion peptide;  
 KW Cdc2-related kinase; barrel medic; immunosuppressant; antibody.  
 XX  
 OS Medicago truncatula.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc difference 1 /label= X  
 FT /note= "V, WV, FWV or absent"  
 FT Misc-difference 9 /label= X  
 FT /note= "E, EG, EGR, EGRE, EGREK,  
 FT EGREKK, EGREKKOT, EGREKKOT or absent"  
 FT  
 PN WO200196579-A1.  
 XX  
 PD 20-DEC-2001.  
 XX  
 PF 15-JUN-2001: 2001WO-EP06771.  
 XX  
 PR 16-JUN-2000: 2000EP-087013.  
 PR 11-JUL-2000: 2000US-217603P.  
 XX  
 PA (CROP-) CROPPDESIGN WV.  
 XX  
 PI Miskolczi P., Pettko-szanter A., Horvath G., Budits P., Polter A.;  
 P1 Gyorgyey J;  
 XX  
 DR WPI: 2002-090211/12.  
 XX  
 PT Polynucleotide encoding new plant type D-cyclin and the polypeptide  
 PT useful for modifying cell fate, plant development, plant morphology,  
 PT plant biochemistry and plant physiology  
 XX  
 PS Example 10; Page 75; 151pp; English.  
 XX  
 CC This invention relates to the protein and nucleic acid sequences of a  
 CC new plant type D-cyclin McCycDm which may be used as a plant growth  
 CC regulator or as a herbicide. The nucleotide sequences of the invention  
 CC are useful for production of transgenic plants, plant cells or tissues,  
 CC and for effecting the expression of the McCycDm protein where the  
 CC nucleic acid is operably linked to one or more control sequences. The  
 CC invention also comprises a method for regenerating a plant from the  
 CC plant cell. The nucleic acid sequence of the invention is useful for  
 CC modifying cell fate, plant development, plant morphology, plant  
 CC biochemistry or plant physiology. The McCycDm protein is useful for  
 CC identifying and obtaining proteins interacting with it, comprising a  
 CC screening assay preferably a two-hybrid screening assay. The protein is  
 CC also useful for modulating the interaction between and/or the activity  
 CC of complexes comprising type D-cyclin and Cdc2 type or Cdc2-related  
 CC kinases and/or other D-cyclin interacting protein partners. The protein  
 CC is also useful for identifying compound or mixture of compounds which  
 CC specifically binds to the protein. This sequence represents the  
 CC McCycDm antigenic peptide #68 of the invention. This peptide may be used  
 CC as an immunogen to produce anti-McCycDm antibodies. These antibodies  
 CC may be used to detect the protein of the invention or to alter its  
 CC function.  
 XX  
 SO Sequence 9 AA;

Query Match 36.4%; Score 4; DB 2; length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Unscored 0; E; E-Small; E-S; Indels 0; E-S; E-S  
 QY 5 KINS 8  
 II  
 SD 5 KINS 8  
 XX  
 RESULT 28  
 AAU75715  
 ID AAU75715 standard: Peptide; 9 AA.  
 AC AAU75715:  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE McCycDm antigenic peptide #68.  
 XX  
 KW D-cyclin; McCycDm; plant growth regulator; herbicide; transgenic plant;  
 KW plant regeneration; cell fate; plant development; plant morphology;  
 KW plant biochemistry; plant physiology; Cdc2-type kinase; fusion peptide;  
 KW Cdc2-related kinase; barrel medic; immunosuppressant; antibody.  
 XX  
 OS Medicago truncatula.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc difference 1 /label= X  
 FT /note= "V, WV, FWV or absent"  
 FT Misc-difference 9 /label= X  
 FT /note= "E, EG, EGR, EGRE, EGREK,  
 FT EGREKK, EGREKKOT, EGREKKOT or absent"  
 FT  
 PN WO200196579-A1.  
 XX  
 PD 20-DEC-2001.  
 XX  
 PF 15-JUN-2001: 2001WO-EP06771.  
 XX  
 PR 16-JUN-2000: 2000EP-087013.  
 PR 11-JUL-2000: 2000US-217603P.  
 XX  
 PA (CROP-) CROPPDESIGN WV.  
 XX  
 PI Miskolczi P., Pettko-szanter A., Horvath G., Budits P., Polter A.;  
 P1 Gyorgyey J;  
 XX  
 DR WPI: 2002-090211/12.  
 XX  
 PT Polynucleotide encoding new plant type D-cyclin and the polypeptide  
 PT useful for modifying cell fate, plant development, plant morphology,  
 PT plant biochemistry and plant physiology  
 XX  
 PS Example 10; Page 75; 151pp; English.  
 XX  
 CC This invention relates to the protein and nucleic acid sequences of a  
 CC new plant type D-cyclin McCycDm which may be used as a plant growth  
 CC regulator or as a herbicide. The nucleotide sequences of the invention  
 CC are useful for production of transgenic plants, plant cells or tissues,  
 CC and for effecting the expression of the McCycDm protein where the  
 CC nucleic acid is operably linked to one or more control sequences. The  
 CC invention also comprises a method for regenerating a plant from the  
 CC plant cell. The nucleic acid sequence of the invention is useful for  
 CC modifying cell fate, plant development, plant morphology, plant  
 CC biochemistry or plant physiology. The McCycDm protein is useful for  
 CC identifying and obtaining proteins interacting with it, comprising a  
 CC screening assay preferably a two-hybrid screening assay. The protein is  
 CC also useful for modulating the interaction between and/or the activity  
 CC of complexes comprising type D-cyclin and Cdc2 type or Cdc2-related  
 CC kinases and/or other D-cyclin interacting protein partners. The protein  
 CC is also useful for identifying compound or mixture of compounds which  
 CC specifically binds to the protein. This sequence represents the  
 CC McCycDm antigenic peptide #68 of the invention. This peptide may be used  
 CC as an immunogen to produce anti-McCycDm antibodies. These antibodies  
 CC may be used to detect the protein of the invention or to alter its  
 CC function.  
 XX  
 SO Sequence 9 AA;



CC new plant type D-cyclin McCycdm which may be used as a plant growth  
CC regulator or as a herbicide. The nucleotide sequences of the invention  
CC are useful for production of transgenic plants, plant cells or tissues,  
CC and for effecting the expression of the McCycdm protein where the  
CC nucleic acid is operably linked to one or more control sequences. The  
CC invention also comprises a method for regenerating a plant from the  
CC plant cell. The nucleic acid sequence of the invention is useful for  
CC modifying cell fate, plant development, plant morphology, plant  
CC biochemistry or plant physiology. The McCycdm protein is useful for  
CC identifying and obtaining proteins interacting with it, comprising a  
CC screening assay preferably a two-hybrid screening assay. The protein is  
CC also useful for modulating the interaction between and/or the activity  
CC of complexes comprising type D-cyclin and Cdc2-type or Cdc2-related  
CC kinases and/or other D-cyclin interacting protein partners. The protein  
CC is also useful for identifying compound or mixture of compounds which  
CC specifically binds to the protein. This sequence represents the  
CC McCycdm antigenic peptide #71 of the invention. This peptide may be used  
CC as an immunogen to produce anti-McCycdm antibodies, these antibodies  
CC may be used to detect the protein of the invention or to alter its  
CC function.

XX Sequence 9 AA:

Query Match 36.4%; Score 47; E-Value 1.0e-10; Length 71  
Best Local Similarity 100.0%; Pred. Num. 9; Length 71  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 KGNS 8  
DQ 2 KGNS 5

RESULT 31

ABB74310

ID ABB74310 standard; Peptide; 9 AA.

XX AC ABB74310;

XX DT 18-APR-2002 (first entry)

XX DE Simple nuclear localisation signal peptide SEQ ID NO:74.

XX KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogenic;  
XX liposome; micelle; karyophilic; cytotax; actinomycin; solid tumour;  
XX peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
XX breast carcinoma; prostate carcinoma.

XX OS Synthetic.

XX PN W020619836-A2.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US18657.

XX PR 09 JUN 2000; 2000US-210925P.

XX PA (H03L7) ROULIKAS T.

XX PI Roulukas T;

XX DR WPI: 2002-164295/21.

XX PT Encapsulation of plasmid DNA (Liposomes) and therapeutic agents with  
XX nuclear localization signal/fusogenic peptide conjugates into targeted  
XX liposome complexes -

XX PS Claim 14; Page 56; 107pp; English.

XX CC The present invention describes a method for producing micelles with  
XX entrapped therapeutic agents. The method comprises: (i) combining  
XX negatively charged agent with a cationic lipid in a ratio where 40-90 %  
XX of the negatively charged atoms are neutralised by positive charges on.

CC nucleic acids, proteins, and other substances complexed with the  
CC antibody and (2) entering the micelle complex of (4) with the antibody  
CC karyophilic peptide complex in a 1:1 or 1:2 ratio, therefore producing  
CC a complex with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent in vivo, comprising the administration  
CC of the micelle complex. Antibodies represent specifically oriented  
CC agent localisation signal (NLS) peptides for use in the method as the  
CC fusogenic karyophilic peptides. The micelles produced can have cytarabine  
CC and antitumor activities. The method for the production of the micelle  
CC produced are useful for identifying the production of the micelle  
CC diseases. The micelle complex is the field of gene therapy and as  
CC directed repair agents for promoting peptide lipid polynucleotide  
CC complexes signal and delivery of polynucleotides. The micelle complex  
CC complexes display a directed activity in eradicated solid tumours  
CC including but not limited to prostate carcinoma or prostate carcinoma  
CC ABB74310 to ABB74310 is used for the identification of the protein  
XX function.

XX Sequence 9 AA:

Query Match 36.4%; Score 47; E-Value 1.0e-10; Length 71  
Best Local Similarity 100.0%; Pred. Num. 9; Length 71  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 KSEK 9

DQ 2 KSEK 9

RESULT 32

ABB74310

ID ABB74310 standard; Peptide; 9 AA.

XX AC ABB74310;

XX DT 18-APR-2002 (first entry)

XX DE Simple nuclear localisation signal peptide SEQ ID NO:74.

XX KW Protease; detection; protein screening; cysteine; apoptosis; inhibition;  
XX nuclear localisation signal; NLS.

XX OS Synthetic.

XX PN W020619836-A2.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US18657.

XX PR 09 JUN 2000; 2000US-210925P.

XX PA (H03L7) ROULIKAS T.

XX PI Roulukas T;

XX DR WPI: 2002-164295/21.

XX PT Detect and the production of a cysteine protease in a cell for use of protease  
XX activity detection and drug screening applications, by using a protease  
XX detection assay on protein.

XX PS Detect and the production of a cysteine protease in a cell for use of protease

XX CC The invention relates to a cell comprising a protease detected and fusion  
XX protein containing first and second subcellular localisation domains. (1)  
XX (b2) separated by a cleavage domain (b2) recognised by the protease,  
XX (where b2 is domain b2) and a label domain is present between the  
XX (b2 and b2). The fusion protein is maintained for a period of time sufficient  
XX for b2 to be cleaved by protease if present in the cell, and subsequently the  
XX location of label domain is detected. The method is useful for  
XX determining whether a cell contains an active protease. The method finds  
XX applications, including monitoring activity of a protease in a cell.

CC monitoring the effect of an agent on the activity of a protease, including  
 CC drug screening applications to identify agents that modulate the activity  
 CC of a particular protease and studying the effect of a factor on  
 CC expression of the protease-encoding gene, detecting protease activity of  
 CC interest in a cell is useful for determining the particular state of the  
 CC cell associated with the particular protease, e.g. certain active  
 CC caspases indicate that a cell is undergoing an apoptotic event. Protease  
 CC detection applications can be used in diagnostic applications, including  
 CC diagnosis of bacterial and/or viral pathogenic infection. The present  
 CC sequence is that of a nuclear localisation signal (NLS) containing  
 CC peptide disclosed in illustrations of the invention.

XX Sequence 9 AA:

Query Match 36.4%; Score 4; DN 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; Gap 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KSKK 5  
 IIII  
 DB 3 KSKK 6

RESULT 33

ABJ19497  
 ID ABJ19497 standard; Peptide: 9 AA.

XX ABJ19497;

XX 27-MAR-2003 (first entry)

XX COGHEP generated degenerate primer: pep:line #14.

XX Panel: degenerate primer pair; screening: virus family:  
 XX high throughput screening; ULIS DNA packaging protein: vHA.

XX Unidentified.

XX W0200299129-A2.

XX 12-DEC-2002.

XX 07-JUN-2002: 2002WO-CR02640.

XX 07-JUN-2001: 2001GB-0013908.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Griffiths DJ, Kellam P, Weiss RA;

XX WPI: 2003-148676/14.

XX Designing a panel of degenerate primer pairs, useful for screening new  
 PT members of multiple known virus families in a biological sample,  
 PT comprises deducing the sequences of the primers using computer based  
 PT calculations.

XX Disclosure: Page 26; 31pp; English.

XX The invention relates to a novel method for designing a panel of  
 CC degenerate primer pairs for screening for new members of multiple known  
 CC virus families in a biological sample. The method can be used in high  
 CC throughput screening to detect viruses. This sequence represents a  
 CC peptide derived from a degenerate per primer of the invention.

XX Sequence 9 AA:

Query Match 36.4%; Score 4; DN 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; Gap 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GNSS 9  
 IIII

DB 2 GNSS 6

RESULT 44

ABJ19442

XX ABJ19442 standard; Peptide: 9 AA.

XX ABJ19442;

XX 27-MAR-2003 (first entry)

XX COGHEP generated degenerate primer: pep:line #14.

XX Panel: degenerate primer pair; screening: virus family:  
 XX high throughput screening; ULIS DNA packaging protein: vHA.

XX Unidentified.

XX W0200299129-A2.

XX 12-DEC-2002.

XX 07-JUN-2002: 2002WO-CR02640.

XX 07-JUN-2001: 2001GB-0013908.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Griffiths DJ, Kellam P, Weiss RA;

XX WPI: 2003-148676/14.

XX Designing a panel of degenerate primer pairs, useful for screening new  
 PT members of multiple known virus families in a biological sample,  
 PT comprises deducing the sequences of the primers using computer based  
 PT calculations.

XX Disclosure: Page 26; 31pp; English.

XX The invention relates to a novel method for designing a panel of  
 CC degenerate primer pairs for screening for new members of multiple known  
 CC virus families in a biological sample. The method can be used in high  
 CC throughput screening to detect viruses. This sequence represents a  
 CC peptide derived from a degenerate per primer of the invention.

XX Sequence 9 AA:

Query Match 36.4%; Score 4; DN 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; Gap 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GNSS 6

DB 2 GNSS 6

RESULT 45

ABJ19448

XX ABJ19448 standard; Peptide: 9 AA.

XX ABJ19448;

XX 27-MAR-2003 (first entry)

XX COGHEP generated degenerate primer: pep:line #14.  
 XX Panel: degenerate primer pair; screening: virus family:  
 XX high throughput screening; ULIS DNA packaging protein: vHA.  
 XX Unidentified.

XX W0200299129-A2.

XX 12-DEC-2002.

XX 07-JUN-2002: 2002WO-CR02640.

XX 07-JUN-2001: 2001GB-0013908.

XX (UNLO ) UNIV COLLEGE LONDON.

XX Griffiths DJ, Kellam P, Weiss RA;

XX WPI: 2003-148676/14.

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FT      /note= "Ac-D2Nal"
FT      /label= OTHER
FT      /note= "D4Clphe"
FT      /note= "D-form, omega-amino
FT      gp, linked to side chain carboxy gp, of
FT      Glu10 via peptide bond"
FT      /note= "Lys(Nicotinyl)
FT      D-form residue"
FT      /note= "Lys(N-epsilon-Isopropyl)"
FT      /note= "D-form reiside, side chain carboxy gp,
FT      linked to omega-amino gp, of LysG3 via
FT      peptide bond, the C-terminal carboxy
FT      is in amide form"
XX
XX      W09524424-A1.
XX
XX      14-SEP-1995.
XX
XX      27-FEB-1995; 95WO-US02410.
XX
XX      09-MAR-1994; 94US-0208544.
XX
XX      (ABRO ) ABBOTT LAB.
XX
XX      Haviv F, Sauer DR;
XX
XX      WPI; 1995-328233/42.
XX
XX      New cyclic peptide LHRH antagonists used for treating conditions
XX      mediated by sex hormones, e.g. prostate cancer, endometriosis and
XX      uterine fibroids
XX
XX      Claim 4; Page 43; 50pp; English.
XX
XX      The cyclic peptide luteinising hormone releasing hormone (LHRH)
XX      antagonists AAR88990-R89073 inhibit the release of LHRH in mamma's,
XX      useful in the treatment of conditions which are mediated by sex
XX      hormones, e.g. prostate cancer, endometriosis, uterine fibroids
XX      and precocious puberty.
XX
XX      Sequence 10 AA;
XX
XX      Query Match 36.48; Score 4; DH 16; Length 10;
XX      Best Local Similarity 100.0%; Pred. No. 7.5e+02;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 2 KSRK 5
XX      Db 3 KSRK 6
XX
XX      RESULT 36
XX      ABP11602
XX      ID ABP11602 standard; Peptide: 10 AA.
XX      AC ABP11602;
XX      XX
XX      DT 15-JUL-2002 (first entry)
XX
XX      HIV A01 super motif env peptide #85.
XX
XX      HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;
XX      vpr; vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
XX      antigen; vaccine; HIV infection; immunisation; viricide.
XX
XX      Human immunodeficiency virus type 1.
XX      OS
XX      PN W0200124810-A1.

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XX      12-APR-2001
XX
XX      05-OCT-2000; 2000US-2423404.
XX
XX      05-OCT-1999; 95US-312444
XX      (PTM-) EMMEN; EN
XX
XX      Sette A, Sidney J, Southwood S, Thompson RO, Chesham R,
XX      Baker DM, Chittam K, Kato RT, Gray BM.
XX
XX      WPI; 2001 354857/51
XX
XX      Vaccine composition for combating human immunodeficiency virus 1 (HIV-1)
XX      peptide groups, used in the vaccination against HIV 1
XX
XX      Claim 32; Para 106, 117-119; Def. 1-5b.
XX
XX      The present invention describes a composition (i) comprising a protein-
XX      human immunodeficiency virus (HIV-1) group comprising an amino acid
XX      sequence selected from a group of amino acid sequences (AA25447 to
XX      AB925457); (ii) a vaccine adjuvant and can be used in vaccines; (i)
XX      may be used for immunisation against HIV-1 infections. The use of
XX      group-based vaccines has several advantages over traditional vaccines,
XX      particularly when compared to the use of whole antigens in vaccine
XX      compositions. There is evidence that the immune response to whole
XX      antigens is directed largely toward variable regions of the antigen,
XX      allowing for immune escape due to mutations. The groups for inclusion in
XX      an group-based vaccine may be selected from conserved regions of viral or
XX      tumour-associated antigens, which therefore reduces the likelihood of
XX      escape mutants. Furthermore, immunosuppressive groups that may be present
XX      in whole antigens can be avoided with the use of group-based vaccines.
XX      An additional advantage of an group-based vaccine approach is the ability
XX      to combine selected groups (vif and tat), and further, to modify the
XX      composition of the groups, deconvolving, for example, enhanced
XX      immunogenicity. Accordingly, the immune response can be modulated, as
XX      appropriate, for the target disease. Similar engineering of the response
XX      is not possible with traditional approaches. ABP11531 to ABP25412
XX      represent peptide sequences used in the exemplification of the present
XX      invention.
XX
XX      Sequence 10 AA.
XX
XX      Query Match 36.48; Score 4; DH 22; Length 10;
XX      Best Local Similarity 100.0%; Pred. No. 7.5e+02;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 6 GNSS 9
XX      Db 111
XX      4 GNSS 7
XX
XX      RESULT 47
XX      ABP12404
XX      DT ABP12404 standard; Peptide: 10 AA.
XX      AC ABP12404;
XX      XX
XX      DT 15-JUL-2002 (first entry)
XX
XX      HIV A02 super motif env peptide #441.
XX
XX      HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;
XX      vpr; vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
XX      antigen; vaccine; HIV infection; immunisation; viricide.
XX
XX      Human immunodeficiency virus type 1
XX      OS
XX      PN W0200124810-A1.
XX      PD 12-APR-2001.
XX

```





PI Sette A, Sidney J, Southwood S, Livingston B, Chesnut R,  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 DR WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccination against HIV;  
 XX Claim 12; Page 185; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV 1) group comprising a prepared  
 CC sequence selected from 51 defined amino acid sequences (A1-2547 to  
 CC A1-2547). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV 1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunopressure groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (C1 and B1), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. A1-1561 to A1-2547  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;

Query Match 36.4%; Score 4; DR 22; Length 17;  
 Best local Similarity 100.0%; Pred. No. 7.5e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
 I I I I  
 DB 4 GNSS 7

RESULT 4C  
 A1-17602  
 ID A1-17602 standard; Peptide; 10 AA.  
 AC A1-17602;  
 XX 15-JUL-2002 (first entry)  
 DE HIV B58 super motif env peptide #1.  
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif; vpr;  
 KW vpr; vif; tat; cytoxic T lymphocyte; C1b; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virus; virus;  
 XX Human immunodeficiency virus type 1.  
 OS  
 XX W0200124810-A1.  
 PN 12-APR-2001.  
 XX 05-OCT-2000: 2000W0-US27766.  
 PF 05-OCT-1999: 99US-0412863.  
 PR (EPIM-) EPIMMUNE INC.  
 PA Sette A, Sidney J, Southwood S, Livingston B, Chesnut R,  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)

PI Sette A, Sidney J, Southwood S, Livingston B, Chesnut R,  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 DR WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccination against HIV;  
 XX Claim 12; Page 185; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV 1) group comprising a prepared  
 CC sequence selected from 51 defined amino acid sequences (A1-2547 to  
 CC A1-2547). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV 1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunopressure groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (C1 and B1), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. A1-1561 to A1-2547  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 Query Match 36.4%; Score 4; DR 22; Length 17;  
 Best local Similarity 100.0%; Pred. No. 7.5e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GNSS 9  
 I I I I  
 DB 4 GNSS 7  
 RESULT 4C  
 A1-17602  
 ID A1-17602 standard; Peptide; 10 AA.  
 AC A1-17602;  
 XX 15-JUL-2002 (first entry)  
 DE HIV B58 super motif env peptide #1.  
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif; vpr;  
 KW vpr; vif; tat; cytoxic T lymphocyte; C1b; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virus; virus;  
 XX Human immunodeficiency virus type 1.  
 OS  
 XX W0200124810-A1.  
 PN 12-APR-2001.  
 XX 05-OCT-2000: 2000W0-US27766.  
 PF 05-OCT-1999: 99US-0412863.  
 PR (EPIM-) EPIMMUNE INC.  
 PA Sette A, Sidney J, Southwood S, Livingston B, Chesnut R,  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)

PT peptide groups, useful for vaccinating against HIV 1;  
 PS Claim 32: Page 233; 448pp; English.  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25437 to  
 CC ABP25497). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of virus,  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be tailored, as  
 CC appropriate, for the target disease. Similar requirements of the response  
 CC is not possible with traditional approaches. Abbreviations: ABP25437 to ABP25497  
 CC represent peptide sequences used in the experimental evaluation of the present  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; 10 22; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 7,6062;  
 Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0  
 QY 6 GNSS 9  
 Db IIII  
 Db 5 GNSS 8  
 RESULT 42  
 ABP19695  
 ID ABP19695 standard; Peptide: 10 AA.  
 XX  
 AC ABP19695;  
 DT 15 JUL 2002 (first entry)  
 XX  
 DE HIV A01 motif env peptide #5.  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W0200124810-A1.  
 XX  
 PD 12 APR 2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livinaston SB, Chishti A;  
 PI Baker DM, Cellis E, Kubo RT, Grey HW.  
 XX  
 DR WPI: 2001-354887/37.  
 XX  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccinating against HIV 1.  
 PT  
 PS Claim 32: Page 273; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25437 to  
 CC ABP25497). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of virus,  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be tailored, as  
 CC appropriate, for the target disease. Similar requirements of the response  
 CC is not possible with traditional approaches. Abbreviations: ABP25437 to ABP25497  
 CC represent peptide sequences used in the experimental evaluation of the present  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; 10 22; Length 1;  
 Best Local Similarity 100.0%; Pred. No. 7,6062;  
 Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 0  
 QY 6 GNSS 9  
 Db IIII  
 Db 5 GNSS 8  
 RESULT 42  
 ABP19695  
 ID ABP19695 standard; Peptide: 10 AA.  
 XX  
 AC ABP19695;  
 DT 15 JUL 2002 (first entry)  
 XX  
 DE HIV A01 motif env peptide #5.  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; tat; vif;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W0200124810-A1.  
 XX  
 PD 12 APR 2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
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 PA (EPIM) EPIMMUNE INC.  
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 PI Sette A, Sidney J, Southwood S, Livinaston SB, Chishti A;  
 PI Baker DM, Cellis E, Kubo RT, Grey HW.  
 XX  
 DR WPI: 2001-354887/37.  
 XX  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccinating against HIV 1.  
 PT  
 PS Claim 32: Page 273; 448pp; English.

sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion of an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

Query Match 36.4%; Score 4; UP 22; Length 10;

Best Local Similarity 100.0%; Prod. No. 7 5e-02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9

DB 1 GNSS 4

RESULT 44

ABP19814

ID ABP19814 standard; Peptide: 10 AA.

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Sequence 10 AA

Query Match 36.4%; Score 4; UP 22; Length 10;

Best Local Similarity 100.0%; Prod. No. 7 5e-02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 GNSS 9

DB 1 GNSS 4

RESULT 44

ABP19814

ID ABP19814 standard; Peptide: 10 AA

XX

XX

XX

XX

XX

XX

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CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP2542  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; PB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GNSS 9  
 Db 3 GNSS 6  
 RESULT 46  
 ABP19819  
 ID ABP19819 standard; Peptide: 10 AA.  
 XX  
 AC ABP19819;  
 DT 15-JUL-2002 (first entry)  
 DE HIV A03 motif env peptide #23.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W0200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston B0, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV 1.  
 XX  
 PS Claim 32; Page 276; 448pp; English.  
 XX  
 CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.

CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP2542  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 36.4%; Score 4; PB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GNSS 9  
 Db 3 GNSS 6  
 RESULT 47  
 ABP25395  
 ID ABP25395 standard; Peptide: 10 AA.  
 XX  
 AC ABP25395;  
 DT 16-JUL-2002 (first entry)  
 DE HIV A03 motif env peptide #26.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W2012481 A1.  
 XX  
 PD 12-APR-2001  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston B0, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1  
 XX  
 PS Claim 32; Page 283; 448pp; English  
 XX  
 CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability  
CC to combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

XX Sequence 10 AA:  
SQ  
Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNS5 9  
Db 2 GNS5 5

RESULT 48  
ABP22288  
ID ABP22288 standard; Peptide: 10 AA.  
XX  
AC ABP22288;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV All motif env peptide #11.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; asq; nef; vif;  
KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; virucide;  
XX  
OS Human immunodeficiency virus type 1.

XX W0200124810-A1.  
PN  
XX 12-APR-2001.  
PD  
XX 05-OCT-2000; 2000WO-US27766.  
PF  
XX 05-OCT-1999; 99US-0412863.  
PR  
XX {EPIM-} EPIMUNE INC.  
PA  
XX Settle A, Sidney J, Southwood S, Livingston RD, Chesnut R;  
PI Baker DM, Cells E, Kubo RT, Grey HM;  
PI WP1: 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
XX peptide groups, useful for vaccinating against HIV-1.  
XX  
XX Claim 32; Page 326; 448pp; English.

XX The present invention describes a composition: (i) comprising a prepared  
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
XX sequence selected from 51 defined amino acid sequences (ABP25347 to  
XX ABP25397); (ii) has virucide activity and can be used in vaccines; (iii)  
XX may be used for immunising subjects against HIV-1 infections; the use of  
XX group-based vaccines has several advantages over traditional vaccines,  
XX particularly when compared to the use of whole antigens in vaccine  
XX compositions. There is evidence that the immune response to whole  
XX antigens is directed largely toward variable regions of the antigen,  
XX allowing for immune escape due to mutations. The groups for inclusion in  
XX an group-based vaccine may be selected from conserved regions of viral or  
XX tumour-associated antigens, which therefore reduces the likelihood of  
XX escape mutants. Furthermore, immunosuppressive groups that may be present  
XX in whole antigens can be avoided with the use of group-based vaccines.  
XX An additional advantage of an group-based vaccine approach is the ability  
XX to combine selected groups (CTL and HTL), and further, to modify the  
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CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP11501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention.

XX Sequence 10 AA:  
SQ  
Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNS5 9  
Db 2 GNS5 5

RESULT 49  
ABP22289  
ID ABP22289 standard; Peptide: 10 AA.  
XX  
AC ABP22289;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE HIV All motif env peptide #12

XX HIV; HIV-1; human immunodeficiency virus; env; pol; asq; nef; vif;  
KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; virucide;  
XX  
OS Human immunodeficiency virus type 1.

XX W0200124810-A1.  
PN  
XX 12-APR-2001.  
PD  
XX 05-OCT-2000; 2000WO-US27766.  
PF  
XX 05-OCT-1999; 99US-0412863.  
PR  
XX {EPIM-} EPIMUNE INC.  
PA  
XX Settle A, Sidney J, Southwood S, Livingston RD, Chesnut R;  
PI Baker DM, Cells E, Kubo RT, Grey HM;  
PI WP1: 2001-354887/37.

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XX peptide groups, useful for vaccinating against HIV-1.  
XX  
XX Claim 32; Page 326; 448pp; English.

XX The present invention describes a composition: (i) comprising a prepared  
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
XX sequence selected from 51 defined amino acid sequences (ABP25347 to  
XX ABP25397); (ii) has virucide activity and can be used in vaccines; (iii)  
XX may be used for immunising subjects against HIV-1 infections; the use of  
XX group-based vaccines has several advantages over traditional vaccines,  
XX particularly when compared to the use of whole antigens in vaccine  
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XX antigens is directed largely toward variable regions of the antigen,  
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XX an group-based vaccine may be selected from conserved regions of viral or  
XX tumour-associated antigens, which therefore reduces the likelihood of  
XX escape mutants. Furthermore, immunosuppressive groups that may be present  
XX in whole antigens can be avoided with the use of group-based vaccines.  
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XX to combine selected groups (CTL and HTL), and further, to modify the  
XX composition of the groups, achieving, for example, enhanced

CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SO Sequence 10 AA;  
 Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;  
 QY 6 GNSS 9  
 Db 4 GNSS 7  
 IIII  
 RESULT 50  
 ID ABP22661 standard; Peptide: 10 AA.  
 XX  
 AC ABP22661;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A11 motif gag peptide #40.  
 XX  
 KW HIV-1; human immunodeficiency virus; HTLV-1; AIDS; HIV-1; HIV-1  
 KW vpr; tat; cytototoxic T lymphocyte (CTL) immune response epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virulence;  
 XX  
 OS Human immunodeficiency virus type 1;  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM ) EPIMUNE INC.  
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 PI Settle A, Sidney J, Southwood S, Livingston BR, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX  
 DR WP1: 2001-354887/17.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccinating against HIV 1.  
 XX  
 PS Claim 42; Page 333; 443pp; English.  
 XX  
 CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (1) has virucide activity and can be used in vaccines. (1)  
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 CC compositions. There is evidence that the immune response to whole  
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 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC A: additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTLV), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX

SO Sequence 10 AA;  
 Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Prod. No. 7.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;  
 QY 6 GNSS 9  
 Db 4 GNSS 7  
 IIII  
 RESULT 50  
 ID ABP22661 standard; Peptide: 10 AA.  
 XX  
 AC ABP22661;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A11 motif gag peptide #40.  
 XX  
 KW HIV-1; human immunodeficiency virus; HTLV-1; AIDS; HIV-1; HIV-1  
 KW vpr; tat; cytototoxic T lymphocyte (CTL) immune response epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virulence;  
 XX  
 OS Human immunodeficiency virus type 1;  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
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 PA (EPIM ) EPIMUNE INC.  
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 PI Settle A, Sidney J, Southwood S, Livingston BR, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX  
 DR WP1: 2001-354887/17.  
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 XX  
 PS Claim 42; Page 333; 443pp; English.  
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 CC particularly when compared to the use of whole viruses in vaccine  
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 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC A: additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTLV), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX















## C49215

urease (EC 3.5.1.5) large subunit. Urea - Helicobacter felis (fragment)

C:Species: Helicobacter felis

C>Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #extl\_change 06-Jan-2003

C:Accession: C49215

R:Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.

Infect. Immun. 60, 5259-5266, 1992

A:Title: Purification and characterization of the urease enzymes of Helicobacter species

A:Reference number: A49215; MUID:93084378; PMID:1452359

A:Accession: C49215

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <PRO>

A:Experimental source: ATCC 49179

A:Note: sequence extracted from NCBI backbone (NCBI:P119464)

C:Superfamily: urease, alpha subunit; urease 62k chain homology

C:Keywords: hydrolase

## Query Match

Best Local Similarity 27.38; Score 3; PB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 SRK 5

DB 5 SRK 7

## RESULT 14

## S26549

T-cell receptor beta chain (clone Cw1/A8, Cw3/Cas1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #extl\_change 17-Mar-1999

C:Accession: S26549; S26550

R:Casanova, J.L.; Cerottini, J.C.; Mathies, M.; Necker, A.; Barnier, B.; Barria, C.

J. Exp. Med. 176, 439-447, 1992

A:Title: H-2 restricted cytolytic T lymphocytes specific for HLA class II T cell receptor

A:Reference number: S26512; MUID:92364545; PMID:1443661

A:Accession: S26549

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Cross-references: EMBL:X67999

A:Experimental source: cytolytic T-lymphocyte, clone Cw1/A8

A:Accession: S26550

A:Molecule type: mRNA

A:Residues: 1-12 <CA2>

A:Cross-references: EMBL:X68000

A:Experimental source: cytolytic T-lymphocyte, clone Cw1/Cas1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

## Query Match

Best Local Similarity 27.38; Score 3; PB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 SSL 10

DB 3 SSL 5

## RESULT 15

## S65409

histone H2B - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #extl\_change 17-Mar-1999

C:Accession: S65409

R:Frohm, M.; Gunne, H.; Bergman, A.C.; Agerterth, R.; Bergman, A.; Lidén, S.

Eur. J. Biochem. 237, 86-92, 1996

A:Title: Biochemical and antibacterial analysis of human waste and bacterium

A:Reference number: S65409; MUID:96203912; PMID:8620898

A:Accession: S65409

A:Molecule type: protein

A:Residues: 1-12 <PRO>

C:Superfamily: histone H2B

C:Keywords: changes of protein; DNA binding; nucleosome core

## Query Match

Best Local Similarity 27.38; Score 3; PB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 SRK 3

DB 4 SRK 3

## RESULT 16

## A44874

prokaryotic protein (Pseudomonas fluorescens Pf-0) (fragment)

C:Species: Pseudomonas fluorescens

C>Date: 31-Mar-1993 #sequence\_revision 18-Mar-1994 #extl\_change 16-Oct-1999

C:Accession: A44874

R:Rauda-Zozor, E.M.; Zozor, E.; Kallio, J.

Development 11, 253-254, 1993

A:Title: Biosynthesis of a protein (Pseudomonas fluorescens Pf-0) (fragment)

A:Reference number: A44874; MUID:1684732

A:Accession: A44874

A:Molecule type: DNA

A:Residues: 1-12 <PRO>

A:Cross-references: EMBL:X67999

A:Note: Sequence extracted from 9701 backdoor (N-HIN 77429; N-HIN 77433)

C:Keywords: changes of protein

## Query Match

Best Local Similarity 27.38; Score 3; PB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 SRK 3

DB 4 SRK 3

## RESULT 17

## S29634

gene (P.0) protein - human (fragment) (nucleolar protein synthesis virus (fragment))

C:Species: Human (fragment) (nucleolar protein synthesis virus (fragment))

C>Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #extl\_change 24-Mar-1999

C:Accession: S29634

R:Ritter, J.; Ritz, K.; Ritz, J.; Ritz, J.; Ritz, J.; Ritz, J.; Ritz, J.; Ritz, J.

Biochem. Biophys. Acta 1172, 189-194, 1994

A:Title: Nucleolar protein synthesis virus (P.0) gene (P.0) protein

A:Reference number: S29634; MUID:841659

A:Accession: S29634

A:Note: not a standard nucleolar protein

A:Molecule type: DNA

A:Residues: 1-12 <PRO>

A:Experimental source: human (fragment)

## Query Match

Best Local Similarity 27.38; Score 3; PB 2; Length 12;

Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 SRK 3

DB 4 SRK 3

## RESULT 18

## S47362

T-cell antigen receptor V (human) (nucleolar protein synthesis virus (fragment))

C:Species: Homo sapiens (man)

C>Date: 30-Jul-1996 #sequence\_revision 26-Jan-1998 #extl\_change 05-Nov-1999

C:Accession: S47362

R: Lechner, P.J.

Submitted to the EMBL Data Library, August 1994

A: Description: Human HLA-A\*0201 restricted recognition of influenza A is determined by T-

A: Reference number: S47355

A: Accession: S47360

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-12 <LEH>

A: Cross references: EMBL:235684; NID:Q527457; EDB:2AA4756.1; EDB:Q527456

C: Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 12;

Best local Similarity 100.0%; Pred. No. 2.6000;

Matches 3; Conservative 0; Mismatches 0; Gaps 0

QY 8 SSL 12

DB 10 SSL 12

#### RESULT 19

PH1463

T-cell receptor beta chain (clone A24/10.1) - mouse (Tramont)

C: Species: Mus musculus (house mouse)

C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995

C: Accession: PH1463

R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K-

J. Exp. Med. 177, 811-820, 1993

A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility

A: Reference number: PH1430; MUID:94171821; EMBL:245611

A: Accession: PH1463

A: Molecule type: mRNA

A: Residues: 1-12 <CAS>

A: Experimental source: cytolytic T-lymphocyte

A: Superfamily: immunoglobulin homology

C: Keywords: receptor; T-cell

Query Match 27.3% Score 3; DB 2; Length 12;

Best local Similarity 100.0%; Pred. No. 2.6000;

Matches 3; Conservative 0; Mismatches 0; Gaps 0

QY 8 SSL 10

DB 4 SSL 5

#### RESULT 20

PH1466

T-cell receptor beta chain (clone A3/74.1) - mouse (Tramont)

C: Species: Mus musculus (house mouse)

C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995

C: Accession: PH1466

R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K-

J. Exp. Med. 177, 811-820, 1993

A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility

A: Reference number: PH1430; MUID:94171821; EMBL:245611

A: Accession: PH1466

A: Molecule type: mRNA

A: Residues: 1-12 <CAS>

A: Experimental source: cytolytic T-lymphocyte

A: Superfamily: immunoglobulin homology

C: Keywords: receptor; T-cell

Query Match 27.3% Score 3; DB 2; Length 12;

Best local Similarity 100.0%; Pred. No. 2.6000;

Matches 3; Conservative 0; Mismatches 0; Gaps 0

QY 8 SSL 10

DB 3 SSL 5

#### RESULT 21

PH1466

T-cell receptor beta chain (clone A3/74.1) - mouse (Tramont)

C: Species: Mus musculus (house mouse)

C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 11 Apr-1995

C: Accession: PH1466

R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K-

J. Exp. Med. 177, 811-820, 1993

A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility

A: Reference number: PH1430; MUID:94171821; EMBL:245611

A: Accession: PH1466

A: Molecule type: mRNA

A: Residues: 1-12 <CAS>

A: Experimental source: cytolytic T-lymphocyte

A: Superfamily: immunoglobulin homology

C: Keywords: receptor; T-cell

Query Match 27.3% Score 3; DB 2; Length 12;

Best local Similarity 100.0%; Pred. No. 2.6000;

Matches 3; Conservative 0; Mismatches 0; Gaps 0

QY 8 SSL 10

DB 3 SSL 5

PH1466

T-cell receptor beta chain (clone A24/10.1) - mouse (Tramont)

C: Species: Mus musculus (house mouse)

C: Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text change 12 Sep-2000

C: Accession: PH1466

R: Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, O.; Fournier, C.; Renard, A.; K-

J. Exp. Med. 177, 811-820, 1993

A: Title: T cell receptor selection by and recognition of two classes of major histocompatibility

A: Reference number: PH1430; MUID:94171821; EMBL:245611

A: Accession: PH1466

A: Molecule type: mRNA

A: Residues: 1-12 <CAS>

A: Experimental source: cytolytic T-lymphocyte

A: Superfamily: immunoglobulin homology

C: Keywords: receptor; T-cell

C: Keywords: receptor; T-cell

C: Keywords: receptor; T-cell

C: Keywords: receptor; T-cell

C: Keywords: receptor; T-cell

C: Keywords: receptor; T-cell

C: Keywords: receptor; T-cell

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C: Keywords: receptor; T-cell

C: Keywords: receptor; T-cell

## RESULT 24

S09395  
 hypothetical protein - fruit fly (Drosophila melanogaster) (fragment)  
 C:Species: Drosophila melanogaster  
 C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 24-Jul-1997  
 C:Accession: S09395  
 R:Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mailart, A.; Ancelet-Petit, D.; Mueller-Helber  
 EMBO J. 8, 2359-2364, 1989  
 A>Title: The interference of truncated with normal potassium channel subunits leads to a  
 A:Reference number: S09395; MUID:90005442; PMID:2551680  
 A:Accession: S09395  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-13 <GIS>

Query Match 27.3% Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9  
 |||  
 DB 11 NSS 13

## RESULT 25

A49018  
 myosin heavy chain, fast skeletal muscle type X - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 18-A-q-1994  
 C:Accession: A49018; S32161  
 R:DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Veileca, M.; Buckingham, M.; Schiaffino  
 J. Cell Biol. 123, 823-835, 1993  
 A>Title: Type 2X-myosin heavy chain is coded by a muscle fiber type specific and develop  
 A:Reference number: A49018; MUID:94043465; PMID:8227143  
 A:Accession: A49018  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <DEN>  
 A:Cross-references: GB:X72591; NID:q288645; PIDN:CAA51189.1; PID:q288646  
 R:DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Veileca, M.; Morille, J.; Buckingham,  
 submitted to the EMBL Data Library, March 1993  
 A:Description: Type 2X myosin heavy chain is coded by a muscle fiber type-specific and c  
 A:Reference number: S32161  
 A:Accession: S32161  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <DEN2>  
 A:Cross-references: EMBL:X72591; NID:q288645; PIDN:CAA51189.1; PID:q288646  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: skeletal muscle

Query Match 27.3% Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSR 4  
 |||  
 DB 2 KSR 4

## RESULT 26

B34135  
 DNA-binding protein q - Crithidia fasciculata mitochondrion (fragment)  
 C:Species: mitochondrion Crithidia fasciculata  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 07-Dec-1999  
 C:Accession: B34135  
 R:Tittawella, I.  
 FEBS Lett. 260, 57-61, 1990  
 A>Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fas  
 A:Reference number: A34135  
 A:Accession: B34135

A:Molecule type: protein  
 A:Residues: 1-14 <GIS>  
 A:Genetics:  
 A:Genome: mitochondrial  
 A:Genetic code: S036  
 C:Keywords: mitochondrion

Query Match 27.3% Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NSS 5  
 |||  
 DB 10 NSS 6

## RESULT 27

A42421  
 leukotriene B-4 synthase (leukotriene synthase) (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1994  
 C:Accession: A42421  
 R:Yokoyama, C.; Smith, W.L.; Smith, W.L.; Kusama, T.; Kobayashi, Y.; Saito, F.; Tasei  
 J. Biol. Chem. 269, 16124-16128, 1994  
 A>Title: Enzymatic activation of leukotriene B-4 by a novel enzyme coded for the p  
 A:Reference number: A42421; MUID:8452600; PMID:8494363  
 A:Accession: A42421  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <GIS>  
 C:Keywords: oxidized arase

Query Match 27.3% Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 4  
 |||  
 DB 3 AKS 5

## RESULT 28

PH1658  
 12 B chain V-D-J region, mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1994  
 C:Accession: PH1658; PH1658  
 R:Levinson, L.A.; Camps-Corcos, L.; Lock, P.  
 J. Exp. Med. 178, 457-469, 1993  
 A>Title: Molecular characterization of T-uniques induced by antigenic peptide in P  
 A:Reference number: PH1658; MUID:8400000; PMID:8415487  
 A:Accession: PH1658  
 A:Molecule type: DNA  
 A:Residues: 1-14 <LEV>  
 A:Experimental source: bone marrow pro-B lymphocytes, wild type clone 405  
 A:Accession: PH1658  
 A:Molecule type: DNA  
 A:Residues: 1-14 <LEV>  
 A:Experimental source: bone marrow pro-B lymphocytes, wild type clone 423  
 C:Keywords: lymphocyte bcl-10

## Query Match

27.3% Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3, 2e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CNS 8  
 |||  
 DB 6 CNS 7

## RESULT 29

S16886  
 Mitosomal protein S12 - Mycobacterium bovis (fragment)



C:Species: Mycobacterium bovis  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 31-Jan-1997  
 C:Accession: S36888  
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
 FEBS Lett. 331, 9-14, 1993  
 A:Title: Isolation and amino acid sequence of the 6S ribosomal protein S19 from Mycobacterium bovis  
 A:Reference number: S36887; MUID:94009653; PMID:8495418  
 A:Accession: S36888  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <OHA>  
 A:Superfamily: Escherichia coli ribosomal protein S12  
 C:Keywords: protein biosynthesis; ribosome

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RKG 6  
 III  
 DB 8 RKG 10

RESULT 30  
 S21411  
 nodulation protein noda - Rhizobium loti (fragment)  
 C:Species: Rhizobium loti  
 C:Date: 22-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 08-Oct-1999  
 C:Accession: S21411  
 R:Scott, D.H.; Young, C.A.; Collins-Emerson, J.M.; Torzadeh, E.A.; Rockwell, E.S.; Low, L.  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Mutational and structural analysis of Rhizobium loti nodulation genes.  
 A:Reference number: S21410  
 A:Accession: S21411  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-15 <SCO>  
 A:Cross-references: EMBL:X65620; NID:q46240; FIDN:CAA3674.1; FID:q46240; FID:q46242  
 C:Genetics:  
 C:Gene: noda

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RKG 6  
 III  
 DB 10 RKG 12

RESULT 31  
 PA0102  
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - humans (Fusarium sporotrichoides)  
 C:Species: Fusarium sporotrichoides  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0102  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichoides  
 A:Reference number: PA0051  
 A:Accession: PA0102  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: aldohyde-lyase; carbon-carbon lyase

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SRK 5  
 III  
 DB 7 SRK 9

RESULT 32  
 FA0004  
 proteinase 2000-2 (proteinase 2000-2) (proteinase 2000-2) (proteinase 2000-2)  
 C:Species: Escherichia coli  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: FA0004  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Escherichia coli  
 A:Reference number: FA0004  
 A:Accession: FA0004  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: aldohyde-lyase; carbon-carbon lyase

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RKG 6  
 III  
 DB 8 RKG 10

RESULT 33  
 FA0004  
 proteinase 2000-2 (proteinase 2000-2) (proteinase 2000-2) (proteinase 2000-2)  
 C:Species: Escherichia coli  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: FA0004  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Escherichia coli  
 A:Reference number: FA0004  
 A:Accession: FA0004  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: aldohyde-lyase; carbon-carbon lyase

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RKG 6  
 III  
 DB 8 RKG 10

RESULT 34  
 FA0004  
 proteinase 2000-2 (proteinase 2000-2) (proteinase 2000-2) (proteinase 2000-2)  
 C:Species: Escherichia coli  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: FA0004  
 R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Escherichia coli  
 A:Reference number: FA0004  
 A:Accession: FA0004  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHO>  
 C:Keywords: aldohyde-lyase; carbon-carbon lyase

Query Match 27.3%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RKG 6  
 III  
 DB 8 RKG 10

RESULT 35



Query Match 18.2% Score 21 Bb 21 Length 87  
 Best Local Similarity 100.0% Pred. No. 2 40-05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 SR 4  
 II  
 DB 1 SR 2

RESULT 41  
 JS0315  
 Leucokinin V - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0315  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A:Title: Isolation, primary structure, and synthesis of leucokinin V and VII from the cockroach  
 A:Reference number: JS0315  
 A:Accession: JS0315  
 A:Molecule type: protein  
 A:Residues: 1-8 <HOL>  
 C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile and  
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 18.2% Score 21 Bb 21 Length 87  
 Best Local Similarity 100.0% Pred. No. 2 40-05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 SS 9  
 II  
 DB 5 SS 6

RESULT 42  
 JS0316  
 Leucokinin VI - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0316  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A:Title: Isolation, primary structure, and synthesis of leucokinin V and VII from the cockroach  
 A:Reference number: JS0315  
 A:Accession: JS0316  
 A:Molecule type: protein  
 A:Residues: 1-8 <HOL>  
 C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile and  
 C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 18.2% Score 21 Bb 21 Length 87  
 Best Local Similarity 100.0% Pred. No. 2 40-05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 SS 9  
 II  
 DB 2 SS 3

RESULT 43  
 JS0317  
 Leucokinin VII - Madeira cockroach  
 C:Species: Leucophaea maderae (Madeira cockroach)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0317  
 R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 31-34, 1987  
 A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII from the cockroach  
 A:Reference number: JS0317



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 6.25 seconds  
(without alignments)  
82.767 Million cell updates/sec

Title: DS-09-787-443-21

Perfect score: 11

Sequence: 1 AKSRKGNSSLW 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 757

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt\_41\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	8	1 RS7_MYCT	P1554 mycobacteri
2	3	27.3	9	1 THYF_PIG	P1255 sus scrofa
3	3	27.3	11	1 Q20A_COME	P0464 romanosus
4	3	27.3	13	1 C1_APLCA	Q1096 aplisia cal
5	3	27.3	13	1 NEUT_CAVPO	P12560 cavia porce
6	3	27.3	15	1 48KD_BACE	P0173 bacillus co
7	2	18.2	8	1 ACT_CARMA	P0709 carcinus ma
8	2	18.2	8	1 ALL3_CYDPO	P02154 cydia pomon
9	2	18.2	8	1 CAD1_ENTFA	P13266 enterococcu
10	2	18.2	8	1 CLP_THICU	P04086 thiobacilli
11	2	18.2	8	1 LCK1_LEUMA	P21140 leucophaea
12	2	18.2	8	1 LCK2_LEUMA	P21141 leucophaea
13	2	18.2	8	1 LCK3_LEUMA	P1142 leucophaea
14	2	18.2	8	1 LCK5_LEUMA	P19987 leucophaea
15	2	18.2	8	1 LCK6_LEUMA	P19989 leucophaea
16	2	18.2	8	1 LCK7_LEUMA	P19989 leucophaea
17	2	18.2	8	1 NS3_MYCTU	P1152 mycobacteri
18	2	18.2	8	1 RSL_FAWCH	P17985 ewinia chr
19	2	18.2	9	1 CONG_CONGE	P05486 coccolus geogr
20	2	18.2	9	1 PAR5_PENMO	P1320 penaeus mon
21	2	18.2	9	1 FIBB_MACFU	P19145 macaria fusc
22	2	18.2	9	1 LFCA_STACU	P16884 staphylococ
23	2	18.2	9	1 NEF_HV128	P12481 human immun
24	2	18.2	9	1 PTSP_BOMMO	P2003 bombyx mori
25	2	18.2	9	1 RT33_BOVIN	P02926 bos taurus
26	2	18.2	9	1 SMP_MUSCA	P19045 mustelus ca
27	2	18.2	9	1 ULAK_MOUSE	P09031 mus muscula
28	2	18.2	9	1 UPA7_HUMAN	P10093 homo sapien
29	2	18.2	10	1 AH3_PRUSE	P19261 prunus sero
30	2	18.2	10	1 AKHX_LOCMI	P1626 locusta mig
31	2	18.2	10	1 ANCT_CHICK	P01018 gallus gall
32	2	18.2	10	1 COXA_ONCMW	P03128 oncornynchu
33	2	18.2	10	1 COXQ_SHEEP	P03137 ovis aries

34	2	18.2	1	1 GNL_LFIMA	P14376 polioviru
35	2	18.2	1	1 GNL_THFPR	P1578 polioviru
36	2	18.2	1	1 KRP_RANRI	P2460 rana tigris
37	2	18.2	1	1 KRS_RACSE	P0243 bacillus s
38	2	18.2	1	1 HUF_HFZE	P1654 bacillus s
39	2	18.2	1	1 MAL_E_KLEEN	P0564 klebsiella
40	2	18.2	1	1 NLI_MYCTU	P0135 mycobacteri
41	2	18.2	1	1 KAL_F_NPS	P0184 pinus pinas
42	2	18.2	1	1 KAL_NUGA	P2421 acheloplasm
43	2	18.2	1	1 KAL_NUGA	P2421 acheloplasm
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45	2	18.2	1	1 SYK_CAME	P1545 dictyostel
46	2	18.2	1	1 KMK_RANFI	P1545 dictyostel
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48	2	18.2	1	1 KKA_SUGA	P1545 dictyostel
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107	2	18.2	13	1	BRK_PARID	P42717	parapolybia	180	2	18.2	15	1	RNS	USCR	P59033	psuedoaria
108	2	18.2	13	1	CD71_LITEW	P82051	litorea cwi	181	2	18.2	15	1	USCR	USCR	P83420	solanum fol
109	2	18.2	13	1	DM0_CANFA	P49818	canis famli	182	2	18.2	15	1	USCR	USCR	P63287	ocorhycton
110	2	18.2	13	1	CHEP_PARID	P42718	parapolybia	183	2	18.2	15	1	USCR	USCR	P27034	sus scrofa
111	2	18.2	13	1	CRBL_VESAN	P17233	vespa anali	184	2	18.2	15	1	USCR	USCR	P95064	polipoliet
112	2	18.2	13	1	CRBL_VESCR	P01518	vespa crabr	185	2	18.2	15	1	USCR	USCR	P82544	spinaetia ol
113	2	18.2	13	1	CRBL_VESLE	P01735	vespola lew	186	2	18.2	15	1	USCR	USCR	P59684	laccellius st
114	2	18.2	13	1	CRBL_VESXA	P17234	vespa xanth	187	2	18.2	15	1	USCR	USCR	P59681	laccellius st
115	2	18.2	13	1	EP65_HUMAN	P54963	homo sapien	188	2	18.2	15	1	USCR	USCR	P59682	laccellius st
116	2	18.2	13	1	LPAA_PORGI	P81411	porphyromon	189	2	18.2	15	1	USCR	USCR	P01159	callosus m
117	2	18.2	13	1	NO40_PEA	P55959	pisum sativ	190	2	18.2	15	1	USCR	USCR	P41782	pinus pinas
118	2	18.2	13	1	NO40_VICSA	P55961	vicia sativ	191	2	18.2	15	1	USCR	USCR	P41770	tremelilla ol
119	2	18.2	13	1	NPL_LYMST	P80176	lymaea sta	192	2	18.2	15	1	USCR	USCR	P59897	varicella zo
120	2	18.2	13	1	NP2_LYMST	P80179	lymaea sta	193	2	18.2	15	1	USCR	USCR	P81783	laccellius st
121	2	18.2	13	1	NP4_LYMST	P80181	lymaea sta	194	2	18.2	15	1	USCR	USCR	P55633	vea mays (c
122	2	18.2	13	1	NP5_LYMST	P80182	lymaea sta	195	2	18.2	15	1	USCR	USCR	P49348	herodum vul
123	2	18.2	13	1	SA2A_ONCMY	P82238	oncorhynch	196	2	18.2	15	1	USCR	USCR	P17337	marquellia
124	2	18.2	13	1	SA2B_ONCMY	P82239	oncorhynch	197	2	18.2	15	1	USCR	USCR	P53907	acthancbac
125	2	18.2	13	1	SODM_CANFA	P54712	canis famli	198	2	18.2	15	1	USCR	USCR	P16691	thomus alb
126	2	18.2	13	1	TAL3_TREME	P81476	tremelilla ol	199	2	18.2	15	1	USCR	USCR	P14080	acthancbac
127	2	18.2	13	1	TEJA_RANJA	P83307	rana japoni	200	2	18.2	15	1	USCR	USCR	P54418	laccellius st
128	2	18.2	13	1	TEMD_RANTE	P56918	rana tempor	201	2	18.2	15	1	USCR	USCR	P54420	laccellius st
129	2	18.2	13	1	TEMD_RANTE	P56919	rana tempor	202	2	18.2	15	1	USCR	USCR	P14595	talacous aff
130	2	18.2	13	1	TEMD_RANTE	P56920	rana tempor	203	2	18.2	15	1	USCR	USCR	P18115	caroleus md
131	2	18.2	13	1	UHAI_HUMAN	P40528	homo sapien	204	2	18.2	15	1	USCR	USCR	P18116	caroleus md
132	2	18.2	13	1	YPE2_LACLC	P40221	lactococcus	205	2	18.2	15	1	USCR	USCR	P18117	caroleus md
133	2	18.2	13	1	ALYT_ALYOB	P08944	alytes obs:	206	2	18.2	15	1	USCR	USCR	P18118	caroleus md
134	2	18.2	13	1	ATP6_SPIOL	P80386	spinaetia ol	207	2	18.2	15	1	USCR	USCR	P18119	caroleus md
135	2	18.2	13	1	CAL3_CALGI	P23228	calotropis	208	2	18.2	15	1	USCR	USCR	P18120	caroleus md
136	2	18.2	13	1	CRBL_VESOR	P17236	vespa orien	209	2	18.2	15	1	USCR	USCR	P18121	caroleus md
137	2	18.2	13	1	GLGS_SPIOL	P55245	spinaetia ol	210	2	18.2	15	1	USCR	USCR	P18122	caroleus md
138	2	18.2	13	1	GLPK_STRGR	P25815	streptomyce	211	2	18.2	15	1	USCR	USCR	P18123	caroleus md
139	2	18.2	13	1	HCYA_MEGCR	GL583	megathura c	212	2	18.2	15	1	USCR	USCR	P18124	caroleus md
140	2	18.2	13	1	HY14_PIG	P01155	sus scrofa	213	2	18.2	15	1	USCR	USCR	P18125	caroleus md
141	2	18.2	13	1	LPW_ECOLI	P03053	escherichia	214	2	18.2	15	1	USCR	USCR	P18126	caroleus md
142	2	18.2	13	1	MST_VESBA	P21654	vespa basal	215	2	18.2	15	1	USCR	USCR	P18127	caroleus md
143	2	18.2	13	1	MST_VESIE	P21516	vespa crabr	216	2	18.2	15	1	USCR	USCR	P18128	caroleus md
144	2	18.2	13	1	MST_VESIE	P21517	vespa lew	217	2	18.2	15	1	USCR	USCR	P18129	caroleus md
145	2	18.2	13	1	MST_VESMA	P04205	vespa mand	218	2	18.2	15	1	USCR	USCR	P18130	caroleus md
146	2	18.2	13	1	MST_VESKA	P04206	vespa xanth	219	2	18.2	15	1	USCR	USCR	P18131	caroleus md
147	2	18.2	13	1	PSAG_CUCSA	P42047	cucumis sat	220	2	18.2	15	1	USCR	USCR	P18132	caroleus md
148	2	18.2	13	1	RS19_CLOPP	P46228	clover prol	221	2	18.2	15	1	USCR	USCR	P18133	caroleus md
149	2	18.2	13	1	RS19_CLOPP	P46228	clover prol	222	2	18.2	15	1	USCR	USCR	P18134	caroleus md
150	2	18.2	13	1	SCK3_LEIQU	P45561	leiurus qui	223	2	18.2	15	1	USCR	USCR	P18135	caroleus md
151	2	18.2	13	1	TAT_HV128	P12511	human immu	224	2	18.2	15	1	USCR	USCR	P18136	caroleus md
152	2	18.2	13	1	TKN1_SCHGR	P82470	schistocerc	225	2	18.2	15	1	USCR	USCR	P18137	caroleus md
153	2	18.2	13	1	TKNM_RANNA	P40551	rana rargar	226	2	18.2	15	1	USCR	USCR	P18138	caroleus md
154	2	18.2	13	1	UHAI_CANFA	P55506	canis famli	227	2	18.2	15	1	USCR	USCR	P18139	caroleus md
155	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	228	2	18.2	15	1	USCR	USCR	P18140	caroleus md
156	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	229	2	18.2	15	1	USCR	USCR	P18141	caroleus md
157	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	230	2	18.2	15	1	USCR	USCR	P18142	caroleus md
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159	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	232	2	18.2	15	1	USCR	USCR	P18144	caroleus md
160	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	233	2	18.2	15	1	USCR	USCR	P18145	caroleus md
161	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	234	2	18.2	15	1	USCR	USCR	P18146	caroleus md
162	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	235	2	18.2	15	1	USCR	USCR	P18147	caroleus md
163	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	236	2	18.2	15	1	USCR	USCR	P18148	caroleus md
164	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	237	2	18.2	15	1	USCR	USCR	P18149	caroleus md
165	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	238	2	18.2	15	1	USCR	USCR	P18150	caroleus md
166	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	239	2	18.2	15	1	USCR	USCR	P18151	caroleus md
167	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	240	2	18.2	15	1	USCR	USCR	P18152	caroleus md
168	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	241	2	18.2	15	1	USCR	USCR	P18153	caroleus md
169	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	242	2	18.2	15	1	USCR	USCR	P18154	caroleus md
170	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	243	2	18.2	15	1	USCR	USCR	P18155	caroleus md
171	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	244	2	18.2	15	1	USCR	USCR	P18156	caroleus md
172	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	245	2	18.2	15	1	USCR	USCR	P18157	caroleus md
173	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	246	2	18.2	15	1	USCR	USCR	P18158	caroleus md
174	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	247	2	18.2	15	1	USCR	USCR	P18159	caroleus md
175	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	248	2	18.2	15	1	USCR	USCR	P18160	caroleus md
176	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	249	2	18.2	15	1	USCR	USCR	P18161	caroleus md
177	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	250	2	18.2	15	1	USCR	USCR	P18162	caroleus md
178	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	251	2	18.2	15	1	USCR	USCR	P18163	caroleus md
179	2	18.2	13	1	UHAI_CLOPA	P1152	clostridium	252	2	18.2	15	1	USCR	USCR	P18164	caroleus md



399	1	9.1	10	1	SLAP_BACTG	P45025 bacillus th	472	1	9.1	10	1	US09-787-443-21.oli.rsp
400	1	9.1	10	1	SP1_RALRO	Q16997 bacynynhia	473	1	9.1	10	1	US09-787-443-21.oli.rsp
401	1	9.1	10	1	TKL2_L0CM1	P16224 locusta miq	474	1	9.1	10	1	US09-787-443-21.oli.rsp
402	1	9.1	10	1	TKL3_L0CM1	P40245 locusta miq	475	1	9.1	10	1	US09-787-443-21.oli.rsp
403	1	9.1	10	1	TKU2_URFUN	P40752 urechis uai	476	1	9.1	10	1	US09-787-443-21.oli.rsp
404	1	9.1	10	1	TR0F_AEDAE	P19425 uedes aedyp	477	1	9.1	10	1	US09-787-443-21.oli.rsp
405	1	9.1	10	1	TRP5_LEUMA	P81737 leucophaea	478	1	9.1	10	1	US09-787-443-21.oli.rsp
406	1	9.1	10	1	TRP6_LEUMA	P81738 leucophaea	479	1	9.1	10	1	US09-787-443-21.oli.rsp
407	1	9.1	10	1	TRP7_LEUMA	P81739 leucophaea	480	1	9.1	10	1	US09-787-443-21.oli.rsp
408	1	9.1	10	1	TRP8_LEUMA	P81740 leucophaea	481	1	9.1	10	1	US09-787-443-21.oli.rsp
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410	1	9.1	10	1	UH05_PAT	P56573 uctus uari	483	1	9.1	10	1	US09-787-443-21.oli.rsp
411	1	9.1	10	1	UH03_HUMAN	P40946 homo sapien	484	1	9.1	10	1	US09-787-443-21.oli.rsp
412	1	9.1	10	1	UPA2_HUMAN	P30088 homo sapien	485	1	9.1	10	1	US09-787-443-21.oli.rsp
413	1	9.1	10	1	UPA4_HUMAN	P30090 homo sapien	486	1	9.1	10	1	US09-787-443-21.oli.rsp
414	1	9.1	10	1	UPA5_HUMAN	P30091 homo sapien	487	1	9.1	10	1	US09-787-443-21.oli.rsp
415	1	9.1	10	1	UPA8_HUMAN	P30094 homo sapien	488	1	9.1	10	1	US09-787-443-21.oli.rsp
416	1	9.1	10	1	UPA9_HUMAN	P30095 homo sapien	489	1	9.1	10	1	US09-787-443-21.oli.rsp
417	1	9.1	10	1	URA1_HUMAN	P32118 homo sapien	490	1	9.1	10	1	US09-787-443-21.oli.rsp
418	1	9.1	10	1	URA6_HUMAN	P32286 homo sapien	491	1	9.1	10	1	US09-787-443-21.oli.rsp
419	1	9.1	10	1	URA7_HUMAN	P34596 homo sapien	492	1	9.1	10	1	US09-787-443-21.oli.rsp
420	1	9.1	10	1	URE3_MORMO	P37339 morquandilla	493	1	9.1	10	1	US09-787-443-21.oli.rsp
421	1	9.1	10	1	URX2_CHELR	P36007 cheilomydia	494	1	9.1	10	1	US09-787-443-21.oli.rsp
422	1	9.1	10	1	URX6_CHELR	P36007 cheilomydia	495	1	9.1	10	1	US09-787-443-21.oli.rsp
423	1	9.1	10	1	V0G6_BACSU	P36599 bacillus su	496	1	9.1	10	1	US09-787-443-21.oli.rsp
424	1	9.1	10	1	ANGT_CRICE	P36537 cricetia quai	497	1	9.1	10	1	US09-787-443-21.oli.rsp
425	1	9.1	10	1	ASL1_BACSE	P31146 bacteroides	498	1	9.1	10	1	US09-787-443-21.oli.rsp
426	1	9.1	10	1	ASL2_BACSE	P31147 bacteroides	499	1	9.1	10	1	US09-787-443-21.oli.rsp
427	1	9.1	10	1	BPP3_BOTIN	P33423 botriopsis in	500	1	9.1	10	1	US09-787-443-21.oli.rsp
428	1	9.1	10	1	BPP4_BOTIN	P33424 botriopsis in	501	1	9.1	10	1	US09-787-443-21.oli.rsp
429	1	9.1	10	1	BPPB_AGRUA	P31021 agastrophys	502	1	9.1	10	1	US09-787-443-21.oli.rsp
430	1	9.1	10	1	BPP_AGRUP	P31022 agastrophys	503	1	9.1	10	1	US09-787-443-21.oli.rsp
431	1	9.1	10	1	CA21_LITIC	P32087 littoria lit	504	1	9.1	10	1	US09-787-443-21.oli.rsp
432	1	9.1	10	1	CA22_LITIC	P32088 littoria lit	505	1	9.1	10	1	US09-787-443-21.oli.rsp
433	1	9.1	10	1	CA31_LITIC	P32089 littoria lit	506	1	9.1	10	1	US09-787-443-21.oli.rsp
434	1	9.1	10	1	CA32_LITIC	P32090 littoria lit	507	1	9.1	10	1	US09-787-443-21.oli.rsp
435	1	9.1	10	1	CA41_LITIC	P32091 littoria lit	508	1	9.1	10	1	US09-787-443-21.oli.rsp
436	1	9.1	10	1	CA42_LITIC	P32092 littoria lit	509	1	9.1	10	1	US09-787-443-21.oli.rsp
437	1	9.1	10	1	CEP1_AGRUP	P32290 agastrophys	510	1	9.1	10	1	US09-787-443-21.oli.rsp
438	1	9.1	10	1	CEX1_CANEA	P30501 canis famil	511	1	9.1	10	1	US09-787-443-21.oli.rsp
439	1	9.1	10	1	CS15_BACSU	P30095 bacillus su	512	1	9.1	10	1	US09-787-443-21.oli.rsp
440	1	9.1	10	1	CS5B_CONAL	P38848 conus anilis	513	1	9.1	10	1	US09-787-443-21.oli.rsp
441	1	9.1	10	1	CS5B_CONAL	P38849 conus anilis	514	1	9.1	10	1	US09-787-443-21.oli.rsp
442	1	9.1	10	1	CXD1_CONMP	P31350 costitridim	515	1	9.1	10	1	US09-787-443-21.oli.rsp
443	1	9.1	10	1	EFG_CLOPA	P31350 costitridim	516	1	9.1	10	1	US09-787-443-21.oli.rsp
444	1	9.1	10	1	ESI_RAT	P36571 rattus norv	517	1	9.1	10	1	US09-787-443-21.oli.rsp
445	1	9.1	10	1	FAR6_FENMO	P36571 rattus norv	518	1	9.1	10	1	US09-787-443-21.oli.rsp
446	1	9.1	10	1	FAR6_FENMO	P36571 rattus norv	519	1	9.1	10	1	US09-787-443-21.oli.rsp
447	1	9.1	10	1	FAR6_FENMO	P36571 rattus norv	520	1	9.1	10	1	US09-787-443-21.oli.rsp
448	1	9.1	10	1	LADD_ONCHY	P31163 leucophaea	521	1	9.1	10	1	US09-787-443-21.oli.rsp
449	1	9.1	10	1	LADD_ONCHY	P31163 leucophaea	522	1	9.1	10	1	US09-787-443-21.oli.rsp
450	1	9.1	10	1	LSK1_LEUMA	P30524 thermus the	523	1	9.1	10	1	US09-787-443-21.oli.rsp
451	1	9.1	10	1	LSKP_PERAM	P34428 leucophaea	524	1	9.1	10	1	US09-787-443-21.oli.rsp
452	1	9.1	10	1	MHL1_KLEIN	P31885 periplaneta	525	1	9.1	10	1	US09-787-443-21.oli.rsp
453	1	9.1	10	1	MLG_THETS	P31989 thermomyza	526	1	9.1	10	1	US09-787-443-21.oli.rsp
454	1	9.1	10	1	MORN_HUMAN	P31163 leucophaea	527	1	9.1	10	1	US09-787-443-21.oli.rsp
455	1	9.1	10	1	NORM_HUMAN	P31163 leucophaea	528	1	9.1	10	1	US09-787-443-21.oli.rsp
456	1	9.1	10	1	PKC1_CARM	P30820 canis famil	529	1	9.1	10	1	US09-787-443-21.oli.rsp
457	1	9.1	10	1	POQC_PSEEL	P30820 canis famil	530	1	9.1	10	1	US09-787-443-21.oli.rsp
458	1	9.1	10	1	POQC_PSEEL	P30820 canis famil	531	1	9.1	10	1	US09-787-443-21.oli.rsp
459	1	9.1	10	1	RANC_FANFI	P31885 periplaneta	532	1	9.1	10	1	US09-787-443-21.oli.rsp
460	1	9.1	10	1	R22_CONAM	P30274 littoria lit	533	1	9.1	10	1	US09-787-443-21.oli.rsp
461	1	9.1	10	1	R22_CONAM	P30274 littoria lit	534	1	9.1	10	1	US09-787-443-21.oli.rsp
462	1	9.1	10	1	RRPL_CHAV	P31163 leucophaea	535	1	9.1	10	1	US09-787-443-21.oli.rsp
463	1	9.1	10	1	T2P1_PRAWU	P31163 leucophaea	536	1	9.1	10	1	US09-787-443-21.oli.rsp
464	1	9.1	10	1	TIN1_HOPTI	P32651 leptodactyl	537	1	9.1	10	1	US09-787-443-21.oli.rsp
465	1	9.1	10	1	TIN4_HOPTI	P32651 leptodactyl	538	1	9.1	10	1	US09-787-443-21.oli.rsp
466	1	9.1	10	1	TKND_RANCA	P32651 leptodactyl	539	1	9.1	10	1	US09-787-443-21.oli.rsp
467	1	9.1	10	1	UF05_MOUSE	P38641 ues musciu	540	1	9.1	10	1	US09-787-443-21.oli.rsp
468	1	9.1	10	1	ULAG_HUMAN	P31163 leucophaea	541	1	9.1	10	1	US09-787-443-21.oli.rsp
469	1	9.1	10	1	CALM_TETRA	P30555 carthymena	542	1	9.1	10	1	US09-787-443-21.oli.rsp
470	1	9.1	10	1	CD11_LITXA	P36246 littoria lit	543	1	9.1	10	1	US09-787-443-21.oli.rsp
471	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	544	1	9.1	10	1	US09-787-443-21.oli.rsp
472	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	545	1	9.1	10	1	US09-787-443-21.oli.rsp
473	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	546	1	9.1	10	1	US09-787-443-21.oli.rsp
474	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	547	1	9.1	10	1	US09-787-443-21.oli.rsp
475	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	548	1	9.1	10	1	US09-787-443-21.oli.rsp
476	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	549	1	9.1	10	1	US09-787-443-21.oli.rsp
477	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	550	1	9.1	10	1	US09-787-443-21.oli.rsp
478	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	551	1	9.1	10	1	US09-787-443-21.oli.rsp
479	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	552	1	9.1	10	1	US09-787-443-21.oli.rsp
480	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	553	1	9.1	10	1	US09-787-443-21.oli.rsp
481	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	554	1	9.1	10	1	US09-787-443-21.oli.rsp
482	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	555	1	9.1	10	1	US09-787-443-21.oli.rsp
483	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	556	1	9.1	10	1	US09-787-443-21.oli.rsp
484	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	557	1	9.1	10	1	US09-787-443-21.oli.rsp
485	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	558	1	9.1	10	1	US09-787-443-21.oli.rsp
486	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	559	1	9.1	10	1	US09-787-443-21.oli.rsp
487	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	560	1	9.1	10	1	US09-787-443-21.oli.rsp
488	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	561	1	9.1	10	1	US09-787-443-21.oli.rsp
489	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	562	1	9.1	10	1	US09-787-443-21.oli.rsp
490	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	563	1	9.1	10	1	US09-787-443-21.oli.rsp
491	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	564	1	9.1	10	1	US09-787-443-21.oli.rsp
492	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	565	1	9.1	10	1	US09-787-443-21.oli.rsp
493	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	566	1	9.1	10	1	US09-787-443-21.oli.rsp
494	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	567	1	9.1	10	1	US09-787-443-21.oli.rsp
495	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	568	1	9.1	10	1	US09-787-443-21.oli.rsp
496	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	569	1	9.1	10	1	US09-787-443-21.oli.rsp
497	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	570	1	9.1	10	1	US09-787-443-21.oli.rsp
498	1	9.1	10	1	CD14_LITXA	P36246 littoria lit	571	1	9.1	10	1	US09-787-443-21.oli.rsp
499	1	9.1	10	1								



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DR HAMAP: MF_00480: -: 1.
DR InterPro: IPR000235: Ribosomal_S7.
DR PROSITE: PS00052: RIBOSOMAL_S7: PARTIAL.
KW Ribosomal protein: RNA-binding: tRNA binding.
FT INIT_MET 0 BY SIMILARITY.
FT NON_TER 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match
Best Local Similarity 27.3%; Score 3; DB 1; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKG 6
DB 2 RKG 4

RESULT 2
THYF_PIG
ID THYF_PIG STANDARD: PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;
OX NCBI_TaxID:9823;
RN [1]
RP SEQUENCE.
RX MEDLINE:78026571; PubMed-914862;
RA Pleau J.-M., Dardenne M., Blouquin Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
RT from pig serum. II. Amino acid sequence."
RL J. Biol. Chem. 252:8045-8047(1977).
CC -I- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR: A01523; YFPG.
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1
SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;

Query Match
Best Local Similarity 27.3%; Score 3; DB 1; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 3
DB 2 AKS 4

RESULT 3
Q2OA_COMTE
ID Q2OA_COMTE STANDARD: PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinolone 2-oxido-reductase, alpha chain (EC 1.1.1.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID:285;
RN [1]
RP SEQUENCE.
RC STRAIN-63;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxido-reductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation."
RL Eur. J. Biochem. 232:536-544(1995).

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QY 1 AKS 3
DB 1 AKS 4

RESULT 4
PCT_APLA
ID PCT_APLA STANDARD: PRT; 18 AA.
AC Q10902;
DT 01-OCT-1996 (Rel. 41, Created)
DT 01-OCT-1996 (Rel. 41, Last sequence update)
DT 01-OCT-1996 (Rel. 41, Last annotation update)
DE Cortical protein 1 (P1).
OS Aplysia californica (California sea slug).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Anusplousa;
OC Aplysioidae; Aplysiidae; Aplysia;
OX NCBI_TaxID:4509;
RN [1]
RP SEQUENCE.
RX MEDLINE:9706171; PubMed-8644264;
RA Phares G.A., Lloyd F.E.;
RT "Partial cDNA, primary structure, and function, localization of
RT cortical protein 1 from Aplysia."
RL Biophys. J. 70:763-765(1996).
CC -I- FUNCTION: MAY FUNCTION AS A PERMEIC TRANSMITTER.
CC -I- TISSUE SPECIFICITY: HIGHLY PREPOTENTIALLY IN THE PERIPHERAL AND PERI-
CC SANGUINE.
SQ SEQUENCE 11 AA; 1144 MW; 90FC68267605 CRC64;

Query Match
Best Local Similarity 27.3%; Score 3; DB 1; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 0 RSG 11
DB 0 RSG 11

RESULT 5
NEPT_PAVL
ID NEPT_PAVL STANDARD: PRT; 15 AA.
AC P42571;
DT 01-OCT-1994 (Rel. 33, Created)
DT 01-OCT-1994 (Rel. 33, Last sequence update)
DT 28-FEB-2004 (Rel. 41, Last annotation update)
DE Neurotensin (NT).
OS Canis potens (Golden Retriever).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriomathia; Canidae; Canis;
OX NCBI_TaxID:10141;
RN [1]
RP SEQUENCE.

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RC TISSUE=Small intestine;  
 RX MEDLINE=86248085; PubMed=308775;  
 RA Shaw C., Thim L., Conlon J.M.;  
 RT \* [Ser7]neurotensin: isolation from guinea pig intestine.\*;  
 RL FEBS Lett. 202:187-192(1986).  
 CC -!- FUNCTION: Smooth muscle-contracting peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.  
 DR PIR: A53608.  
 KW Vasoactive; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA: 1680 MW: 4C8314644C4115B3 CRC64:

Query Match 27.3% Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSR 4  
 DB 6 KSR 8

## RESULT 6

48KD\_BACCE  
 ID 48KD\_BACCE STANDARD; PRT: 15 AA.  
 AC P80173;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-OCT-1993 (Rel. 27, Last annotation update)  
 DE 48 kDa protein (fragment).  
 OS Bacillus cereus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1396;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=1210-98;  
 RX MEDLINE=93307641; PubMed=8319899;  
 RA Granum P.E., Nissen H.;  
 RT \*Sphingomyelinase is part of the 'enterotoxin complex' produced by  
 RT Bacillus cereus.\*;  
 RL FEMS Microbiol. Lett. 110:97-100(1993).  
 CC -!- FUNCTION: NOT KNOWN, PART OF THE ENTEROTOXIN COMPLEX.  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA: 1644 MW: 88442960R4H0FR62 CRC64:

Query Match 27.3% Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10  
 DB 11 SSL 13

## RESULT 7

ACT\_CARMA  
 ID ACT\_CARMA STANDARD; PRT: 8 AA.  
 AC P80709;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin (Fragment).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
 RA Baghdassarian D.;  
 RT \*A transaldolase. An enzyme implicated in crab steroidogenesis.\*;  
 RL Endocrine 5:23-32(1996).

CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE BIOCHEMICALLY EXPRESSED  
 CC IN ALL EUKARYOTIC CELLS.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: ON THE EDGEL THE DETERMINED PI OF THIS PROTEIN IS  
 CC 6.8. ITS MW IS 46 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.  
 DR InterPro: IPR004501; Actin.  
 DR InterPro: IPR004501; Actin Iso.  
 DR PROSITE: PS00406; ACTIN 1; PARTIAL.  
 DR PROSITE: PS00432; ACTIN 2; PARTIAL.  
 DR PROSITE: PS1152; ACTINS ACT LIKE PARTIAL.  
 KW Structural protein.  
 FT K\_NTER 1  
 FT K\_NTER 8  
 SQ SEQUENCE 8 AA: 926 MW: 11490ANDAAER5 CRC64:

Query Match 100% Score 4; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSL 1  
 DB 7 SSL 6

## RESULT 8

ALLA\_CYDIN  
 ID ALLA\_CYDIN STANDARD; PRT: 4 AA.  
 AC P82154;  
 DT 30-MAY-2000 (Rel. 34, Created)  
 DT 30-MAY-2000 (Rel. 34, Last sequence update)  
 DT 30-MAY-2000 (Rel. 34, Last annotation update)  
 DE Cydiastatin A.  
 OS Cydia pomonella (Common moth).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Lepidoptera;  
 OC Noctuidae; Pterophyllini; Lepidoptera; Noctuidae; Dioryctini;  
 OC Tortricidae; Tortricinae; Tortricinae; Cydia.  
 OX NCBI\_TaxID=4200;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Leaf.  
 EX MEDLINE=9455479; PubMed=947229;  
 RA Davey M., East P.D., Harper A.;  
 RT \*Lepidopteran peptides of the allatostatin superfamily.\*;  
 RL Peptides 14:101-104(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 4  
 SQ SEQUENCE 4 AA: 926 MW: 92674DGAH4774.5 CRC64:

Query Match 100% Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SP 4  
 DB 1 SP 2

## RESULT 9

CADL\_ENTFA  
 ID CADL\_ENTFA STANDARD; PRT: 8 AA.  
 AC F13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 12, Last annotation update)  
 DE Sex pheromone (AL1).  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1451;  
 RN [1]

RP SEQUENCE  
 RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
 induces plasmid transfer in *Streptococcus faecalis*.";  
 RL FEBS Lett. 178:97-100(1984).  
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PAD1.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA: 819 MW: 047DD732C735B9C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SL 10  
 Db 3 SL 4

RESULT 10  
 ID CLP\_THICU STANDARD; PRI: 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Chemolithotroph-specific protein (Fragment).  
 OS Thiobacillus cuprinus.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Thiomonas.  
 OX NCBI\_TaxID=36860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;  
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC CHEMOLITHOTROPHICALLY.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 785 MW: 91487B06DDC2D76D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GN 7  
 Db 7 GN 8

RESULT 11  
 ID LCK1\_LEUMA STANDARD; PRI: 8 AA.  
 AC P21140;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-1).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatteroida;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 RT from *Leucophaea maderae*: members of a new family of  
 RT Cephalomyotropeptides."  
 RL Comp. Biochem. Physiol. 84C:205-211(1986).

CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKS AND PTERODROM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidated;  
 FT MOD\_RES 8 R AMINATION  
 SQ SEQUENCE 8 AA: 804 MW: 006050P41C1A276A CRC64;

Query Match 14.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NS 8  
 Db 5 NS 7

RESULT 12  
 ID LCK2\_LEUMA STANDARD; PRI: 8 AA.  
 AC P21141;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-1).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatteroida;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 RT from *Leucophaea maderae*: members of a new family of  
 RT Cephalomyotropeptides."  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PTERODROM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidated;  
 FT MOD\_RES 8 R AMINATION  
 SQ SEQUENCE 8 AA: 802 MW: 006050P41C1A276A CRC64;

Query Match 14.2%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SS 9  
 Db 5 SS 7

RESULT 13  
 ID LCK3\_LEUMA STANDARD; PRI: 8 AA.  
 AC P21142;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-1).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatteroida;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two additional neopeptides  
 RT from *Leucophaea maderae*: members of a new family of  
 RT Cephalomyotropeptides."







\*Nucleotide sequence analysis of the env gene of a new Zairian  
 isolate of HIV-1.\*  
 RT AIDS Res. Hum. Retroviruses 4:165-173(1988).  
 RL -1- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating  
 CC activities. It seems to down-regulate the CD4(T4) antigen.  
 CC -1- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD  
 CC ZAIREAN MALE.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL: J03653; AAA44687.1; -  
 DR HIV: J03653; NEFSJVL  
 KW AIDS: Myristate; GTP-binding.  
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 967 MW: 319CB325A4733878 CRG64;  
 Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 KS 3  
 Db 7 KS 8  
 RESULT 24  
 PTSP\_BOMMO STANDARD; PRT; 9 AA.  
 AC P82003;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Prothoracicostatic peptide (Bom-PTSP).  
 OS Bombyx mori (Silk moth).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombyx  
 CC Bombycidae; Bombyx.  
 CC NCBI\_TaxID:7091;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN:C145 X N140; TISSUE=Brain;  
 RX MEDLINE=20002634; PubMed=10531308;  
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,  
 RA Kataoka H.;  
 RT "Identification of a prothoracicostatic peptide in the larval brain of  
 RT the silkworm, Bombyx mori.";  
 RL J. Biol. Chem. 274:31169-31173(1999).  
 RN [2]  
 RP ERRATUM.  
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,  
 RA Kataoka H.;  
 RL J. Biol. Chem. 275:9892-9892(2000).  
 CC -1- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic  
 CC gland.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.  
 KW Hormone: Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 1090 MW: 3878C5M472A96C3 CRG64;  
 Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 NS 8  
 Db 11

DB 7 NS 7  
 RESULT 25  
 PT33\_BOMMO STANDARD; PRT; 9 AA.  
 AC P82926;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S24 (S24mt) (MRP S24) (Pentaxin).  
 GN MRP53.  
 GN MRP53.  
 OS Bos taurus (cow).  
 CC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Eutelestomi;  
 CC Mammalia; Ruminantia; Bovidae; Bovinae; Bovinae; Bovinae; Bovinae;  
 CC Bovidae; Ruminantia; Bovidae; Bovinae; Bovinae; Bovinae;  
 CC NCBI\_TaxID:9913;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=212364; PubMed=10531308;  
 RA KESLER, Burkhardt, W., KESLER, K., KESLER, A., STRANDBERG, L.,  
 RA "The S24 protein of the mammalian mitochondrial ribosome.  
 RA Identification of the full complement of ribosomal proteins present in  
 RA the S24 protein." 274:31443-31474(2001).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial ribosome S24 subunit  
 CC (28S) which comprises a 12S RNA and about 40 distinct proteins.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
 KW Ribosomal protein; Mitochondrial.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1092 MW: 104117477636589 CRG64;  
 Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AK 2  
 Db 9 AK 4  
 RESULT 26  
 SAMP\_MUSCA STANDARD; PRT; 9 AA.  
 AC P39075;  
 DT 01-NOV-1992 (Rel. 16, Created)  
 DT 01-NOV-1992 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serum amyloid P component (SAP) (Frequent).  
 OS Musculus musculus (House mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;  
 CC Elasmobranchii; Chondrichthyes; Galeorhinidae; Chondrichthyes; Triakidae;  
 CC Mustelus.  
 CC NCBI\_TaxID:7912;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=8816352; PubMed=10531308;  
 RA Kober F.A., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,  
 RA "Isolation and characterization of a cDNA for serum amyloid P  
 RA component."  
 RL J. Biol. Chem. 267:6869-6874(1992).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DISEASE: SAP is a precursor of amyloid component F WHICH IS FOUND  
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 DR InterPro: IPR001759; Pentaxin.  
 DR PROSITE: PS00289; PENTAXIN PARTIAL.  
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.

FT DOMAIN 1 >9 PENTAXIN.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA: 965 MW; D05B5735B386769 CIRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1 to 05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KS 3  
 II  
 DB 5 KS 6

## RESULT 27

ULAK\_MOUSE  
 ID ULAK\_MOUSE STANDARD; PRT; 9 AA.  
 AC P99031;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spec. 28 G041D)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Van E. X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser P.F.,  
 RA Cowthorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED pI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.  
 DR SWISS-2DPAGE: P99031; MOUSE.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA: 1106 MW; E1E842C1240B145A CIRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1 to 05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RK 5  
 II  
 DB 5 RK 6

## RESULT 28

UPA7\_HUMAN  
 ID UPA7\_HUMAN STANDARD; PRT; 9 AA.  
 AC P30093;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spec. 18) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Xavier F., Pasquari C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED pI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.  
 DR SWISS-2DPAGE: P30093; HUMAN.  
 FT NON\_TER 1

FT UNSURE 5  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA: 1443 MW; 1443 FASB077277 CIRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1 to 05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KS 3  
 II  
 DB 5 KS 6

## RESULT 29

AB\_CROUSE  
 ID AB\_CROUSE SCAN.AVL; PRT; 10 AA.  
 AC P29261;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-NOV-1992 (Rel. 23, Last annotation update)  
 DE Amyloid-like beta-amyloid protein (A210-117) (Amyloid-like protein)  
 DE (Fragment).  
 OS Prionus serotinus (Beetle).  
 OC Eukaryota; Viridiplantae; Streptophyta; Equisetophyta; Equisetopsida;  
 OC Sphenocarpales; Madoniellales; Equisetales; Equisetaceae; Equisetum;  
 OC Equisetum; Equisetum; Equisetum; Amygdalaceae; Prunus.  
 OX NCBI\_TaxID=23202;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Spore;  
 RA Frutiger S., Sanchez J.-C., Binz P.-A., Hochstrasser P.F.,  
 RA Cowthorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -!- CATALYTIC ACTIVITY: (E)-hydroxy-3-methyl-2-oxo-4-oxo-5-oxo-6-oxo-7-oxo-8-oxo-9-oxo-10-oxo-11-oxo-12-oxo-13-oxo-14-oxo-15-oxo-16-oxo-17-oxo-18-oxo-19-oxo-20-oxo-21-oxo-22-oxo-23-oxo-24-oxo-25-oxo-26-oxo-27-oxo-28-oxo-29-oxo-30-oxo-31-oxo-32-oxo-33-oxo-34-oxo-35-oxo-36-oxo-37-oxo-38-oxo-39-oxo-40-oxo-41-oxo-42-oxo-43-oxo-44-oxo-45-oxo-46-oxo-47-oxo-48-oxo-49-oxo-50-oxo-51-oxo-52-oxo-53-oxo-54-oxo-55-oxo-56-oxo-57-oxo-58-oxo-59-oxo-60-oxo-61-oxo-62-oxo-63-oxo-64-oxo-65-oxo-66-oxo-67-oxo-68-oxo-69-oxo-70-oxo-71-oxo-72-oxo-73-oxo-74-oxo-75-oxo-76-oxo-77-oxo-78-oxo-79-oxo-80-oxo-81-oxo-82-oxo-83-oxo-84-oxo-85-oxo-86-oxo-87-oxo-88-oxo-89-oxo-90-oxo-91-oxo-92-oxo-93-oxo-94-oxo-95-oxo-96-oxo-97-oxo-98-oxo-99-oxo-100-oxo-101-oxo-102-oxo-103-oxo-104-oxo-105-oxo-106-oxo-107-oxo-108-oxo-109-oxo-110-oxo-111-oxo-112-oxo-113-oxo-114-oxo-115-oxo-116-oxo-117-oxo-118-oxo-119-oxo-120-oxo-121-oxo-122-oxo-123-oxo-124-oxo-125-oxo-126-oxo-127-oxo-128-oxo-129-oxo-130-oxo-131-oxo-132-oxo-133-oxo-134-oxo-135-oxo-136-oxo-137-oxo-138-oxo-139-oxo-140-oxo-141-oxo-142-oxo-143-oxo-144-oxo-145-oxo-146-oxo-147-oxo-148-oxo-149-oxo-150-oxo-151-oxo-152-oxo-153-oxo-154-oxo-155-oxo-156-oxo-157-oxo-158-oxo-159-oxo-160-oxo-161-oxo-162-oxo-163-oxo-164-oxo-165-oxo-166-oxo-167-oxo-168-oxo-169-oxo-170-oxo-171-oxo-172-oxo-173-oxo-174-oxo-175-oxo-176-oxo-177-oxo-178-oxo-179-oxo-180-oxo-181-oxo-182-oxo-183-oxo-184-oxo-185-oxo-186-oxo-187-oxo-188-oxo-189-oxo-190-oxo-191-oxo-192-oxo-193-oxo-194-oxo-195-oxo-196-oxo-197-oxo-198-oxo-199-oxo-200-oxo-201-oxo-202-oxo-203-oxo-204-oxo-205-oxo-206-oxo-207-oxo-208-oxo-209-oxo-210-oxo-211-oxo-212-oxo-213-oxo-214-oxo-215-oxo-216-oxo-217-oxo-218-oxo-219-oxo-220-oxo-221-oxo-222-oxo-223-oxo-224-oxo-225-oxo-226-oxo-227-oxo-228-oxo-229-oxo-230-oxo-231-oxo-232-oxo-233-oxo-234-oxo-235-oxo-236-oxo-237-oxo-238-oxo-239-oxo-240-oxo-241-oxo-242-oxo-243-oxo-244-oxo-245-oxo-246-oxo-247-oxo-248-oxo-249-oxo-250-oxo-251-oxo-252-oxo-253-oxo-254-oxo-255-oxo-256-oxo-257-oxo-258-oxo-259-oxo-260-oxo-261-oxo-262-oxo-263-oxo-264-oxo-265-oxo-266-oxo-267-oxo-268-oxo-269-oxo-270-oxo-271-oxo-272-oxo-273-oxo-274-oxo-275-oxo-276-oxo-277-oxo-278-oxo-279-oxo-280-oxo-281-oxo-282-oxo-283-oxo-284-oxo-285-oxo-286-oxo-287-oxo-288-oxo-289-oxo-290-oxo-291-oxo-292-oxo-293-oxo-294-oxo-295-oxo-296-oxo-297-oxo-298-oxo-299-oxo-300-oxo-301-oxo-302-oxo-303-oxo-304-oxo-305-oxo-306-oxo-307-oxo-308-oxo-309-oxo-310-oxo-311-oxo-312-oxo-313-oxo-314-oxo-315-oxo-316-oxo-317-oxo-318-oxo-319-oxo-320-oxo-321-oxo-322-oxo-323-oxo-324-oxo-325-oxo-326-oxo-327-oxo-328-oxo-329-oxo-330-oxo-331-oxo-332-oxo-333-oxo-334-oxo-335-oxo-336-oxo-337-oxo-338-oxo-339-oxo-340-oxo-341-oxo-342-oxo-343-oxo-344-oxo-345-oxo-346-oxo-347-oxo-348-oxo-349-oxo-350-oxo-351-oxo-352-oxo-353-oxo-354-oxo-355-oxo-356-oxo-357-oxo-358-oxo-359-oxo-360-oxo-361-oxo-362-oxo-363-oxo-364-oxo-365-oxo-366-oxo-367-oxo-368-oxo-369-oxo-370-oxo-371-oxo-372-oxo-373-oxo-374-oxo-375-oxo-376-oxo-377-oxo-378-oxo-379-oxo-380-oxo-381-oxo-382-oxo-383-oxo-384-oxo-385-oxo-386-oxo-387-oxo-388-oxo-389-oxo-390-oxo-391-oxo-392-oxo-393-oxo-394-oxo-395-oxo-396-oxo-397-oxo-398-oxo-399-oxo-400-oxo-401-oxo-402-oxo-403-oxo-404-oxo-405-oxo-406-oxo-407-oxo-408-oxo-409-oxo-410-oxo-411-oxo-412-oxo-413-oxo-414-oxo-415-oxo-416-oxo-417-oxo-418-oxo-419-oxo-420-oxo-421-oxo-422-oxo-423-oxo-424-oxo-425-oxo-426-oxo-427-oxo-428-oxo-429-oxo-430-oxo-431-oxo-432-oxo-433-oxo-434-oxo-435-oxo-436-oxo-437-oxo-438-oxo-439-oxo-440-oxo-441-oxo-442-oxo-443-oxo-444-oxo-445-oxo-446-oxo-447-oxo-448-oxo-449-oxo-450-oxo-451-oxo-452-oxo-453-oxo-454-oxo-455-oxo-456-oxo-457-oxo-458-oxo-459-oxo-460-oxo-461-oxo-462-oxo-463-oxo-464-oxo-465-oxo-466-oxo-467-oxo-468-oxo-469-oxo-470-oxo-471-oxo-472-oxo-473-oxo-474-oxo-475-oxo-476-oxo-477-oxo-478-oxo-479-oxo-480-oxo-481-oxo-482-oxo-483-oxo-484-oxo-485-oxo-486-oxo-487-oxo-488-oxo-489-oxo-490-oxo-491-oxo-492-oxo-493-oxo-494-oxo-495-oxo-496-oxo-497-oxo-498-oxo-499-oxo-500-oxo-501-oxo-502-oxo-503-oxo-504-oxo-505-oxo-506-oxo-507-oxo-508-oxo-509-oxo-510-oxo-511-oxo-512-oxo-513-oxo-514-oxo-515-oxo-516-oxo-517-oxo-518-oxo-519-oxo-520-oxo-521-oxo-522-oxo-523-oxo-524-oxo-525-oxo-526-oxo-527-oxo-528-oxo-529-oxo-530-oxo-531-oxo-532-oxo-533-oxo-534-oxo-535-oxo-536-oxo-537-oxo-538-oxo-539-oxo-540-oxo-541-oxo-542-oxo-543-oxo-544-oxo-545-oxo-546-oxo-547-oxo-548-oxo-549-oxo-550-oxo-551-oxo-552-oxo-553-oxo-554-oxo-555-oxo-556-oxo-557-oxo-558-oxo-559-oxo-560-oxo-561-oxo-562-oxo-563-oxo-564-oxo-565-oxo-566-oxo-567-oxo-568-oxo-569-oxo-570-oxo-571-oxo-572-oxo-573-oxo-574-oxo-575-oxo-576-oxo-577-oxo-578-oxo-579-oxo-580-oxo-581-oxo-582-oxo-583-oxo-584-oxo-585-oxo-586-oxo-587-oxo-588-oxo-589-oxo-590-oxo-591-oxo-592-oxo-593-oxo-594-oxo-595-oxo-596-oxo-597-oxo-598-oxo-599-oxo-600-oxo-601-oxo-602-oxo-603-oxo-604-oxo-605-oxo-606-oxo-607-oxo-608-oxo-609-oxo-610-oxo-611-oxo-612-oxo-613-oxo-614-oxo-615-oxo-616-oxo-617-oxo-618-oxo-619-oxo-620-oxo-621-oxo-622-oxo-623-oxo-624-oxo-625-oxo-626-oxo-627-oxo-628-oxo-629-oxo-630-oxo-631-oxo-632-oxo-633-oxo-634-oxo-635-oxo-636-oxo-637-oxo-638-oxo-639-oxo-640-oxo-641-oxo-642-oxo-643-oxo-644-oxo-645-oxo-646-oxo-647-oxo-648-oxo-649-oxo-650-oxo-651-oxo-652-oxo-653-oxo-654-oxo-655-oxo-656-oxo-657-oxo-658-oxo-659-oxo-660-oxo-661-oxo-662-oxo-663-oxo-664-oxo-665-oxo-666-oxo-667-oxo-668-oxo-669-oxo-670-oxo-671-oxo-672-oxo-673-oxo-674-oxo-675-oxo-676-oxo-677-oxo-678-oxo-679-oxo-680-oxo-681-oxo-682-oxo-683-oxo-684-oxo-685-oxo-686-oxo-687-oxo-688-oxo-689-oxo-690-oxo-691-oxo-692-oxo-693-oxo-694-oxo-695-oxo-696-oxo-697-oxo-698-oxo-699-oxo-700-oxo-701-oxo-702-oxo-703-oxo-704-oxo-705-oxo-706-oxo-707-oxo-708-oxo-709-oxo-710-oxo-711-oxo-712-oxo-713-oxo-714-oxo-715-oxo-716-oxo-717-oxo-718-oxo-719-oxo-720-oxo-721-oxo-722-oxo-723-oxo-724-oxo-725-oxo-726-oxo-727-oxo-728-oxo-729-oxo-730-oxo-731-oxo-732-oxo-733-oxo-734-oxo-735-oxo-736-oxo-737-oxo-738-oxo-739-oxo-740-oxo-741-oxo-742-oxo-743-oxo-744-oxo-745-oxo-746-oxo-747-oxo-748-oxo-749-oxo-750-oxo-751-oxo-752-oxo-753-oxo-754-oxo-755-oxo-756-oxo-757-oxo-758-oxo-759-oxo-760-oxo-761-oxo-762-oxo-763-oxo-764-oxo-765-oxo-766-oxo-767-oxo-768-oxo-769-oxo-770-oxo-771-oxo-772-oxo-773-oxo-774-oxo-775-oxo-776-oxo-777-oxo-778-oxo-779-oxo-780-oxo-781-oxo-782-oxo-783-oxo-784-oxo-785-oxo-786-oxo-787-oxo-788-oxo-789-oxo-790-oxo-791-oxo-792-oxo-793-oxo-794-oxo-795-oxo-796-oxo-797-oxo-798-oxo-799-oxo-800-oxo-801-oxo-802-oxo-803-oxo-804-oxo-805-oxo-806-oxo-807-oxo-808-oxo-809-oxo-810-oxo-811-oxo-812-oxo-813-oxo-814-oxo-815-oxo-816-oxo-817-oxo-818-oxo-819-oxo-820-oxo-821-oxo-822-oxo-823-oxo-824-oxo-825-oxo-826-oxo-827-oxo-828-oxo-829-oxo-830-oxo-831-oxo-832-oxo-833-oxo-834-oxo-835-oxo-836-oxo-837-oxo-838-oxo-839-oxo-840-oxo-841-oxo-842-oxo-843-oxo-844-oxo-845-oxo-846-oxo-847-oxo-848-oxo-849-oxo-850-oxo-851-oxo-852-oxo-853-oxo-854-oxo-855-oxo-856-oxo-857-oxo-858-oxo-859-oxo-860-oxo-861-oxo-862-oxo-863-oxo-864-oxo-865-oxo-866-oxo-867-oxo-868-oxo-869-oxo-870-oxo-871-oxo-872-oxo-873-oxo-874-oxo-875-oxo-876-oxo-877-oxo-878-oxo-879-oxo-880-oxo-881-oxo-882-oxo-883-oxo-884-oxo-885-oxo-886-oxo-887-oxo-888-oxo-889-oxo-890-oxo-891-oxo-892-oxo-893-oxo-894-oxo-895-oxo-896-oxo-897-oxo-898-oxo-899-oxo-900-oxo-901-oxo-902-oxo-903-oxo-904-oxo-905-oxo-906-oxo-907-oxo-908-oxo-909-oxo-910-oxo-911-oxo-912-oxo-913-oxo-914-oxo-915-oxo-916-oxo-917-oxo-918-oxo-919-oxo-920-oxo-921-oxo-922-oxo-923-oxo-924-oxo-925-oxo-926-oxo-927-oxo-928-oxo-929-oxo-930-oxo-931-oxo-932-oxo-933-oxo-934-oxo-935-oxo-936-oxo-937-oxo-938-oxo-939-oxo-940-oxo-941-oxo-942-oxo-943-oxo-944-oxo-945-oxo-946-oxo-947-oxo-948-oxo-949-oxo-950-oxo-951-oxo-952-oxo-953-oxo-954-oxo-955-oxo-956-oxo-957-oxo-958-oxo-959-oxo-960-oxo-961-oxo-962-oxo-963-oxo-964-oxo-965-oxo-966-oxo-967-oxo-968-oxo-969-oxo-970-oxo-971-oxo-972-oxo-973-oxo-974-oxo-975-oxo-976-oxo-977-oxo-978-oxo-979-oxo-980-oxo-981-oxo-982-oxo-983-oxo-984-oxo-985-oxo-986-oxo-987-oxo-988-oxo-989-oxo-990-oxo-991-oxo-992-oxo-993-oxo-994-oxo-995-oxo-996-oxo-997-oxo-998-oxo-999-oxo-1000-oxo-1001-oxo-1002-oxo-1003-oxo-1004-oxo-1005-oxo-1006-oxo-1007-oxo-1008-oxo-1009-oxo-1010-oxo-1011-oxo-1012-oxo-1013-oxo-1014-oxo-1015-oxo-1016-oxo-1017-oxo-1018-oxo-1019-oxo-1020-oxo-1021-oxo-1022-oxo-1023-oxo-1024-oxo-1025-oxo-1026-oxo-1027-oxo-1028-oxo-1029-oxo-1030-oxo-1031-oxo-1032-oxo-1033-oxo-1034-oxo-1035-oxo-1036-oxo-1037-oxo-1038-oxo-1039-oxo-1040-oxo-1041-oxo-1042-oxo-1043-oxo-1044-oxo-1045-oxo-1046-oxo-1047-oxo-1048-oxo-1049-oxo-1050-oxo-1051-oxo-1052-oxo-1053-oxo-1054-oxo-1055-oxo-1056-oxo-1057-oxo-1058-oxo-1059-oxo-1060-oxo-1061-oxo-1062-oxo-1063-oxo-1064-oxo-1065-oxo-1066-oxo-1067-oxo-1068-oxo-1069-oxo-1070-oxo-1071-oxo-1072-oxo-1073-oxo-1074-oxo-1075-oxo-1076-oxo-1077-oxo-1078-oxo-1079-oxo-1080-oxo-1081-oxo-1082-oxo-1083-oxo-1084-oxo-1085-oxo-1086-oxo-1087-oxo-1088-oxo-1089-oxo-1090-oxo-1091-oxo-1092-oxo-1093-oxo-1094-oxo-1095-oxo-1096-oxo-1097-oxo-1098-oxo-1099-oxo-1100-oxo-1101-oxo-1102-oxo-1103-oxo-1104-oxo-1105-oxo-1106-oxo-1107-oxo-1108-oxo-1109-oxo-1110-oxo-1111-oxo-1112-oxo-1113-oxo-1114-oxo-1115-oxo-1116-oxo-1117-oxo-1118-oxo-1119-oxo-1120-oxo-1121-oxo-1122-oxo-1123-oxo-1124-oxo-1125-oxo-1126-oxo-1127-oxo-1128-oxo-1129-oxo-1130-oxo-1131-oxo-1132-oxo-1133-oxo-1134-oxo-1135-oxo-1136-oxo-1137-oxo-1138-oxo-1139-oxo-1140-oxo-1141-oxo-1142-oxo-1143-oxo-1144-oxo-1145-oxo-1146-oxo-1147-oxo-1148-oxo-1149-oxo-1150-oxo-1151-oxo-1152-oxo-1153-oxo-1154-oxo-1155-oxo-1156-oxo-1157-oxo-1158-oxo-1159-oxo-1160-oxo-1161-oxo-1162-oxo-1163-oxo-1164-oxo-1165-oxo-1166-oxo-1167-oxo-1168-oxo-1169-oxo-1170-oxo-1171-oxo-1172-oxo-1173-oxo-1174-oxo-1175-oxo-1176-oxo-1177-oxo-1178-oxo-1179-oxo-1180-oxo-1181-oxo-1182-oxo-1183-oxo-1184-oxo-1185-oxo-1186-oxo-1187-oxo-1188-oxo-1189-oxo-1190-oxo-1191-oxo-1192-oxo-1193-oxo-1194-oxo-1195-oxo-1196-oxo-1197-oxo-1198-oxo-1199-oxo-1200-oxo-1201-oxo-1202-oxo-1203-oxo-1204-oxo-1205-oxo-1206-oxo-1207-oxo-1208-oxo-1209-oxo-1210-oxo-1211-oxo-1212-oxo-1213-oxo-1214-oxo-1215-oxo-1216-oxo-1217-oxo-1218-oxo-1219-oxo-1220-oxo-1221-oxo-1222-oxo-1223-oxo-1224-oxo-1225-oxo-1226-oxo-1227-oxo-1228-oxo-1229-oxo-1230-oxo-1231-oxo-1232-oxo-1233-oxo-1234-oxo-1235-oxo-1236-oxo-1237-oxo-1238-oxo-1239-oxo-1240-oxo-1241-oxo-1242-oxo-1243-oxo-1244-oxo-1245-oxo-1246-oxo-1247-oxo-1248-oxo-1249-oxo-1250-oxo-1251-oxo-1252-oxo-1253-oxo-1254-oxo-1255-oxo-1256-oxo-1257-oxo-1258-oxo-1259-oxo-1260-oxo-1261-oxo-1262-oxo-1263-oxo-1264-oxo-1265-oxo-1266-oxo-1267-oxo-1268-oxo-1269-oxo-1270-oxo-1271-oxo-1272-oxo-1273-oxo-1274-oxo-1275-oxo-1276-oxo-1277-oxo-1278-oxo-1279-oxo-1280-oxo-1281-oxo-1282-oxo-1283-oxo-1284-oxo-1285-oxo-1286-oxo-1287-oxo-1288-oxo-1289-oxo-1290-oxo-1291-oxo-1292-oxo-1293-oxo-1294-oxo-1295-oxo-1296-oxo-1297-oxo-1298-oxo-1299-oxo-1300-oxo-1301-oxo-1302-oxo-1303-oxo-1304-oxo-1305-oxo-1306-oxo-1307-oxo-1308-oxo-1309-oxo-1310-oxo-1311-oxo-1312-oxo-1313-oxo-1314-oxo-1315-oxo-1316-oxo-1317-oxo-1318-oxo-1319-oxo-1320-oxo-1321-oxo-1322-oxo-1323-oxo-1324-oxo-1325-oxo-1326-oxo-1327-oxo-1328-oxo-1329-oxo-1330-oxo-1331-oxo-1332-oxo-1333-oxo-1334-oxo-1335-oxo-1336-oxo-1337-oxo-1338-oxo-1339-oxo-1340-oxo-1341-oxo-1342-oxo-1343-oxo-1344-oxo-1345-oxo-1346-oxo-1347-oxo-1348-oxo-1349-oxo-1350-oxo-1351-oxo-1352-oxo-1353-oxo-1354-oxo-1355-oxo-1356-oxo-1357-oxo-1358-oxo-1359-oxo-1360-oxo-1361-oxo-1362-oxo-1363-oxo-1364-oxo-1365-oxo-1366-oxo-1367-oxo-1368-oxo-1369-oxo-1370-oxo-1371-oxo-1372-oxo-1373-oxo-1374-oxo-1375-oxo-1376-oxo-1377-oxo-1378-oxo-1379-oxo-1380-oxo-1381-oxo-1382-oxo-1383-oxo-1384-oxo-1385-oxo-1386-oxo-1387-oxo-1388-oxo-1389-oxo-1390-oxo-



CC INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.  
 CC InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1222 MW; 81BF67AB415B9D1 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 3 SR 4  
 DB 5 SR 6

## RESULT 31

ANGT\_CHICK  
 ID ANGT\_CHICK STANDARD; PRI: 10 AA.  
 AC P01618;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1,7]-angiotensin I); (Ang I) (Fragment).  
 GN AGT OR SERPIN8.  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OX NCBI\_TaxID=9031, 93934;  
 RN [1];  
 RP SEQUENCE.  
 RC SPECIES=Chicken;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sakabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of [Ile] angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RN [2];  
 RP SEQUENCE.  
 RC SPECIES=C. japonica;  
 RX MEDLINE=90284684; PubMed=2191893;  
 RA Takai Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and inhibition of these effects in the Japanese quail.";  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN I, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR: A60624; A60624.  
 DR PIR: A90917; A90917.  
 DR InterPro: IPR000215; Serpin.  
 DR PROSITE: PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0;  
 QY 3 SR 4  
 DB 5 SR 6

RESULT 42

COXA\_SHEEP  
 ID COXA\_SHEEP STANDARD; PRI: 10 AA.  
 AC P80328;  
 DT 01-OCT-1994 (Rel. 40, Last sequence update)  
 DT 01-OCT-1994 (Rel. 40, Last annotation update)  
 DE Cytochrome c oxidase (EC 1.1.3.1) (Fragment)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Euteleostei; Euteleostei;  
 CC Percaridactylia; Salmoniformes; Salmonidae; Cyprinodontes;  
 OX NCBI\_TaxID=6223;  
 RN [1];  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=9410710; PubMed=1251000;  
 RA Froud R., Kadonaga R.;  
 RT "Identification of cytochrome c oxidase subunits Va and Vb of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1117(1994).  
 CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT CHAIN. CATALYTICALLY 4 tetrahydrochrome c + O(2) -> 4 tetrahydrochrome c + 2 H(2)O.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrion; Inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
 DR PIR: S43625; S43625.  
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane;  
 RN [1];  
 RP SEQUENCE 10 AA; 1343 MW; 05C694A40284D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 3 SR 4  
 DB 5 SR 6

## RESULT 43

COXQ\_SHEEP  
 ID COXQ\_SHEEP STANDARD; PRI: 10 AA.  
 AC P80337;  
 DT 01-OCT-1994 (Rel. 40, Last sequence update)  
 DT 01-OCT-1994 (Rel. 40, Last annotation update)  
 DE Cytochrome c oxidase (EC 1.1.3.1) (Fragment)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Caprinae; Vis.  
 OX NCBI\_TaxID=6223;  
 RN [1];  
 RP SEQUENCE.  
 RC TISSUE=Heart; and Liver.  
 RX MEDLINE=9410710; PubMed=1251000;  
 RA Froud R., Kadonaga R.;  
 RT "Identification of cytochrome c oxidase subunits Va and Vb of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1117(1994).  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-ENCODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT CHAIN. CATALYTICALLY 4 tetrahydrochrome c + O(2) -> 4 tetrahydrochrome c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.

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KW Oxdicredutase: Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1027 MW: C4E9FCA43D76A5C45764

Query Match 18.2% Score 21.05 (100.0% identity)
Best Local Similarity 100.0% Pred. No. 9.76e-03
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 AK 2
   11
Db 3 AK 4

RESULT 34
GON1_PETMA STANDARD; PRT: 10 AA.
AC P04378;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone 1) (Chain 1)
DE (Luliberin I).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperostei;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID:7757;
RN [1]
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE: 86168192; PubMed: 3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser P.A., Brownstein M.J.
RT "Primary structure of gonadotropin-releasing hormone from lamprey brain."
RL J. Biol. Chem. 261:4812-4819(1986).
CC 1- FUNCTION: Stimulates the secretion of gonadotropins: it stimulates the secretion of both luteinizing and follicle stimulating hormones.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: belongs to the GnRH family.
DR PIR: A01412; RHIMGS.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1244 MW: 184836237R175A3 (P04378)

Query Match 18.2% Score 21.05 (100.0% identity)
Best Local Similarity 100.0% Pred. No. 9.76e-03
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 9 SL 10
   11
Db 4 SL 5

RESULT 35
GON2_CHEPR STANDARD; PRT: 10 AA.
AC P0678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone 2) (Chain 1)
DE (Luliberin II).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID:71177;
RN [1]
RP SEQUENCE.
RX MEDLINE: 96413669; PubMed: 8816823;

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RA Park M., Fraser P.A., Sherwood N.M., Fletcher M., Fischer W.H.,
RA "Two new forms of the luteinizing hormone releasing hormone 1 gene and the expression of the gene in the brain of the lamprey, Petromyzon marinus."
RA J. Biol. Chem. 261:4812-4819(1986).
SQ SEQUENCE 10 AA: 1027 MW: C4E9FCA43D76A5C45764 (P04378)
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone 1) (Chain 1)
DE (Luliberin I).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperostei;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID:7757;
RN [1]
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE: 86168192; PubMed: 3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser P.A., Brownstein M.J.
RT "Primary structure of gonadotropin-releasing hormone from lamprey brain."
RL J. Biol. Chem. 261:4812-4819(1986).
CC 1- FUNCTION: Stimulates the secretion of gonadotropins: it stimulates the secretion of both luteinizing and follicle stimulating hormones.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: belongs to the GnRH family.
DR PIR: A01412; RHIMGS.
DR InterPro: IPR002012; GnRH.
DR Pfam: PF00446; GnRH; 1.
DR PROSITE: PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1244 MW: 184836237R175A3 (P04378)

Query Match 18.2% Score 21.05 (100.0% identity)
Best Local Similarity 100.0% Pred. No. 9.76e-03
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 10 IR 11
   11
Db 9 IR 11

RESULT 37
GON3_CHEPR STANDARD; PRT: 10 AA.
AC P0678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin II (Gonadotropin-releasing hormone 2) (Chain 1)
DE (Luliberin II).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi.
OC Phlebobranchia; Corellidae; Chelyosoma.
OX NCBI_TaxID:71177;
RN [1]
RP SEQUENCE.
RX MEDLINE: 96413669; PubMed: 8816823;

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GS09_BACSU
ID GS09_BACSU STANDARD: PRT: 10 AA.
AC P80243:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE General stress protein 9 (GSP9) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1].
RP SEQUENCE.
RC STRAIN=168 / 1558;
RX MEDLINE=94282319; PubMed=8012595;
RA Voelker U., Engelmann S., Maul B., Rietdorf S., Voelker A.,
RA Schmid R., Mach H., Hecker M.
RT *Analysis of the induction of general stress proteins of Bacillus
RT subtilis*.
RL Microbiology 140:741-752(1994).
CC -1- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GROWTH OF
CC -1- LIMITATION AND OXYGEN LIMITATION.
CC -1- CAUTION: Could not be found in the genome of B.subtilis 168.
KW Heat shock.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1168 MW: 997664425EAZ0DA CR644;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4
DB 1 SR 2

RESULT 39
HTF_HELZE
ID HTF_HELZE STANDARD: PRT: 10 AA.
AC p16353:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosemic hormone (HEZ-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Hymenoptera.
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1].
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=88426324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird J.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.
RT *Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosemic and adipokinetic activities.*.
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / HCH FAMILY.
DR PIR: A31571; A31571.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH: 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1096 MW: 8670367865A5B9C1 CR764;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 SR 4
DB 1 SR 2

RESULT 40
NSL_MST29
ID NSL_MST29 STANDARD: PRT: 10 AA.
AC p81143:
DT 15-JUN-1994 (Rel. 30, Created)
DT 15-JUN-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2003 (Rel. 40, Last annotation update)
DE 59 kDa non-specificity protein 1 (Protein 1).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1774;
RN [1].
RP SEQUENCE.
RC STRAIN=H37Rv;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4
DB 1 SR 2

RESULT 41
NSL_MST29
ID NSL_MST29 STANDARD: PRT: 10 AA.
AC p81143:
DT 15-JUN-1994 (Rel. 30, Created)
DT 15-JUN-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2003 (Rel. 40, Last annotation update)
DE 59 kDa non-specificity protein 1 (Protein 1).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1774;
RN [1].
RP SEQUENCE.
RC STRAIN=H37Rv;

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RESULT 47
TKL4_LOCMI
ID TKL4_LOCMI STANDARD: PRT: 10 AA.
AC P30250;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin IV (TK-IV).
OS Locustatachykinin (migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kechiansky J.P., Nachman R.J.
RA de Loof A.;
RT "Locustatachykinin III and IV: two additional insect neuropeptides
RT with homology to peptides of the vertebrate tachykinin family."
RL Regul. Pept. 31:199-212(1990).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR: H60073; ECL04M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA: 1040 MW: 9526D71F9C87735 CRQ64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9; Maps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SL 10
DB 3 SL 4

RESULT 48
TKNL_SCYCA
ID TKNL_SCYCA STANDARD: PRT: 10 AA.
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Scyllorhinin I.
OS Scyllorhinus canicula (spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carharniiformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=66192829; PubMed=2422058;
RA Conlon J.M., Beacon C.F., O'Toole L., Tim L.J.
RA "Scyllorhinin I and II: two novel tachykinins from dogfish
RL FEBS Lett. 200:111-116(1986).
RN [2]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;
RA "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyllorhinus canicula".
RL Eur. J. Biochem. 214:469-474(1993).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.

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-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
PIR: A24867; A24867.
InfoPro: P0802040; Tachykinin I.
PROSITE: PS00267; TACHYKININ_1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA: 1040 MW: 9526D71F9C87735 CRQ64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9; Maps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 1 AK 2

RESULT 49
TKNP_CHICK
ID TKNP_CHICK STANDARD: PRT: 10 AA.
AC P10833;
DT 01-FEB-1991 (Rel. 12, Created)
DT 01-FEB-1991 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurtakinin A (Substance K) (Neurokinin A).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Accipitriformes; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
FT MOD_RES 10 10
FT SEQUENCE 10 AA: 114 MW: 8460D620C0F0A8176064;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9; Maps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 11
DB 4 AK 11

RESULT 50
TKNR_GNMY
ID TKNR_GNMY STANDARD: PRT: 10 AA.
AC P28590;
DT 01-DEC-1992 (Rel. 21, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurtakinin A (Substance K) (Neurokinin A).
OS Caracanthus myxus (rainbow trout) (Salmo gairdneri); and
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model:

Run on: September 30, 2003, 10:07:04 : Search time 31.6667 Seconds  
(without alignments)  
69,639 Million cell updates/sec

Title: US-09-787-443-21

Perfect score: 11

Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4479

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

SPTREMBL\_23:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp-organelle:  
9: sp-organism:  
10: sp-plant:  
11: sp-rodent:  
12: sp-virus:  
13: sp-vertebrate:  
14: sp-unclassified:  
15: sp-rvirus:  
16: sp\_bacteriap:  
17: sp-archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	14	3 Q8J1G2	Q8J1G2 asl1y1 quos
2	3	27.3	8	2 P77556	P77556 escherichia
3	3	27.3	9	2 Q45852	Q45852 ribostidim
4	3	27.3	9	4 Q9UKJ6	Q9UKJ6 homo sapien
5	3	27.3	9	4 Q8NHL3	Q8NHL3 homo sapien
6	3	27.3	9	6 Q9TRW2	Q9TRW2 oryctolagus
7	3	27.3	9	10 Q8S3C6	Q8S3C6 glycine max
8	3	27.3	10	2 Q47651	Q47651 escherichia
9	3	27.3	10	2 Q9X533	Q9X533 escherichia
10	3	27.3	10	2 Q9X534	Q9X534 leclercia a
11	3	27.3	10	2 Q9F5W1	Q9F5W1 vibrio chol
12	3	27.3	10	3 Q8TG88	Q8TG88 pleurotus o
13	3	27.3	10	5 Q8WPL6	Q8WPL6 okopileura
14	3	27.3	10	15 P82080	P82080 limnodynast
15	3	27.3	10	15 Q8UT83	Q8UT83 human immun
16	3	27.3	11	2 Q9R872	Q9R872 escherichia

Q8J1G2 asl1y1 quos	17	4	36.4	14	3 Q8J1G2	Q8J1G2 asl1y1 quos
Q45852 ribostidim	18	3	27.3	8	2 P77556	P77556 escherichia
Q9UKJ6 homo sapien	19	3	27.3	9	4 Q9UKJ6	Q9UKJ6 homo sapien
Q8NHL3 homo sapien	20	3	27.3	9	4 Q8NHL3	Q8NHL3 homo sapien
Q9TRW2 oryctolagus	21	3	27.3	9	6 Q9TRW2	Q9TRW2 oryctolagus
Q8S3C6 glycine max	22	3	27.3	9	10 Q8S3C6	Q8S3C6 glycine max
Q47651 escherichia	23	3	27.3	10	2 Q47651	Q47651 escherichia
Q9X533 escherichia	24	3	27.3	10	2 Q9X533	Q9X533 escherichia
Q9X534 leclercia a	25	3	27.3	10	2 Q9X534	Q9X534 leclercia a
Q9F5W1 vibrio chol	26	3	27.3	10	2 Q9F5W1	Q9F5W1 vibrio chol
Q8TG88 pleurotus o	27	3	27.3	10	3 Q8TG88	Q8TG88 pleurotus o
Q8WPL6 okopileura	28	3	27.3	10	5 Q8WPL6	Q8WPL6 okopileura
P82080 limnodynast	29	3	27.3	10	15 P82080	P82080 limnodynast
Q8UT83 human immun	30	3	27.3	10	15 Q8UT83	Q8UT83 human immun
Q9R872 escherichia	31	3	27.3	11	2 Q9R872	Q9R872 escherichia
Q8J1G2 asl1y1 quos	32	3	27.3	14	3 Q8J1G2	Q8J1G2 asl1y1 quos
Q45852 ribostidim	33	3	27.3	8	2 P77556	P77556 escherichia
Q9UKJ6 homo sapien	34	3	27.3	9	4 Q9UKJ6	Q9UKJ6 homo sapien
Q8NHL3 homo sapien	35	3	27.3	9	4 Q8NHL3	Q8NHL3 homo sapien
Q9TRW2 oryctolagus	36	3	27.3	9	6 Q9TRW2	Q9TRW2 oryctolagus
Q8S3C6 glycine max	37	3	27.3	9	10 Q8S3C6	Q8S3C6 glycine max
Q47651 escherichia	38	3	27.3	10	2 Q47651	Q47651 escherichia
Q9X533 escherichia	39	3	27.3	10	2 Q9X533	Q9X533 escherichia
Q9X534 leclercia a	40	3	27.3	10	2 Q9X534	Q9X534 leclercia a
Q9F5W1 vibrio chol	41	3	27.3	10	2 Q9F5W1	Q9F5W1 vibrio chol
Q8TG88 pleurotus o	42	3	27.3	10	3 Q8TG88	Q8TG88 pleurotus o
Q8WPL6 okopileura	43	3	27.3	10	5 Q8WPL6	Q8WPL6 okopileura
P82080 limnodynast	44	3	27.3	10	15 P82080	P82080 limnodynast
Q8UT83 human immun	45	3	27.3	10	15 Q8UT83	Q8UT83 human immun
Q9R872 escherichia	46	3	27.3	11	2 Q9R872	Q9R872 escherichia
Q8J1G2 asl1y1 quos	47	3	27.3	14	3 Q8J1G2	Q8J1G2 asl1y1 quos
Q45852 ribostidim	48	3	27.3	8	2 P77556	P77556 escherichia
Q9UKJ6 homo sapien	49	3	27.3	9	4 Q9UKJ6	Q9UKJ6 homo sapien
Q8NHL3 homo sapien	50	3	27.3	9	4 Q8NHL3	Q8NHL3 homo sapien
Q9TRW2 oryctolagus	51	3	27.3	9	6 Q9TRW2	Q9TRW2 oryctolagus
Q8S3C6 glycine max	52	3	27.3	9	10 Q8S3C6	Q8S3C6 glycine max
Q47651 escherichia	53	3	27.3	10	2 Q47651	Q47651 escherichia
Q9X533 escherichia	54	3	27.3	10	2 Q9X533	Q9X533 escherichia
Q9X534 leclercia a	55	3	27.3	10	2 Q9X534	Q9X534 leclercia a
Q9F5W1 vibrio chol	56	3	27.3	10	2 Q9F5W1	Q9F5W1 vibrio chol
Q8TG88 pleurotus o	57	3	27.3	10	3 Q8TG88	Q8TG88 pleurotus o
Q8WPL6 okopileura	58	3	27.3	10	5 Q8WPL6	Q8WPL6 okopileura
P82080 limnodynast	59	3	27.3	10	15 P82080	P82080 limnodynast
Q8UT83 human immun	60	3	27.3	10	15 Q8UT83	Q8UT83 human immun
Q9R872 escherichia	61	3	27.3	11	2 Q9R872	Q9R872 escherichia
Q8J1G2 asl1y1 quos	62	3	27.3	14	3 Q8J1G2	Q8J1G2 asl1y1 quos
Q45852 ribostidim	63	3	27.3	8	2 P77556	P77556 escherichia
Q9UKJ6 homo sapien	64	3	27.3	9	4 Q9UKJ6	Q9UKJ6 homo sapien
Q8NHL3 homo sapien	65	3	27.3	9	4 Q8NHL3	Q8NHL3 homo sapien
Q9TRW2 oryctolagus	66	3	27.3	9	6 Q9TRW2	Q9TRW2 oryctolagus
Q8S3C6 glycine max	67	3	27.3	9	10 Q8S3C6	Q8S3C6 glycine max
Q47651 escherichia	68	3	27.3	10	2 Q47651	Q47651 escherichia
Q9X533 escherichia	69	3	27.3	10	2 Q9X533	Q9X533 escherichia
Q9X534 leclercia a	70	3	27.3	10	2 Q9X534	Q9X534 leclercia a
Q9F5W1 vibrio chol	71	3	27.3	10	2 Q9F5W1	Q9F5W1 vibrio chol
Q8TG88 pleurotus o	72	3	27.3	10	3 Q8TG88	Q8TG88 pleurotus o
Q8WPL6 okopileura	73	3	27.3	10	5 Q8WPL6	Q8WPL6 okopileura
P82080 limnodynast	74	3	27.3	10	15 P82080	P82080 limnodynast
Q8UT83 human immun	75	3	27.3	10	15 Q8UT83	Q8UT83 human immun
Q9R872 escherichia	76	3	27.3	11	2 Q9R872	Q9R872 escherichia
Q8J1G2 asl1y1 quos	77	3	27.3	14	3 Q8J1G2	Q8J1G2 asl1y1 quos
Q45852 ribostidim	78	3	27.3	8	2 P77556	P77556 escherichia
Q9UKJ6 homo sapien	79	3	27.3	9	4 Q9UKJ6	Q9UKJ6 homo sapien
Q8NHL3 homo sapien	80	3	27.3	9	4 Q8NHL3	Q8NHL3 homo sapien
Q9TRW2 oryctolagus	81	3	27.3	9	6 Q9TRW2	Q9TRW2 oryctolagus
Q8S3C6 glycine max	82	3	27.3	9	10 Q8S3C6	Q8S3C6 glycine max
Q47651 escherichia	83	3	27.3	10	2 Q47651	Q47651 escherichia
Q9X533 escherichia	84	3	27.3	10	2 Q9X533	Q9X533 escherichia
Q9X534 leclercia a	85	3	27.3	10	2 Q9X534	Q9X534 leclercia a
Q9F5W1 vibrio chol	86	3	27.3	10	2 Q9F5W1	Q9F5W1 vibrio chol
Q8TG88 pleurotus o	87	3	27.3	10	3 Q8TG88	Q8TG88 pleurotus o
Q8WPL6 okopileura	88	3	27.3	10	5 Q8WPL6	Q8WPL6 okopileura
P82080 limnodynast	89	3	27.3	10	15 P82080	P82080 limnodynast
Q8UT83 human immun	90	3	27.3	10	15 Q8UT83	Q8UT83 human immun
Q9R872 escherichia	91	3	27.3	11	2 Q9R872	Q9R872 escherichia



90	2	18.2	8	8	8	P93957	P93957 testucopsis	163	2	18.2	4	04036	Q9406 homo sapien
91	2	18.2	8	8	8	P92222	P92222 bromas iner	164	2	18.2	4	04097	Q9497 homo sapien
92	2	18.2	8	8	8	P92388	P92388 henrardia p	165	2	18.2	4	04058	Q9458 archidardi
93	2	18.2	8	8	8	P92441	P92441 thriopyrum	166	2	18.2	4	04012	Q9412 bos tauris
94	2	18.2	8	8	8	Q94000	Q94000 masoala mad	167	2	18.2	4	04016	Q9416 eubedia fy
95	2	18.2	8	8	8	P92404	P92404 lophopyrum	168	2	18.2	4	04036	Q9436 aotus azara
96	2	18.2	8	8	8	P93961	P93961 psathyrosta	169	2	18.2	4	04036	Q9436 aotus azara
97	2	18.2	8	8	8	P93970	P93970 eremopyrum	170	2	18.2	4	04036	Q9436 aotus azara
98	2	18.2	8	8	8	P93955	P93955 testucopsis	171	2	18.2	4	04036	Q9436 aotus azara
99	2	18.2	8	8	8	P93965	P93965 secale stri	172	2	18.2	4	04036	Q9436 aotus azara
100	2	18.2	8	8	8	P92394	P92394 hordeum val	173	2	18.2	4	04036	Q9436 aotus azara
101	2	18.2	8	8	8	P92382	P92382 hordeum bre	174	2	18.2	4	04036	Q9436 aotus azara
102	2	18.2	8	8	8	P93966	P93966 aequilops sp	175	2	18.2	4	04036	Q9436 aotus azara
103	2	18.2	8	8	8	Q94472	Q94472 asterina po	176	2	18.2	4	04036	Q9436 aotus azara
104	2	18.2	8	8	8	P92227	P92227 crithopsis	177	2	18.2	4	04036	Q9436 aotus azara
105	2	18.2	8	8	8	P92373	P92373 baynaldia v	178	2	18.2	4	04036	Q9436 aotus azara
106	2	18.2	8	8	8	P92211	P92211 atropyrone e	179	2	18.2	4	04036	Q9436 aotus azara
107	2	18.2	8	8	8	P92428	P92428 peridictyon	180	2	18.2	4	04036	Q9436 aotus azara
108	2	18.2	8	8	8	P92386	P92386 hordeum mar	181	2	18.2	4	04036	Q9436 aotus azara
109	2	18.2	8	8	8	P93959	P93959 hordeum ere	182	2	18.2	4	04036	Q9436 aotus azara
110	2	18.2	8	8	8	P92219	P92219 australopyr	183	2	18.2	4	04036	Q9436 aotus azara
111	2	18.2	8	8	8	P93985	P93985 aequilops fo	184	2	18.2	4	04036	Q9436 aotus azara
112	2	18.2	8	8	8	P92443	P92443 faenariae	185	2	18.2	4	04036	Q9436 aotus azara
113	2	18.2	8	8	8	Q94482	Q94482 varanus sal	186	2	18.2	4	04036	Q9436 aotus azara
114	2	18.2	8	8	8	P92391	P92391 heteranthel	187	2	18.2	4	04036	Q9436 aotus azara
115	2	18.2	8	8	8	P93981	P93981 crithodum	188	2	18.2	4	04036	Q9436 aotus azara
116	2	18.2	8	8	8	P93992	P93992 australopyr	189	2	18.2	4	04036	Q9436 aotus azara
117	2	18.2	8	8	8	Q94006	Q94006 boophilus m	190	2	18.2	4	04036	Q9436 aotus azara
118	2	18.2	8	8	8	P92426	P92426 pseudoroecq	191	2	18.2	4	04036	Q9436 aotus azara
119	2	18.2	8	8	8	P92431	P92431 aequilops ta	192	2	18.2	4	04036	Q9436 aotus azara
120	2	18.2	8	8	8	Q94477	Q94477 varanus sal	193	2	18.2	4	04036	Q9436 aotus azara
121	2	18.2	8	8	8	Q94485	Q94485 varanus sal	194	2	18.2	4	04036	Q9436 aotus azara
122	2	18.2	8	8	8	P92422	P92422 psathyrosta	195	2	18.2	4	04036	Q9436 aotus azara
123	2	18.2	8	8	8	Q93784	Q93784 bacterioph	196	2	18.2	4	04036	Q9436 aotus azara
124	2	18.2	8	8	8	Q93944	Q93944 bacterioph	197	2	18.2	4	04036	Q9436 aotus azara
125	2	18.2	8	8	8	Q93939	Q93939 bacterioph	198	2	18.2	4	04036	Q9436 aotus azara
126	2	18.2	8	8	8	Q93917	Q93917 bacterioph	199	2	18.2	4	04036	Q9436 aotus azara
127	2	18.2	8	8	8	Q93915	Q93915 bacterioph	200	2	18.2	4	04036	Q9436 aotus azara
128	2	18.2	8	8	8	Q93913	Q93913 bacterioph	201	2	18.2	4	04036	Q9436 aotus azara
129	2	18.2	8	8	8	Q93911	Q93911 bacterioph	202	2	18.2	4	04036	Q9436 aotus azara
130	2	18.2	8	8	8	Q93919	Q93919 bacterioph	203	2	18.2	4	04036	Q9436 aotus azara
131	2	18.2	8	8	8	Q93918	Q93918 bacterioph	204	2	18.2	4	04036	Q9436 aotus azara
132	2	18.2	8	8	8	Q93916	Q93916 bacterioph	205	2	18.2	4	04036	Q9436 aotus azara
133	2	18.2	8	8	8	Q93914	Q93914 bacterioph	206	2	18.2	4	04036	Q9436 aotus azara
134	2	18.2	8	8	8	Q93912	Q93912 bacterioph	207	2	18.2	4	04036	Q9436 aotus azara
135	2	18.2	8	8	8	Q93910	Q93910 bacterioph	208	2	18.2	4	04036	Q9436 aotus azara
136	2	18.2	8	8	8	Q93908	Q93908 bacterioph	209	2	18.2	4	04036	Q9436 aotus azara
137	2	18.2	8	8	8	Q93905	Q93905 bacterioph	210	2	18.2	4	04036	Q9436 aotus azara
138	2	18.2	8	8	8	Q93903	Q93903 bacterioph	211	2	18.2	4	04036	Q9436 aotus azara
139	2	18.2	8	8	8	Q93901	Q93901 bacterioph	212	2	18.2	4	04036	Q9436 aotus azara
140	2	18.2	8	8	8	Q93900	Q93900 bacterioph	213	2	18.2	4	04036	Q9436 aotus azara
141	2	18.2	8	8	8	Q93900	Q93900 bacterioph	214	2	18.2	4	04036	Q9436 aotus azara
142	2	18.2	8	8	8	Q93900	Q93900 bacterioph	215	2	18.2	4	04036	Q9436 aotus azara
143	2	18.2	8	8	8	Q93900	Q93900 bacterioph	216	2	18.2	4	04036	Q9436 aotus azara
144	2	18.2	8	8	8	Q93900	Q93900 bacterioph	217	2	18.2	4	04036	Q9436 aotus azara
145	2	18.2	8	8	8	Q93900	Q93900 bacterioph	218	2	18.2	4	04036	Q9436 aotus azara
146	2	18.2	8	8	8	Q93900	Q93900 bacterioph	219	2	18.2	4	04036	Q9436 aotus azara
147	2	18.2	8	8	8	Q93900	Q93900 bacterioph	220	2	18.2	4	04036	Q9436 aotus azara
148	2	18.2	8	8	8	Q93900	Q93900 bacterioph	221	2	18.2	4	04036	Q9436 aotus azara
149	2	18.2	8	8	8	Q93900	Q93900 bacterioph	222	2	18.2	4	04036	Q9436 aotus azara
150	2	18.2	8	8	8	Q93900	Q93900 bacterioph	223	2	18.2	4	04036	Q9436 aotus azara
151	2	18.2	8	8	8	Q93900	Q93900 bacterioph	224	2	18.2	4	04036	Q9436 aotus azara
152	2	18.2	8	8	8	Q93900	Q93900 bacterioph	225	2	18.2	4	04036	Q9436 aotus azara
153	2	18.2	8	8	8	Q93900	Q93900 bacterioph	226	2	18.2	4	04036	Q9436 aotus azara
154	2	18.2	8	8	8	Q93900	Q93900 bacterioph	227	2	18.2	4	04036	Q9436 aotus azara
155	2	18.2	8	8	8	Q93900	Q93900 bacterioph	228	2	18.2	4	04036	Q9436 aotus azara
156	2	18.2	8	8	8	Q93900	Q93900 bacterioph	229	2	18.2	4	04036	Q9436 aotus azara
157	2	18.2	8	8	8	Q93900	Q93900 bacterioph	230	2	18.2	4	04036	Q9436 aotus azara
158	2	18.2	8	8	8	Q93900	Q93900 bacterioph	231	2	18.2	4	04036	Q9436 aotus azara
159	2	18.2	8	8	8	Q93900	Q93900 bacterioph	232	2	18.2	4	04036	Q9436 aotus azara
160	2	18.2	8	8	8	Q93900	Q93900 bacterioph	233	2	18.2	4	04036	Q9436 aotus azara
161	2	18.2	8	8	8	Q93900	Q93900 bacterioph	234	2	18.2	4	04036	Q9436 aotus azara
162	2	18.2	8	8	8	Q93900	Q93900 bacterioph	235	2	18.2	4	04036	Q9436 aotus azara

236	2	18.2	10	4	060912	Q60912 homo sapien	309	2	18.2	11	2	P27404	Q27404 escherichia
237	2	18.2	10	4	Q90C53	Q90C53 homo sapien	310	2	18.2	11	2	Q46053	Q46053 escherichia
238	2	18.2	10	4	Q9H115	Q9H115 homo sapien	311	2	18.2	11	2	Q47600	Q47600 escherichia
239	2	18.2	10	4	Q9UCP3	Q9UCP3 homo sapien	312	2	18.2	11	2	Q9H115	Q9H115 escherichia
240	2	18.2	10	4	Q9UCU6	Q9UCU6 homo sapien	313	2	18.2	11	2	P21226	P21226 escherichia
241	2	18.2	10	4	Q8N6B1	Q8N6B1 homo sapien	314	2	18.2	11	2	Q95514	Q95514 pseudomonas
242	2	18.2	10	5	Q9TXK1	Q9TXK1 dermatophag	315	2	18.2	11	2	Q47344	Q47344 escherichia
243	2	18.2	10	5	P82384	P82384 drosophila	316	2	18.2	11	2	Q47424	Q47424 escherichia
244	2	18.2	10	5	P82217	P82217 bombyx mori	317	2	18.2	11	2	Q96414	Q96414 pseudomonas
245	2	18.2	10	6	Q9TS43	Q9TS43 sus scrofa	318	2	18.2	11	2	Q96434	Q96434 homo sapien
246	2	18.2	10	6	Q8M78	Q8M78 bos taurus q	319	2	18.2	11	4	Q47344	Q47344 homo sapien
247	2	18.2	10	6	Q9TR48	Q9TR48 bos taurus	320	2	18.2	11	4	Q95524	Q95524 homo sapien
248	2	18.2	10	8	Q9TRF7	Q9TRF7 agonis gran	321	2	18.2	11	4	Q95524	Q95524 homo sapien
249	2	18.2	10	8	Q9TRF9	Q9TRF9 metaleuca v	322	2	18.2	11	4	Q16427	Q16427 homo sapien
250	2	18.2	10	8	Q9TRG2	Q9TRG2 callistemon	323	2	18.2	11	4	Q95811	Q95811 homo sapien
251	2	18.2	10	8	Q9TRF5	Q9TRF5 agonis sp	324	2	18.2	11	4	Q47344	Q47344 homo sapien
252	2	18.2	10	8	Q94VG5	Q94VG5 varanus gri	325	2	18.2	11	4	Q47344	Q47344 homo sapien
253	2	18.2	10	8	Q9TRF1	Q9TRF1 homioleperg	326	2	18.2	11	4	Q95811	Q95811 homo sapien
254	2	18.2	10	8	Q9TRF3	Q9TRF3 tristatopsis	327	2	18.2	11	4	Q95811	Q95811 homo sapien
255	2	18.2	10	8	Q9TRF3	Q9TRF3 anagasmyrin	328	2	18.2	11	4	Q95811	Q95811 homo sapien
256	2	18.2	10	8	Q9TRF3	Q9TRF3 asferomyitru	329	2	18.2	11	4	Q95811	Q95811 homo sapien
257	2	18.2	10	8	Q9TRF0	Q9TRF0 neofabricia	330	2	18.2	11	4	Q95811	Q95811 homo sapien
258	2	18.2	10	8	Q9TRF0	Q9TRF0 kunzea arbi	331	2	18.2	11	4	Q95811	Q95811 homo sapien
259	2	18.2	10	8	Q94VD5	Q94VD5 varanus oli	332	2	18.2	11	4	Q95811	Q95811 homo sapien
260	2	18.2	10	8	Q9TRP4	Q9TRP4 varus sp	333	2	18.2	11	4	Q95811	Q95811 homo sapien
261	2	18.2	10	8	Q92707	Q92707 platysaurus	334	2	18.2	11	4	Q95811	Q95811 homo sapien
262	2	18.2	10	8	Q9TRF6	Q9TRF6 agonis obtu	335	2	18.2	11	4	Q95811	Q95811 homo sapien
263	2	18.2	10	8	Q9TRM7	Q9TRM7 leptosperu	336	2	18.2	11	4	Q95811	Q95811 homo sapien
264	2	18.2	10	8	P92733	P92733 tegevaria	337	2	18.2	11	4	Q95811	Q95811 homo sapien
265	2	18.2	10	8	Q9TRF2	Q9TRF2 leptosperu	338	2	18.2	11	4	Q95811	Q95811 homo sapien
266	2	18.2	10	8	Q9TRK3	Q9TRK3 leptosperu	339	2	18.2	11	4	Q95811	Q95811 homo sapien
267	2	18.2	10	8	Q9TRK7	Q9TRK7 kunzea pulc	340	2	18.2	11	4	Q95811	Q95811 homo sapien
268	2	18.2	10	8	Q9TRM6	Q9TRM6 leptosperu	341	2	18.2	11	4	Q95811	Q95811 homo sapien
269	2	18.2	10	8	Q9TRK6	Q9TRK6 leptosperu	342	2	18.2	11	4	Q95811	Q95811 homo sapien
270	2	18.2	10	8	P92576	P92576 bipes bipir	343	2	18.2	11	4	Q95811	Q95811 homo sapien
271	2	18.2	10	8	Q9TR97	Q9TR97 kapiocerus	344	2	18.2	11	4	Q95811	Q95811 homo sapien
272	2	18.2	10	8	Q9TRK8	Q9TRK8 kunzea eric	345	2	18.2	11	4	Q95811	Q95811 homo sapien
273	2	18.2	10	8	Q9TRK9	Q9TRK9 kunzea baxi	346	2	18.2	11	4	Q95811	Q95811 homo sapien
274	2	18.2	10	8	Q8SL54	Q8SL54 aconium haw	347	2	18.2	11	4	Q95811	Q95811 homo sapien
275	2	18.2	10	8	Q9TRF5	Q9TRF5 eublepharus	348	2	18.2	11	4	Q95811	Q95811 homo sapien
276	2	18.2	10	8	Q35013	Q35013 metoidophne	349	2	18.2	11	4	Q95811	Q95811 homo sapien
277	2	18.2	10	8	Q8SHN1	Q8SHN1 bradypodion	350	2	18.2	11	4	Q95811	Q95811 homo sapien
278	2	18.2	10	8	Q9TRK1	Q9TRK1 neofabricia	351	2	18.2	11	4	Q95811	Q95811 homo sapien
279	2	18.2	10	8	P92632	P92632 eromias ara	352	2	18.2	11	4	Q95811	Q95811 homo sapien
280	2	18.2	10	8	Q9TRK4	Q9TRK4 leptosperu	353	2	18.2	11	4	Q95811	Q95811 homo sapien
281	2	18.2	10	8	Q9TRK0	Q9TRK0 lophostemon	354	2	18.2	11	4	Q95811	Q95811 homo sapien
282	2	18.2	10	8	P82136	P82136 spinacia ol	355	2	18.2	11	4	Q95811	Q95811 homo sapien
283	2	18.2	10	8	Q8HUB4	Q8HUB4 anemobryum	356	2	18.2	11	4	Q95811	Q95811 homo sapien
284	2	18.2	10	9	Q38217	Q38217 lactococcus	357	2	18.2	11	4	Q95811	Q95811 homo sapien
285	2	18.2	10	10	Q95926	Q95926 alycino max	358	2	18.2	11	4	Q95811	Q95811 homo sapien
286	2	18.2	10	10	Q8SAC2	Q8SAC2 amblystegiu	359	2	18.2	11	4	Q95811	Q95811 homo sapien
287	2	18.2	10	10	P82434	P82434 nicotiana t	360	2	18.2	11	4	Q95811	Q95811 homo sapien
288	2	18.2	10	10	P82438	P82438 nicotiana t	361	2	18.2	11	4	Q95811	Q95811 homo sapien
289	2	18.2	10	10	Q8GUV6	Q8GUV6 capsella ru	362	2	18.2	11	4	Q95811	Q95811 homo sapien
290	2	18.2	10	11	Q9QW81	Q9QW81 rattus norv	363	2	18.2	11	4	Q95811	Q95811 homo sapien
291	2	18.2	10	11	Q63389	Q63389 rattus norv	364	2	18.2	11	4	Q95811	Q95811 homo sapien
292	2	18.2	10	11	Q8VIL8	Q8VIL8 mus muscariu	365	2	18.2	11	4	Q95811	Q95811 homo sapien
293	2	18.2	10	11	Q9JL15	Q9JL15 mus muscariu	366	2	18.2	11	4	Q95811	Q95811 homo sapien
294	2	18.2	10	11	Q70580	Q70580 mus muscariu	367	2	18.2	11	4	Q95811	Q95811 homo sapien
295	2	18.2	10	12	Q84140	Q84140 influenza v	368	2	18.2	11	4	Q95811	Q95811 homo sapien
296	2	18.2	10	12	Q69347	Q69347 herpes simf	369	2	18.2	11	4	Q95811	Q95811 homo sapien
297	2	18.2	10	12	P90391	P90391 tomato yru	370	2	18.2	11	4	Q95811	Q95811 homo sapien
298	2	18.2	10	13	Q42355	Q42355 brachydanio	371	2	18.2	11	4	Q95811	Q95811 homo sapien
299	2	18.2	10	13	Q9PR09	Q9PR09 sparus aara	372	2	18.2	11	4	Q95811	Q95811 homo sapien
300	2	18.2	10	13	Q73588	Q73588 gallus gall	373	2	18.2	11	4	Q95811	Q95811 homo sapien
301	2	18.2	10	13	Q73594	Q73594 gallus gall	374	2	18.2	11	4	Q95811	Q95811 homo sapien
302	2	18.2	10	13	Q8AXT7	Q8AXT7 xenopus lae	375	2	18.2	11	4	Q95811	Q95811 homo sapien
303	2	18.2	10	15	Q86324	Q86324 rous sarcom	376	2	18.2	11	4	Q95811	Q95811 homo sapien
304	2	18.2	10	15	Q86325	Q86325 rous sarcom	377	2	18.2	11	4	Q95811	Q95811 homo sapien
305	2	18.2	10	15	Q9QKJ0	Q9QKJ0 human immun	378	2	18.2	11	4	Q95811	Q95811 homo sapien
306	2	18.2	10	15	Q86326	Q86326 rous sarcom	379	2	18.2	11	4	Q95811	Q95811 homo sapien
307	2	18.2	11	2	Q9R790	Q9R790 borrelia ga	380	2	18.2	11	4	Q95811	Q95811 homo sapien
308	2	18.2	11	2	Q47602	Q47602 escherichia	381	2	18.2	11	4	Q95811	Q95811 homo sapien

[illegible]

Query Match: 36.4%; Score 4; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7, 9e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SRKG 6  
 Db 7 SRKG 10

RESULT 2  
 P77556  
 ID P77556 PRELIMINARY; PRT: 8 AA.  
 AC P77556;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)  
 DE TRAY (Fragment).  
 GN TRAY.  
 OS Escherichia coli.  
 OG Plasmid IncFII R1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ECOR11;  
 RX MEDLINE=96400908; PubMed=8807284;  
 RA Boyd E.F., Hill C.W., Rich S.W., Hart J.E.;  
 RT "Mosaic structure of plasmids from natural populations of *Escherichia coli*."  
 RL Genetics 141:1091-1100(1996).  
 DR EMBL: U50661; AAC44245.1;  
 DR EMBL: U50650; AAC44234.1;  
 DR EMBL: U50651; AAC44235.1;  
 DR EMBL: U50652; AAC44236.1;  
 DR EMBL: U50653; AAC44237.1;  
 DR EMBL: U50654; AAC44238.1;  
 DR EMBL: U50655; AAC44239.1;  
 DR EMBL: U50656; AAC44240.1;  
 DR EMBL: U50657; AAC44241.1;  
 DR EMBL: U50658; AAC44242.1;  
 DR EMBL: U50659; AAC44243.1;  
 DR EMBL: U50660; AAC44244.1;  
 KW Plasmid.  
 FT NON-TER  
 SQ SEQUENCE 8 AA: 834 MW: D335A580544735A1 CRR44;

Query Match: 27.3%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6, 4e-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 SSL 10  
 Db 6 SSL 8

RESULT 3  
 Q45852  
 ID Q45852 PRELIMINARY; PRT: 9 AA.  
 AC Q45852;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Chloramphenicol acetyltransferase (cat).  
 OS Clostridium butyricum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1492;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93143268; PubMed=1489203;  
 RA Huggins A.S., Bannam T.L., Rood J.I.;

Query Match: 36.4%; Score 4; DB 3; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7, 9e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 SRKG 6  
 Db 7 SRKG 10

RESULT 4  
 Q45852  
 ID Q45852 PRELIMINARY; PRT: 9 AA.  
 AC Q45852;  
 DT 01-MAY-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAY-2002 (TrEMBLrel. 22, Last annotation update)  
 DE K18201 (Fragment).  
 GN K18201.  
 OS Homo sapiens (human).  
 OG Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Primates; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Li X., Li N.;  
 RT "A Splice Site Mutation in the *ADAM10* Gene in a Family with Alzheimer's Disease."  
 RL Submitted (GDB) Entry: 1000000000; dbSNP: 1000000000;  
 DR EMBL: AF240147; AAC48013.1;  
 KW Receptor.  
 FT NON-TER  
 SQ SEQUENCE 9 AA: 1272 MW: 122663.55555555555 CRR44;

Query Match: 27.3%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6, 4e-05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 KSR 4  
 Db 5 KSR 7

RESULT 5  
 Q45852  
 ID Q45852 PRELIMINARY; PRT: 9 AA.  
 AC Q45852;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE K18201 (Fragment).  
 GN K18201.  
 OS Homo sapiens (human).  
 OG Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Primates; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Li X., Li N.;  
 RT "A Splice Site Mutation in the *ADAM10* Gene in a Family with Alzheimer's Disease."  
 RL Submitted (GDB) Entry: 1000000000; dbSNP: 1000000000;  
 DR EMBL: AF240147; AAC48013.1;  
 KW Receptor.  
 FT NON-TER  
 SQ SEQUENCE 9 AA: 1272 MW: 122663.55555555555 CRR44;

Query Match 27.3%, Score 3; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 8 (e=0.01);  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SLM 11  
 Db 2 SLM 4

## RESULT 6

Q9TRW2 PRELIMINARY; PRT: 9 AA;  
 AC Q9TRW2;  
 DT 01-MAY-2000 (TRENBLREL: 13, Created);  
 DT 01-MAY-2000 (TRENBLREL: 13, Last sequence update);  
 DT 01-JUN-2002 (TRENBLREL: 21, Last annotation update);  
 DE CAJESMON-PHOSPHORYLATION site (Fragment);  
 OS Oryctolagus cuniculus (Rabbit);  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cuniculidae;  
 OX NCBI\_TaxID:9986;  
 RN [1];  
 RP SEQUENCE;  
 RX MEDLINE=9,178498; PubMed=1698046;  
 RA Ikebe M., Hornick T.;  
 RT \*Determination of the phosphorylation sites of smooth muscle caldesmon  
 by protein kinase C.\*;  
 RL Arch. Biochem. Biophys. 288:538-542(1991);  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1018 MW: 809018105 6735A5 CRC64;

## Query Match

Best Local Similarity 100.0%; Pred. No. 8 (e=0.01);  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SLM 10  
 Db 2 SLM 4

## RESULT 7

Q8S3C6 PRELIMINARY; PRT: 9 AA;  
 AC Q8S3C6;  
 DT 01-JUN-2002 (TRENBLREL: 21, Created);  
 DT 01-JUN-2002 (TRENBLREL: 21, Last sequence update);  
 DT 01-JUN-2002 (TRENBLREL: 21, Last annotation update);  
 DE SNF RAD 54-like protein (Fragment);  
 OS Glycine max (Soybean);  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudots; Rosidae;  
 OC eurosids I; Fabales; Fabaceae; Papilionaceae; Phaseolidae; Glycine  
 OX NCBI\_TaxID=3847;  
 RN [1];  
 RP SEQUENCE FROM N.A.;  
 RC STRAIN=cv. Forrest;  
 RX MEDLINE=21258784; PubMed=11361330;  
 RA Meksem K., Ruben E., Hylen D., Trivittayakorn K., Lightfoot D.A.;  
 RT \*Conversion of AFLP bands into high-throughput DNA markers.\*;  
 RL Mol. Genet. Genomics 265:207-214(2001);  
 RN [2];  
 RP SEQUENCE FROM N.A.;  
 RC STRAIN=cv. Forrest;  
 RA Meksem K., Lightfoot D., Gibson P.;  
 RT \*Soybean Sudden Death Syndrome resistant soybeans: soybean cyst  
 nematode resistant soybeans and methods of breeding and identifying  
 resistant plants.\*;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases;  
 DR EMBL: AF489439; AAM14563.1;  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1070 MW: DC20A69735A2C699 CRC64;

## Query Match

Best Local Similarity 100.0%; Pred. No. 8 (e=0.01);  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SLM 11  
 Db 2 SLM 4

## RESULT 8

Q47451 PRELIMINARY; PRT: 9 AA;  
 AC Q47451;  
 DT 01-MAY-2000 (TRENBLREL: 13, Created);  
 DT 01-MAY-2000 (TRENBLREL: 13, Last sequence update);  
 DT 01-JUN-2002 (TRENBLREL: 21, Last annotation update);  
 DE CAJESMON-PHOSPHORYLATION site (Fragment);  
 OS Oryctolagus cuniculus (Rabbit);  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cuniculidae;  
 OX NCBI\_TaxID:9986;  
 RN [1];  
 RP SEQUENCE;  
 RX MEDLINE=9,178498; PubMed=1698046;  
 RA Ikebe M., Hornick T.;  
 RT \*Determination of the phosphorylation sites of smooth muscle caldesmon  
 by protein kinase C.\*;  
 RL Arch. Biochem. Biophys. 288:538-542(1991);  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1018 MW: 809018105 6735A5 CRC64;

## Query Match

Best Local Similarity 100.0%; Pred. No. 8 (e=0.01);  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SLM 11  
 Db 2 SLM 4

## RESULT 9

Q47451 PRELIMINARY; PRT: 9 AA;  
 AC Q47451;  
 DT 01-MAY-2000 (TRENBLREL: 13, Created);  
 DT 01-MAY-2000 (TRENBLREL: 13, Last sequence update);  
 DT 01-JUN-2002 (TRENBLREL: 21, Last annotation update);  
 DE CAJESMON-PHOSPHORYLATION site (Fragment);  
 OS Oryctolagus cuniculus (Rabbit);  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cuniculidae;  
 OX NCBI\_TaxID:9986;  
 RN [1];  
 RP SEQUENCE;  
 RX MEDLINE=9,178498; PubMed=1698046;  
 RA Ikebe M., Hornick T.;  
 RT \*Determination of the phosphorylation sites of smooth muscle caldesmon  
 by protein kinase C.\*;  
 RL Arch. Biochem. Biophys. 288:538-542(1991);  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1018 MW: 809018105 6735A5 CRC64;

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RA  Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT  *Phylogeny of mercury resistance (mer) operons of gram-negative
RL  bacteria isolated from the fecal flora of primates.*;
RN  Appl. Environ. Microbiol. 63:1066-1076(1997).
RP  [2]
RX  STRAIN-209A;
RC  MEDLINE-98027386; PubMed-9361435;
RA  Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT  *Association of mercury resistance with antibiotic resistance in the
RL  gram-negative fecal bacteria of primates.*;
RN  Appl. Environ. Microbiol. 63:4494-4503(1997).
RP  [3]
RX  STRAIN-209A;
RC  MEDLINE-20568355; PubMed-11116334;
RA  Liebert C.A., Watson A.L., Summers A.O.;
RT  *The quality of merC, a module of the mer mosaic.*;
RL  J. Mol. Evol. 51:607-622(2000).
DR  EMBL: AF120964; AAD23783.1; -;
FT  NON_TER 1
SQ  SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match      27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 SSL 10
DB  6 SSL 8

RESULT 10
QX534 PRELIMINARY: PRT: 10 AA.
AC QX534;
DT 01-NOV-1999 (TRENBLREL. 12, Created)
DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Periplasmic mercuric ion binding protein (Fragment).
GN MERP.
OS Leclercia adcarboxylata.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Leclercia.
OX NCBI_TaxID=83655;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-742H;
RX MEDLINE-97208220; PubMed-9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT *Phylogeny of mercury resistance (mer) operons of gram-negative
RL bacteria isolated from the fecal flora of primates.*;
RN Appl. Environ. Microbiol. 63:1066-1076(1997).
RP [2]
RX STRAIN-742H;
RC STRAIN-742H;
RX MEDLINE-98027386; PubMed-9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT *Association of mercury resistance with antibiotic resistance in the
RL gram-negative fecal bacteria of primates.*;
RN Appl. Environ. Microbiol. 63:4494-4503(1997).
RP [3]
RX STRAIN-742H;
RC STRAIN-742H;
RX MEDLINE-20568355; PubMed-11116334;
RA Liebert C.A., Watson A.L., Summers A.O.;
RT *The quality of merC, a module of the mer mosaic.*;
RL J. Mol. Evol. 51:607-622(2000).
DR EMBL: AF120965; AAD23785.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match      27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 SSL 10
DB  6 SSL 8

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Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 SSL 10
DB  6 SSL 8

RESULT 11
QX534 PRELIMINARY: PRT: 10 AA.
AC QX534;
DT 01-MAR-2001 (TRENBLREL. 12, Created)
DT 01-MAR-2001 (TRENBLREL. 12, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 19, Last annotation update)
DE Cop (Fragment).
GN CFP.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=696;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-9403;
RA RUI Y.Y., Kan B., Chao S.Y., Liu Y.Q., Li G.M.;
RT *PS region of Vibrio cholerae serotype O1Xp11, includes rsh (RSTK).
RL RSTA (RSTA) and RSTB (RSTB) genes.*;
RI Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF162794; AA12711.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1093 MW; 0F7CA443A7745A5 CRC64;

Query Match      27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 SSL 10
DB  7 SSL 5

RESULT 12
QX534 PRELIMINARY: PRT: 1 AA.
AC QX534;
DT 01-JUN-2002 (TRENBLREL. 21, Created)
DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Manganese peroxidase (Fragment).
GN MNP.
OS Pleurotus ostreatus (cluster mushroom) (White rot fungus).
OC Eukaryota; Basidiomycota; Basidiomycetes; Agaricomycetes;
OC Agaricomycetes; Pleurotus; Pleurotus.
OX NCBI_TaxID=5422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Flora-3;
RA Cohen P., Vandenbergh, Brian V.;
RT *The effect of Mn2+ on transcription of mnp genes in Pleurotus
RL ostreatus.*;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases
DR EMBL: AF156435; AAM-647.1; -;
KW Peroxidase.
FT NON_TER 1
SQ SEQUENCE 1 AA; 100 MW; 0F900A3167E339 CRC64;

Query Match      27.3%; Score 3; DB 3; Length 1;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  8 SSL 10
DB  7 SSL 9

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DR EMBL: AJ001816; CAA05032.1; -.
KW plasmid.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CR664;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SLM 11
DB 4 SLM 6

RESULT 17
Q9BJ61 PRELIMINARY; PRT: 11 AA.
AC Q9BJ61;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE G-box binding factor (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliales; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21290831; PubMed=11397018;
RA Brown J.M., Fitel R.A.;
RT "Functional and regulatory analysis of the Dictyostelium G box binding
factor.";
RL Dev. Biol. 234:521-534(2001).
DR EMBL: AF337815; AAK21290.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1248 MW; 8735635FDE1E1E1F1 CR664;

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNS 8
DB 9 GNS 11

RESULT 18
Q9G622 PRELIMINARY; PRT: 11 AA.
AC Q9G622;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COL.
OS Salea horsfieldii.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Anamniota; Anapsida;
OC Salea.
OX NCBI_TaxID=118233;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genome
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard

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PLYSOENETICS".
RC Syst. Biol. 49:257-277(2000).
DR EMBL: AF128474; AAK21290.1; -.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1248 MW; 56207EE46641A7 CR664;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SLM 10
DB 2 SLM 4

RESULT 19
Q9G616 PRELIMINARY; PRT: 11 AA.
AC Q9G616;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE "Evaluating Trans-Tethys migration: An example using Acrodont lizard".
OS Cytochrome c oxidase subunit I (Fragment).
GN COL.
OX NCBI_TaxID=118196;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard".
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard".
PLYSOENETICS".
RC Syst. Biol. 49:257-277(2000).
DR EMBL: AF128474; AAK21290.1; -.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1248 MW; 56207EE46641A7 CR664;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. Re-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SLM 10
DB 2 SLM 4

RESULT 20
Q9G610 PRELIMINARY; PRT: 11 AA.
AC Q9G610;
DT 01-MAR-2001 (TREMBlrel. 16, Created)

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OC Lepidosauria; Squamata; Iguania; Acrodontia; Anamidae; Eutrocostridae;
OC Ceratophora.
OX NCBI_TaxID=118196;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2165505; PubMed=11796034;
RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.
RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
RT Endemic to Sri Lanka."
RL Mol. Phylogenet. Evol. 22:111-117(2002).
DR EMBL: AF364053; AAL68024.1; .
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33649067 CRC64;

Query Match 27.3%; Score 3; DH 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8000;
Matches 3; Conservative 0; Mismatches 0; Labels 0;

QY 8 SSL 10
DB 2 SSL 4

RESULT 24
O9G613
ID O9G613 PRELIMINARY: PRT; 11 AA.
AC O9G613:
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI
OS Cophotis ceylanica.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodontia; Anamidae; Eutrocostridae;
OC Cophotis.
OX NCBI_TaxID=118202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.
RT "Evolution and information content of the mitochondrial genome
RT structural features illustrated with acrodont lizards."
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Arachchane N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.
RT "Evaluating Trans-Tethys migration: An example using Anamidae lizard
RT phylogenetics."
RL Syst. Biol. 49:233-256(2000).
DR EMBL: AF128493; AAG00716.1; .
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336491A7 CRC64;

Query Match 27.3%; Score 3; DH 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8000;
Matches 3; Conservative 0; Mismatches 0; Labels 0;

QY 8 SSL 10
DB 2 SSL 4

RESULT 25
O9G525
ID O9G525 PRELIMINARY: PRT; 11 AA.
AC O9G525:
DT 01-MAR-2001 (TReMBLrel. 16, Created)

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11 01-MAR-2002 (TReMBLrel. 22, Last sequence update)
11 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
1F Cytochrome c oxidase subunit I (Fragment).
1N [1]
1S Papadaria sphendari
1OS Mitochondrion
1G Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1C Lepidosauria; Squamata; Iguania; Acrodontia; Anamidae; Eutrocostridae;
1X Japalifra
1X NCBI_TaxID=118200;
1N [1]
1S SEQUENCE FROM N.A.
1X MEDLINE=22114081; PubMed=12118408;
1A Macey J.R., Schulte J.A. II, Larson A.
1A "Evolution and information content of the mitochondrial genome
1A structural features illustrated with acrodont lizards."
1S Syst. Biol. 49:257-277(2000).
1N [2]
1S SEQUENCE FROM N.A.
1X MEDLINE=22114081; PubMed=12118407;
1A Macey J.R., Schulte J.A. II, Larson A., Arachchane N.B., Wang Y.,
1A Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.
1A "Evaluating Trans-Tethys migration: An example using Anamidae lizard
1A phylogenetics."
1S Syst. Biol. 49:233-256(2000).
1X EMBL: AF128493; AAG00716.1; .
1KW Mitochondrion
1FT NON_TER 11 11
1SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336491A7 CRC64;

Query Match 27.3%; Score 3; DH 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 8000;
Matches 3; Conservative 0; Mismatches 0; Labels 0;

QY 8 SSL 10
DB 2 SSL 4

RESULT 26
O9G524
ID O9G524 PRELIMINARY: PRT; 11 AA.
AC O9G524:
DT 01-MAR-2002 (TReMBLrel. 22, Created)
DT 01-MAR-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
1E Cytochrome c oxidase subunit I (Fragment).
1N [1]
1S Ceratophora
1OS Mitochondrion
1G Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1C Lepidosauria; Squamata; Iguania; Acrodontia; Anamidae; Eutrocostridae;
1X Ceratophora
1X NCBI_TaxID=118196;
1N [1]
1S SEQUENCE FROM N.A.
1X MEDLINE=22114081; PubMed=12118408;
1A Macey J.R., Schulte J.A. II, Larson A.
1A "Evolution and information content of the mitochondrial genome
1A structural features illustrated with acrodont lizards."
1S Syst. Biol. 49:257-277(2000).
1N [2]
1S SEQUENCE FROM N.A.
1X MEDLINE=22114081; PubMed=12118407;
1A Macey J.R., Schulte J.A. II, Larson A., Arachchane N.B., Wang Y.,
1A Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.
1A "Evaluating Trans-Tethys migration: An example using Anamidae lizard
1A phylogenetics."
1S Syst. Biol. 49:233-256(2000).
1X EMBL: AF128493; AAG00716.1; .
1KW Mitochondrion
1FT NON_TER 11 11
1SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336491A7 CRC64;

```

Query Match 27.3% Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 SSL 10  
 DB 2 SSL 4

## RESULT 27

ID 054226 PRELIMINARY; PRT: 12 AA.  
 AC 054226;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Polyketide synthase (Fragment).  
 GN ERYA.  
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Pseudonocardiaceae; Pseudonocardiaceae; Saccharopolyspora.  
 OX NCBI\_TaxID=1836;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=NRRL2338;  
 RA Salah-Bey K., Doumith M., Michel J.M., Haydock S., Cortes C.,  
 Leadlay P.F., Reynal M.C.;  
 RT "Targeted gene inactivation for the elucidation of cheyA and  
 RT biosynthesis in the erythromycin producer, saccharopolyspora  
 RT erythraea.";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y1432; CAA74712.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1282 MW; D4BA3E57E27747D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GNS 8  
 DB 10 GNS 12

## RESULT 28

ID 046747 PRELIMINARY; PRT: 12 AA.  
 AC 046747;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Malate dehydrogenase (Fragment).  
 GN MDH.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=W3110;  
 RX MEDLINE=96165273; PubMed=8576952;  
 RA Bass S., Gu Q., Christen A.;  
 RT "Multicopy suppressors of pro mutant, Escherichia coli, include two E1A  
 RT (DeqP) protease homologs (HhoAB), DksA, and a truncated alpha."  
 RL J. Bacteriol. 178:1154-1161(1996).  
 DR EMBL; U15661; AAC43994.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1302 MW; D2DRE65218A5B33D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKS 5  
 DB 1  
 DB 5 AKS 5

## RESULT 29

ID 047251 PRELIMINARY; PRT: 12 AA.  
 AC 047251;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 04, Last annotation update)  
 DE Biotin protein (Fragment).  
 GN BMT.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=NRRL2338;  
 RA Salah-Bey K., Doumith M., Michel J.M., Haydock S., Cortes C.,  
 Leadlay P.F., Reynal M.C.;  
 RT "Targeted gene inactivation for the elucidation of cheyA and  
 RT biosynthesis in the erythromycin producer, saccharopolyspora  
 RT erythraea.";  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y1432; CAA74712.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1282 MW; D4BA3E57E27747D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 SSL 1  
 DB 1  
 DB 4 SSL 4

## RESULT 30

ID 046747 PRELIMINARY; PRT: 12 AA.  
 AC 046747;  
 DT 01-MAY-2000 (TrEMBLrel. 04, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 04, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 04, Last annotation update)  
 DE Glucose-1-ATPase (Fragment).  
 GN GlcA.  
 OS Helicobacter pylori (Campylobacter pylori).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Campylobacteriales;  
 OC Helicobacteriaceae; Helicobacteriaceae; Helicobacter.  
 OX NCBI\_TaxID=2347;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=J99;  
 RX MEDLINE=96165273; PubMed=8576952;  
 RA Bass S., Gu Q., Christen A.;  
 RT "Multicopy suppressors of pro mutant, Escherichia coli, include two E1A  
 RT (DeqP) protease homologs (HhoAB), DksA, and a truncated alpha."  
 RL J. Bacteriol. 178:1154-1161(1996).  
 DR EMBL; U15661; AAC43994.1;  
 FT NON\_TER 1  
 FT SEQUENCE 12 AA; 1302 MW; D2DRE65218A5B33D CR664;

Query Match 27.3% Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SSK 5  
 DB 1  
 DB 5 SSK 5

## RESULT 31

Q26429

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ID O26429 PRELIMINARY; PRT: 12 AA.
AC O26429;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PROBOSCPEDIA protein (Fragment).
GN PB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9211389; PubMed=1684932;
RA Randazzo F.M., Cribbs D.L., Kaufman T.C.;
RT "Rescue and regulation of proboscipedia: a homeotic gene of the
RT Antennapedia Complex."
RL Development 113:257-271(1991).
DR EMBL: S77929; AAB20845.1;
DR FlyBase; FBgn0012734; Dpse\pb.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA: 1377 MW: 4608DB18E35A5B3 CR664;

Query Match 27.3%; Score 3; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRK 5
DB 3 SRK 5

RESULT 32
ID Q8AEW7 PRELIMINARY; PRT: 12 AA.
AC Q8AEW7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (Fragment).
GN REV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HAART patient 28;
RA Saurva S.;
RT "Characterization of HIV-1 genes from AIDS patients on combination
RT therapy with discordance between viral load and CD4+ T cell counts."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ496725; CAD43155.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA: C395423D2E4321AD CR664;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9
DB 8 NSS 10

RESULT 33
ID Q9X3E1 PRELIMINARY; PRT: 13 AA.
AC Q9X3E1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).

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GN PTER.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae.
OX NCBI_TaxID=1226;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E.;
RT "Genetic diversity in the natural oceanic populations (New Cymondic) of
RT sorted from the Sargasso Sea and Gulf Stream."
RL Limnol. Oceanogr. 43:1416-1430(1998).
OR EMBL: AF070141; AAL2755.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA: 67E3E802-A466603 CR664;

Query Match 27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRK 5
DB 4 SRK 3

RESULT 34
ID Q90EE4 PRELIMINARY; PRT: 13 AA.
AC Q90EE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE RSGB transcription factor (Fragment).
GN R111.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominoidea;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohta K., Hirota H., Nishida H., Yoshida M.O., Aki S.;
RT "Molecular analysis of the breakpoint region of a 1.1-kb
RT translocation in leuko's sarcoma."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
OR EMBL: AB012624; AAA3455.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA: 6294FE7A64A50B CR664;

Query Match 27.3%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
DB 7 SSL 9

RESULT 35
ID Q29823 PRELIMINARY; PRT: 13 AA.
AC Q29823;
DT 01-NOV-1999 (TrEMBLrel. 13, Created)
DT 01-NOV-1999 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2000 (TrEMBLrel. 16, Last annotation update)
DE GAF-1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominoidea;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144827; PubMed=858858;
RA Beck S., Abdulla S., Aderton K.P., Guyane R.J., Gai J.G.;

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RA Hosking L.K., Jackson A., Kelly A., Newell W.R., Sanson P.,  
 RA Radley E., Thorpe K.L., Trowsdale J.,  
 RT "Evolutionary dynamics of non-coding sequences within the Class II  
 region of the human MHC";  
 RL J. Mol. Biol. 255:11-13(1996).  
 DR EMBL: X87344; CAA60783.1;  
 SQ SEQUENCE 13 AA; 1512 MW; 1F8948507F9CA554 CRC64;

Query Match 27.3%; Score 3; DB 7; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9  
 Db 6 NSS 8

## RESULT 36

Q9AU99 PRELIMINARY: PRT; 13 AA.  
 AC Q9AU99;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE Chalcone synthase (Fragment).  
 OS Aethionema grandiflora.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;  
 OC Eurosids II; Brassicales; Brassicaceae; Arabionema.  
 OX NCBI\_TaxID=72657;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP Koch M., Kroymann J., Haubold B., Weisshaar B., Mitchell-Olds T.,  
 RT "Phylogenetic analysis of promoter sequences from cruciferous  
 plants";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF249000; AAK31935.1;  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1432 MW; 5C444963C4621AA7 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10  
 Db 4 SSL 6

## RESULT 37

Q9FS97 PRELIMINARY: PRT; 13 AA.  
 AC Q9FS97;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2  
 OS Silene noctiflora (night-flowering catchfly).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene  
 OX NCBI\_TaxID=39899;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP Popp M., Oxelman B.,  
 RT "Inferring the history of the polyploid Silene acaqua  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ296140; CAC13021.1;  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1391 MW; D71753428A8B4B2 CRC64;

Query Match 27.4%; Score 3; DB 10; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SSL 11  
 Db 3 SSL 5

## RESULT 38

Q9R274 PRELIMINARY: PRT; 14 AA.  
 AC Q9R274;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
 DE Pseudomonas fluorescens Pf0-1  
 OS Pseudomonas fluorescens Pf0-1  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Gammaproteobacteria;  
 OC Gammaproteobacteria; Gammaproteobacteria  
 OX NCBI\_TaxID=1753;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP Studer E.,  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN 121  
 RA SEQUENCE FROM N.A.  
 RP Studer E., Bolmer M., Wimmer M., Löffler J., Schmid S.,  
 RA Gleditsia L.,  
 RT "REL and sequence analysis of Campylobacter jejuni and Campylobacter  
 coli PCR products amplified directly from environmental samples";  
 RL Food Sci. Technol. 33:367-373(1999).  
 ER EMBL: AJ146772; CAP69422.1;  
 LR EMBL: AJ146772; CAP69422.1;  
 LR EMBL: AJ146772; CAP69422.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1563 MW; 27340E37A724156 CRC64;

Query Match 27.4%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9  
 Db 3 NSS 5

## RESULT 39

Q9A081 PRELIMINARY: PRT; 14 AA.  
 AC Q9A081;  
 DT 01-MAY-1999 (TREMblrel. 1, Created)  
 DT 01-MAY-1999 (TREMblrel. 1, Last sequence update)  
 DT 01-MAY-1999 (TREMblrel. 1, Last annotation update)  
 DE Hypothetical protein  
 OS Saccharomyces cerevisiae (baker's yeast)  
 OC Eukaryota; Archaezoa; Eukaryota; Eukaryota; Eukaryota;  
 OC Bacteria; Actinobacteria; Actinobacteria; Actinobacteria;  
 OC Pseudomonas fluorescens Pf0-1  
 OX NCBI\_TaxID=1753;  
 RN [1]  
 RA SEQUENCE FROM N.A.  
 RP MCDONNELL J.,  
 RA Donadio S., Shalton A.,  
 RT "Distal protein of a thymidine kinase results in a thymidine kinase  
 Saccharomyces cerevisiae";  
 RL J. Bacteriol. 172:4600-4604(1990).  
 DR EMBL: M29612; AA884642.1;  
 KW Hypothetical protein  
 SQ SEQUENCE 14 AA; 1759 MW; 8C6000F9E59BE CRC64;

Query Match 27.4%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 9, 7e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10  
DB 8 SSL 10

## RESULT 40

Q9NFK8 PRELIMINARY; PRT; 14 AA.

AC Q9NFK8  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DI 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DE 01-OCT-2000 (TRENBLrel. 15, Last annotation update)  
DE Mmcl protein (Fragment).  
GN Mmcl.  
OS Brugia pahangi.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filariidae; Onchocercidae; Brugia.  
OX NCBI\_TaxID=6280.  
RN [1]  
RA Enes R.D., Thompson F., Devaney E.  
RT "A novel mRNA up-regulated in mammalian-derived microfilaria of Brugia".  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBS databases.  
DR EMBL: AJ277950; CAB93515.1;  
FT NON\_TER 1 1  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA: 1602 MW: 504062055AB89397 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9, 7e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SLM 11  
DB 6 SLM 8

## RESULT 41

P82220 PRELIMINARY; PRT; 14 AA.

AC P82220  
DT 01-OCT-2001 (TRENBLrel. 18, Created)  
DI 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
DE Unknown protein from 2D-page (Fragment).  
OS Bombyx mori (Silk moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Nymphalidae; Bombycidae; Bombyx.  
OX NCBI\_TaxID=7091;  
RN [1]  
RA STRAIN-XINHANG X KEMING; TISSUE: Body wall, and eye body;  
RX MELLINE-21177481; PubMed11280994;  
RA Zhong B.X.;  
RT "Protein database for several tissues derived from five last instar of silkworm".  
RL 1 Chuan Hsueh Pao 28:217-224(2001).  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA: 1566 MW: 3F6E8265CA86778 CRC64.

Query Match 27.3%; Score 3; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9, 7e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRK 5  
DB 1 SRK 3

## RESULT 42

Q9SMV4 PRELIMINARY; PRT; 14 AA.

AC Q9SMV4  
DT 01 MAY 2000 (TRENBLrel. 14, Created)  
DI 01 MAY 2000 (TRENBLrel. 14, Last sequence update)  
DE Unknown protein from 2D-page (Fragment).  
OS Arabidopsis thaliana (Brassicaceae).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliopsida; Corderiales; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3332.  
RN [1]  
RA SEQUENCE FROM N.A.  
RX STRAIN: Columbia.  
RX MELLINE-9406614; PubMed1076634.  
RA Stadler R., Eickholt F., Gahrz M., Samz N.  
RT "The Arabidopsis sucrose esterase may represent the osmotic drying factor for anther dehiscence and pollen tube growth in Arabidopsis".  
RL Plant J. 19:269-280(1999).  
DR EMBL: AJ001363; CAB93515.1;  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA: 1563 MW: 7FE479976A0A2A4 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9, 7e-03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SLM 10  
DB 6 SLM 8

## RESULT 43

Q9SMV4 PRELIMINARY; PRT; 14 AA.

AC Q9SMV4  
DT 01 MAY 2000 (TRENBLrel. 14, Created)  
DI 01 MAY 2000 (TRENBLrel. 14, Last sequence update)  
DE Unknown protein from 2D-page (Fragment).  
OS Arabidopsis thaliana (Brassicaceae).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliopsida; Corderiales; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3332.  
RN [1]  
RA SEQUENCE FROM N.A.  
RX STRAIN: Columbia.  
RX MELLINE-9406614; PubMed1076634.  
RA Stadler R., Eickholt F., Gahrz M., Samz N.  
RT "The Arabidopsis sucrose esterase may represent the osmotic drying factor for anther dehiscence and pollen tube growth in Arabidopsis".  
RL Plant J. 19:269-280(1999).  
DR EMBL: AJ001363; CAB93515.1;  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA: 1563 MW: 7FE479976A0A2A4 CRC64;

Query Match 27.3% Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 3  
 III  
 DB 12 AKS 14

## RESULT 44

Q9ZRS3 PRELIMINARY: PRT: 14 AA.  
 AC Q9ZRS3  
 DT 01-MAY-1999 (TRENBLREL. 10, Created)  
 DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)  
 DT 01-MAY-2002 (TRENBLREL. 20, Last annotation update)  
 DE Knotted-like homeobox protein (Fragment).  
 GN KNAT1  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eriophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosales;  
 OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsids;  
 OX NCBI\_TaxID:3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:cv. C24;  
 RA Raap M., Heyer A.G.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: AJ131822; CAAL0513.1;  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 14  
 FT 14  
 SQ SEQUENCE 14 AA: 1722 MW: 9814656; HIRSL4A CRC64;

Query Match 27.3% Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9  
 III  
 DB 8 NSS 10

## RESULT 45

P82340 PRELIMINARY: PRT: 14 AA.  
 AC P82340  
 DT 01-JUN-2000 (TRENBLREL. 14, Created)  
 DT 01-JUN-2000 (TRENBLREL. 14, Last sequence update)  
 DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)  
 DE Unknown protein from 2D-page of thylakoid lumen (Spectro); (Fragment).  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eriophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosales;  
 OC Eurosidia I; Fabales; Fabaceae; Papilionoideae; Viciales; Pisum  
 OX NCBI\_TaxID:3886;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND LEVEL: MEN, AT STADP  
 RC STRAIN:cv. DE GRACE; TISSUE:LEAF;  
 RX MEDLINE:20181728; PubMed:10715320;  
 RA Adamska I., van Wijk K.J.;  
 RA Peltier J.-B., Friso G., Kallme D.E., Raapstorf P., Nilsson P.  
 RT Proteomics of the chloroplast: systematic identification and  
 RT targeting analysis of luminal and peripheral thylakoid proteins.  
 RL Plant Cell 12:319-341(2000).  
 CC -/- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE; LUMEN  
 CC -/- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
 KW Chloroplast; Thylakoid membrane.  
 FT NON\_TER 14  
 FT 14  
 SQ SEQUENCE 14 AA: 1505 MW: 2EABFAF980F3D707 CRC64;

Query Match 27.3% Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 AKS 6  
 III  
 DB 11 AKS 14

## RESULT 46

Q06414 PRELIMINARY: PRT: 14 AA.  
 AC Q06414  
 DT 01-NOV-1999 (TRENBLREL. 10, Created)  
 DT 01-NOV-1999 (TRENBLREL. 10, Last sequence update)  
 DT 01-NOV-2002 (TRENBLREL. 20, Last annotation update)  
 DE 2X Tryptophan binding protein.  
 GN BAP1  
 OS Rattus norvegicus (Brown rat).  
 OC Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;  
 OC Muridae; Murinae; Muridae; Muridae; Muridae; Muridae;  
 OX NCBI\_TaxID:10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE:epithelium;  
 RA MEDLINE:1046155; PubMed:1046155; PubMed:1046155;  
 RA BACKUS M., Schmitt M., Schmitt M., Schmitt M., Schmitt M.,  
 PI "Type 2A Myosin Heavy Chain" (S100L10), a muscle fiber type-specific  
 PI protein, is a member of the myosin heavy chain family.  
 RL J Biol Chem 271:11111-11116(1996).  
 DR EMBL: X72561; CAAL0513.1;  
 KW NON\_TER 14  
 FT 14  
 SQ SEQUENCE 14 AA: 1722 MW: 9814656; HIRSL4A CRC64;

Query Match 27.3% Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSP 4  
 I  
 DB 2 KSP 4

## RESULT 47

Q06414 PRELIMINARY: PRT: 14 AA.  
 AC Q06414  
 DT 01-NOV-1999 (TRENBLREL. 10, Created)  
 DT 01-NOV-1999 (TRENBLREL. 10, Last sequence update)  
 DT 01-MAY-2002 (TRENBLREL. 20, Last annotation update)  
 DE MYO15: heavy chain, 2B (fragment)  
 OS Rattus norvegicus (rat)  
 OC Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;  
 OC Muridae; Murinae; Muridae; Muridae; Muridae; Muridae;  
 OX NCBI\_TaxID:10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE:epithelium;  
 RA MEDLINE:1046155; PubMed:1046155; PubMed:1046155;  
 RA BACKUS M., Schmitt M., Schmitt M., Schmitt M., Schmitt M.,  
 PI "Type 2A Myosin Heavy Chain" (S100L10), a muscle fiber type-specific  
 PI protein, is a member of the myosin heavy chain family.  
 RL J Biol Chem 271:11111-11116(1996).  
 DR EMBL: X72561; CAAL0513.1;  
 KW NON\_TER 14  
 FT 14  
 SQ SEQUENCE 14 AA: 1722 MW: 9814656; HIRSL4A CRC64;

Query Match 27.3% Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSP 4

Db 111  
2 KSR 4

## RESULT 48

005003 PRELIMINARY: PRT; 15 AA.  
AC O05003; Q52844;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DI 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Nodulation protein A, 3'END (Fragment) (Fragment).  
GN NODA.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN 11;  
RP SEQUENCE FROM N.A.  
RC STRAIN=NZB2213;  
RX MEDLINE=97002748; PubMed=8850088;  
RA Scott D.B., Young C.A., Collins-Emerson J.M., Terzaghi E.A.,  
RA Rockman E.S., Lewis P.E., Pankhurst C.E.,  
RT "Novel and complex chromosomal arrangement of Rhizobium loti  
RT nodulation genes".  
RL Mol. Plant Microbe Interact. 9:187-197(1996).  
DR EMBL: X65620; CAA46574.1; -;  
DR EMBL: X65620; CAA46573.1; -;  
DR InterPro: IPR003484; NODA.  
DR Pfam: PF02474; Noda; 1.  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1689 MW; 0A729663327794R1 CDS64;

Query Match 27.3%; Score 3; DB 2; Length 15;  
Best local similarity 100.0%; Pred. No. le+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKG 6  
111  
DB 10 RKG 12

## RESULT 49

Q81SC5 PRELIMINARY: PRT; 15 AA.  
AC Q81SC5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DI 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE FCR3 varC3A ligand (Fragment).  
GN VAR.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Kinetoplastida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN 11;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22096013; PubMed=12100556;  
RA Vazquez-Macias A., Martinez Cruz P., Castaneda-Correa M.A.,  
RA Scheidegger C., Gysin J., Schert A., Hernandez-Kirvas R.,  
RT "A distinct 5' flanking var gene region regulates Plasmodium  
RT falciparum variant erythrocyte surface antigen expression in placental  
RT malaria".  
RL Mol. Microbiol. 45:155-167(2002).  
DR EMBL: AY135378; AAN1318.1; -;  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1435 MW; 5DEC3C688309RF2E CDS64;

Query Match 27.3%; Score 3; DB 5; Length 15;  
Best local similarity 100.0%; Pred. No. le+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 3  
111

Db 111  
12 AKS 14

## RESULT 50

Q85C16 PRELIMINARY: PRT; 15 AA.  
AC Q85C16;  
DT 01-DEC-2001 (TrEMBLrel. 10, Created)  
DI 01-DEC-2001 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 10, Last annotation update)  
DE C215 (Fragment).  
GN C215 (Fragment).  
OS Rhizoglyphus sp. 10.  
OC Metazoa; Chordata; Vertebrata; Mammalia; Chiroptera; Chiroptera; Chiroptera;  
OC Eukaryota; Eumetazoa; Chordata; Vertebrata; Mammalia; Chiroptera; Chiroptera;  
OX NCBI\_TaxID=381;  
RN 11;  
RP SEQUENCE FROM N.A.  
RC STRAIN=10;  
PA Forquet L., Bost M., Bost V., Bost V., Bost V., Bost V., Bost V., Bost V.,  
PA "Hydrophobic interaction between a lipid molecule and a lipid molecule in a lipid molecule and an evolutionary link to the lipid molecule".  
RL Mol. Biol. Evol. 19:1000-1000;  
RN 12;  
RP SEQUENCE FROM N.A.  
RC STRAIN=10;  
RA Lang F., Bost V., Bost V., Bost V., Bost V., Bost V., Bost V., Bost V.,  
RL Submitted (10/10/01) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF043303; AAF04303.1;  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 15 AA; 1221 MW; 0A5551AD0B0AE CDS64;

Query Match 27.3%; Score 3; DB 5; Length 15;  
Best local similarity 100.0%; Pred. No. le+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKG 11  
111  
DB 4 RKG 1

Search completed: September 30, 2003, 10:04:14  
Job time: 38.6667 sec



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:05, Search time 11.8333 seconds  
(without alignments)  
39.331 Million cell updates/sec

## Title: US-09-787-443-21

Perfect score: 11

Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO  
Gapop 60.0, Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size: 0

Total number of hits satisfying chosen parameters: 72359

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

## Database:

- 1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles!.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	8	4	US-09-373-157-7
2	4	36.4	9	1	US-08-324-977-24
3	4	36.4	9	2	US-08-384-616-24
4	4	36.4	9	2	US-08-928-558-14
5	4	36.4	9	2	US-09-072-429-19
6	4	36.4	9	2	US-08-342-866A-8
7	4	36.4	9	2	US-08-904-646A-24
8	4	36.4	9	3	US-09-315-850-24
9	4	36.4	9	4	US-09-257-490-8
10	4	36.4	9	4	US-09-593-673A-58
11	4	36.4	10	2	US-08-564-972-71
12	4	36.4	11	4	US-09-381-545-48
13	4	36.4	13	3	US-08-836-075A-164
14	4	36.4	13	3	US-09-248-588-74
15	4	36.4	13	4	US-09-025-596-103
16	4	36.4	13	4	US-09-025-596-103
17	4	36.4	13	4	US-09-155-613A-11
18	4	36.4	13	4	US-09-073-661-101
19	4	36.4	13	4	US-09-073-661-103
20	4	36.4	14	3	US-08-879-565-7
21	4	36.4	14	4	US-09-330-245A-10
22	4	36.4	14	4	US-09-252-404A-21
23	4	36.4	15	2	US-08-616-844-45
24	4	36.4	15	2	US-08-650-262-10
25	4	36.4	15	2	US-08-599-658-45
26	4	36.4	15	3	US-08-944-868A-45
27	4	36.4	15	3	US-08-296-848A-2

15	3	US-08-296-848A-5	28	4	36.4	4	US-08-544-423A-45	Sequence 43, Appl 1
16	3	US-08-544-423A-45	29	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
17	3	US-08-544-423A-45	30	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
18	3	US-08-544-423A-45	31	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
19	3	US-08-544-423A-45	32	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
20	3	US-08-544-423A-45	33	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
21	3	US-08-544-423A-45	34	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
22	3	US-08-544-423A-45	35	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
23	3	US-08-544-423A-45	36	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
24	3	US-08-544-423A-45	37	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
25	3	US-08-544-423A-45	38	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
26	3	US-08-544-423A-45	39	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
27	3	US-08-544-423A-45	40	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
28	3	US-08-544-423A-45	41	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
29	3	US-08-544-423A-45	42	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
30	3	US-08-544-423A-45	43	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
31	3	US-08-544-423A-45	44	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
32	3	US-08-544-423A-45	45	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
33	3	US-08-544-423A-45	46	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
34	3	US-08-544-423A-45	47	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
35	3	US-08-544-423A-45	48	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
36	3	US-08-544-423A-45	49	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
37	3	US-08-544-423A-45	50	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
38	3	US-08-544-423A-45	51	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
39	3	US-08-544-423A-45	52	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
40	3	US-08-544-423A-45	53	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
41	3	US-08-544-423A-45	54	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
42	3	US-08-544-423A-45	55	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
43	3	US-08-544-423A-45	56	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
44	3	US-08-544-423A-45	57	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
45	3	US-08-544-423A-45	58	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
46	3	US-08-544-423A-45	59	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
47	3	US-08-544-423A-45	60	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
48	3	US-08-544-423A-45	61	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
49	3	US-08-544-423A-45	62	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
50	3	US-08-544-423A-45	63	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
51	3	US-08-544-423A-45	64	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
52	3	US-08-544-423A-45	65	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
53	3	US-08-544-423A-45	66	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
54	3	US-08-544-423A-45	67	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
55	3	US-08-544-423A-45	68	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
56	3	US-08-544-423A-45	69	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
57	3	US-08-544-423A-45	70	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
58	3	US-08-544-423A-45	71	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
59	3	US-08-544-423A-45	72	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
60	3	US-08-544-423A-45	73	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
61	3	US-08-544-423A-45	74	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
62	3	US-08-544-423A-45	75	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
63	3	US-08-544-423A-45	76	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
64	3	US-08-544-423A-45	77	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
65	3	US-08-544-423A-45	78	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
66	3	US-08-544-423A-45	79	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
67	3	US-08-544-423A-45	80	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
68	3	US-08-544-423A-45	81	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
69	3	US-08-544-423A-45	82	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
70	3	US-08-544-423A-45	83	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
71	3	US-08-544-423A-45	84	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
72	3	US-08-544-423A-45	85	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
73	3	US-08-544-423A-45	86	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
74	3	US-08-544-423A-45	87	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
75	3	US-08-544-423A-45	88	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
76	3	US-08-544-423A-45	89	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
77	3	US-08-544-423A-45	90	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
78	3	US-08-544-423A-45	91	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
79	3	US-08-544-423A-45	92	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
80	3	US-08-544-423A-45	93	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
81	3	US-08-544-423A-45	94	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
82	3	US-08-544-423A-45	95	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
83	3	US-08-544-423A-45	96	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
84	3	US-08-544-423A-45	97	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
85	3	US-08-544-423A-45	98	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
86	3	US-08-544-423A-45	99	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1
87	3	US-08-544-423A-45	100	4	36.4	4	US-08-544-423A-45	Sequence 45, Appl 1

101	3	27.3	8	3	US-08-582-7760-20	Sequence 20, Appl	27.3	1	US-08-259-441A-4	Sequence 1, Appl
102	3	27.3	8	3	US-09-136-218-10	Sequence 10, Appl	27.3	1	US-08-277-187-2	Sequence 2, Appl
103	3	27.3	8	3	US-08-726-807B-16	Sequence 16, Appl	27.3	1	US-08-217-188A-19	Sequence 19, Appl
104	3	27.3	8	3	US-09-234-163-10	Sequence 10, Appl	27.3	1	US-08-255-456A-9	Sequence 9, Appl
105	3	27.3	8	3	US-08-434-831B-20	Sequence 20, Appl	27.3	1	US-08-256-85A-14	Sequence 14, Appl
106	3	27.3	8	3	US-08-444-618-409	Sequence 409, Appl	27.3	1	US-08-255-805A-24	Sequence 24, Appl
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; NAME: Stevens-Smith, Theresa M.
; REGISTRATION NUMBER: 36,281
; REFERENCE/DOCKET NUMBER: 9007030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-324-977-24

```

```

Query Match 36.4% Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 GNSS 9
Db 4 GNSS 7

```

```

RESULT 3
US-08-384-616-24
; Sequence 24, Application US/08384616
; Patent No. 5847101

```

```

; GENERAL INFORMATION:
; APPLICANT: OKAYAMA, Hiroto
; APPLICANT: FURE, Isao
; APPLICANT: MORI, Chisato
; APPLICANT: TAKAMIZAWA, Akaishi
; APPLICANT: YOSHIDA, Iwao
; TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
; TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armsstrong, Westerman, Hattori, McDaniel &
; ADDRESSEE: Naughton
; STREET: 1725 K St. N.W. Suite 1000
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,977
; FILING DATE: 18-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-167466
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-305605
; FILING DATE: 09-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/769,996
; FILING DATE: 02-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/635,451
; FILING DATE: 28-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens-Smith, Theresa M.
; REGISTRATION NUMBER: 36,281
; REFERENCE/DOCKET NUMBER: 9007030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-384-616-24

```

```

Query Match 36.4% Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 GNSS 9
Db 4 GNSS 7

```

```

RESULT 4
US-08-928-958-19
; Sequence 19, Application US/08928958
; Patent No. 5877282
; GENERAL INFORMATION:
; APPLICANT: NADEAU, STEVEN J.
; APPLICANT: CLEVELAND, JEFFERY S.
; APPLICANT: BLAKE, JAMES

```

APPLICANT: HAFAR, OMAR K.  
 TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
 TITLE OF INVENTION: METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ROBINS & ASSOCIATES  
 STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
 CITY: MENLO PARK  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/928,958  
 FILING DATE: 12-SEP-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/026978  
 FILING DATE: 20-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBINS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 5998-0019  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 325-7812  
 TELEFAX: (650) 325-7823  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-928-958-19

Query Match 36.4%, Score 4; LR 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2, 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Inp-Is 0; Gaps 0

Oy 2 KSRK 5  
 Db 1111  
 3 KSRK 6

RESULT 5  
 US-09 072 429-19  
 Sequence 19, Application US/09072429  
 Patent No. 5962415  
 GENERAL INFORMATION:  
 APPLICANT: Nadler, Steven G.  
 TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
 TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLLOCATION AND AN  
 TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bristol-Myers Squibb Company  
 STREET: P.O. Box 4000  
 CITY: Princeton  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 08543-4000  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/072,429

FILING DATE: 4 MAY 1996  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KROTH, CLAUDIA L.  
 REGISTRATION NUMBER: 41,000  
 REFERENCE/DOCKET NUMBER: 5998-0019  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 325-7812  
 TELEFAX: (650) 325-7823  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-072-429-19  
 Query Match 36.4%, Score 4; LR 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2, 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Inp-Is 0; Gaps 0  
 Oy 2 KSRK 5  
 Db 1111  
 3 KSRK 6  
 RESULT 6  
 US-08-928-958-19  
 Sequence 19, Application US/08-928-958-19  
 Patent No. 5962415  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: TRANSLLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
 TITLE OF INVENTION: METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ROBINS & ASSOCIATES  
 STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
 CITY: MENLO PARK  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/928,958  
 FILING DATE: 12-SEP-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/026978  
 FILING DATE: 20-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBINS, ROBERTA L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 5998-0019  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 325-7812  
 TELEFAX: (650) 325-7823  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-928-958-19

Db 6 KGNS 9

## RESULT 7

US-08-904-686A-24  
: Sequence 24, Application US/08904686A  
: Patent No. 5998130  
: GENERAL INFORMATION:  
: APPLICANT: OKAYAMA, Hiroo  
: APPLICANT: FUKU, Isao  
: APPLICANT: MORI, Chisato  
: APPLICANT: TAKAMIZAWA, Akahisa  
: APPLICANT: YOSHIDA, Iwao  
: TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
: TITLE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE  
: NUMBER OF SEQUENCES: 50  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Armstrong, Westerman, Hattori, McLeod &  
: STREET: 1725 K St. N.W. Suite 1030  
: CITY: Washington  
: STATE: D.C.  
: COUNTRY: U.S.A.  
: ZIP: 20006  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0  
: SOFTWARE: ASCII  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/904,686A  
: FILING DATE: 01-AUG-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/324,977  
: FILING DATE: 18-OCT-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-167466  
: FILING DATE: 25-JUN-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-230921  
: FILING DATE: 31-AUG-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-305605  
: FILING DATE: 09-NOV-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/099,706  
: FILING DATE: 30-JUL-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/769,996  
: FILING DATE: 02-OCT-1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/635,451  
: FILING DATE: 28-DEC-1990  
: ATTORNEY/AGENT INFORMATION:  
: NAME: McLeod, Le-Nhung  
: REGISTRATION NUMBER: 31,541  
: REFERENCE/DOCKET NUMBER: 900703G  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 659-2910  
: TELEFAX: (202) 887-0357  
: INFORMATION FOR SEQ ID NO: 24:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 9 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US-08-904-686A-24

Query Match 36.4%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 6 GNSS 9

Db 4 GNSS 7

RESULT 8  
US-09-415-850-24  
: Sequence 24, Application US/09415850  
: Patent No. 6219624  
: GENERAL INFORMATION:  
: APPLICANT: OKAYAMA, Hiroo  
: APPLICANT: FUKU, Isao  
: APPLICANT: MORI, Chisato  
: APPLICANT: TAKAMIZAWA, Akahisa  
: APPLICANT: YOSHIDA, Iwao  
: TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC  
: TITLE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE  
: NUMBER OF SEQUENCES: 50  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Armstrong, Westerman, Hattori, McLeod &  
: STREET: 1725 K St. N.W. Suite 1030  
: CITY: Washington  
: STATE: D.C.  
: COUNTRY: U.S.A.  
: ZIP: 20006  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0  
: SOFTWARE: ASCII  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/415,850A  
: FILING DATE:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/09/904,686A  
: FILING DATE: 01-AUG-1997  
: APPLICATION NUMBER: US 08/324,977  
: FILING DATE: 18-OCT-1994  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-167466  
: FILING DATE: 25-JUN-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 2-230921  
: FILING DATE: 31-AUG-1990  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/099,706  
: FILING DATE: 30-JUL-1993  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/769,996  
: FILING DATE: 02-OCT-1991  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 07/635,451  
: FILING DATE: 28-DEC-1990  
: ATTORNEY/AGENT INFORMATION:  
: NAME: McLeod, Le-Nhung  
: REGISTRATION NUMBER: 31,541  
: REFERENCE/DOCKET NUMBER: 900703G  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 659-2910  
: TELEFAX: (202) 887-0357  
: INFORMATION FOR SEQ ID NO: 24:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 9 amino acids  
: TYPE: amino acid  
: TOPOLOGY: linear  
: MOLECULE TYPE: protein  
US 09-415-850 24

Query Match 46.4%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

```

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 6 GNSS 9
Db 4 GNSS 7

RESULT 9
US-09-257-490 8
: Sequence 8, Application US/09/257490A
: Patent No. 6248328
: GENERAL INFORMATION
: APPLICANT: Dietrich, Ursula
: APPLICANT: Von Briesen, Hagen
: APPLICANT: Grez, Manuel
: APPLICANT: Rubsamen-Waigmann, Beiga
: TITLE OF INVENTION: HIV-1 virus isolates of a subtype and its 4 Diagnostic
: TITLE OF INVENTION: diagnostics, a vaccine against HIV-1 virus isolates
: TITLE OF INVENTION: of this subtype and method of producing same
: TITLE OF INVENTION: the HIV-1 virus isolates
: FILE REFERENCE: 10496/P58512051
: CURRENT APPLICATION NUMBER: US/09/257-490A
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 8
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus
US-09-257-490-8

Query Match 36.4% Score 4: 18 4: Length 9;
Best Local Similarity 100.0% Pred. No. 2.5e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 5 GNSS 8
Db 6 GNSS 9

RESULT 10
US-09-593-870A-58
: Sequence 58, Application US/09/593870A
: Patent No. 6548643
: GENERAL INFORMATION
: APPLICANT: McKenzie, Ian F.C.
: APPLICANT: Apostolopoulos, Vasso
: APPLICANT: Pictersz, Geoff Allan
: TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
: TITLE OF INVENTION: Use in Immunotherapy
: FILE REFERENCE: 2368-McKenzie
: CURRENT APPLICATION NUMBER: US/09/593,870A
: PRIOR FILING DATE: 2000-06-14
: CURRENT FILING DATE: 1998-12-30
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: FastSeq for Windows Version: 3.0
: SEQ ID NO 58
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-593-870A-58

Query Match 36.4% Score 4: 18 4: Length 9;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 7 NSSL 10
Db 1 NSSL 4

RESULT 11

```

```

US-09-787-443-21
: Sequence 787, Application US/09/787443-21
: Patent No. 6548643
: GENERAL INFORMATION
: APPLICANT: McKenzie, Ian F.C.
: APPLICANT: Apostolopoulos, Vasso
: APPLICANT: Pictersz, Geoff Allan
: TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
: TITLE OF INVENTION: Use in Immunotherapy
: FILE REFERENCE: 2368-McKenzie
: CURRENT APPLICATION NUMBER: US/09/787,443-21
: PRIOR FILING DATE: 2000-06-14
: CURRENT FILING DATE: 1998-12-30
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: Patent In Ver. 2.1
US-09-787-443-21

Query Match 36.4% Score 4: 18 4: Length 10;
Best Local Similarity 100.0% Pred. No. 1.8e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0
QY 6 NSSL 11
Db 6 NSSL 7

RESULT 12
US-09-593-870A-58
: Sequence 48, Application US/09/593870A
: Patent No. 6548643
: GENERAL INFORMATION
: APPLICANT: McKenzie, Ian F.C.
: APPLICANT: Apostolopoulos, Vasso
: APPLICANT: Pictersz, Geoff Allan
: TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
: TITLE OF INVENTION: Use in Immunotherapy
: FILE REFERENCE: 2368-McKenzie
: CURRENT APPLICATION NUMBER: US/09/593,870A
: PRIOR FILING DATE: 2000-06-14
: CURRENT FILING DATE: 1998-12-30
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: Patent In Ver. 2.1
US-09-593-870A-58

```



```

; SEQ ID NO 48
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acids
; OTHER INFORMATION: encoded by bases 921-956 of pBKX-3X
US-09-391-546-48

Query Match          36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2, 4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9
    IIII
DB 8 GNSS 11

RESULT 13
US-08-836-075A-164
; Sequence 164; Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS A VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; NUMBER OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DUKREE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836.075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-075A-164

Query Match          36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2, 4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9
    IIII
DB 4 GNSS 7

```

```

RESULT 14
US-09-218-586-74
; Sequence 74; Application US/09218586
; Patent No. 621864
; GENERAL INFORMATION:
; APPLICANT: MITCHELL, WILLIAM M
; TITLE OF INVENTION: HEPATITIS B CORE PROTEINS AND
; TITLE OF INVENTION: POLYPEPTIDES
; TITLE OF INVENTION: SYNTHETIC ANALOGS
; CURRENT APPLICATION NUMBER: US/09218586
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: US/97-04-04
; EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQUENCES: 1
; SOFTWARE: FASTSEQ FOR WINDOWS Version 1.3
; SEQ ID NO: 74
; LENGTH: 14
; ORGANISM: Artificial Sequence
US-09-218-586-74

Query Match          36.4%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2, 4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 4
    III
DB 6 ASK 9

```

```

RESULT 15
US-09-025-596-14
; Sequence 103; Application US/09025596
; Patent No. 634464
; GENERAL INFORMATION:
; APPLICANT: MITCHELL, WILLIAM M
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: IDENTIFICATION OF ANTI-HEPATIC PERITHE
; TITLE OF INVENTION: SEQUENCES
; FILE REFERENCE NUMBER:
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: US/97-04-04
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: EP/97-04-04
; EARLIER FILING DATE: 1997-04-04
; NUMBER OF SEQUENCES: 1
; SOFTWARE: FASTSEQ FOR WINDOWS Version 1.3
; SEQ ID NO: 103
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-025-596-14

Query Match          36.4%; Score 4; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2, 4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSK 5
    IIII
DB 7 KSK 10

```

```

RESULT 16
US-09-025-596-14
; Sequence 103; Application US/09025596
; Patent No. 634464
; GENERAL INFORMATION:
; APPLICANT: MITCHELL, WILLIAM M
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: IDENTIFICATION OF ANTI-HEPATIC PERITHE
; TITLE OF INVENTION: SEQUENCES

```

FILE REFERENCE: VDB98-01  
 CURRENT APPLICATION NUMBER: US/09/025,596  
 EARLIER FILING DATE: 1998-02-18  
 EARLIER APPLICATION NUMBER: 08/911,593  
 EARLIER FILING DATE: 1997-08-14  
 EARLIER APPLICATION NUMBER: 60/023,921  
 EARLIER FILING DATE: 1996-08-14  
 NUMBER OF SEQ ID NOS: 118  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 103  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Chlamydia trachomatis  
 US-09-025,596-103

Query Match 36.4% Score 4: Db 4: Length 13  
 Best Local Similarity 100.0% Pred. No. 2,400,621  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KSKK 5  
 Db 7 KSKK 10

## RESULT 17

US-09-155-613A-11  
 Sequence 11: Application US/09155613A  
 Patent No. 6420120  
 GENERAL INFORMATION:  
 APPLICANT: Boulanger, Pierre  
 APPLICANT: Hong, Saw See  
 APPLICANT: Karayan, Lucie  
 TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
 FILE REFERENCE: 032751-036  
 CURRENT APPLICATION NUMBER: US/09/155,613A  
 CURRENT FILING DATE: 1998-09-30  
 PRIOR APPLICATION NUMBER: PCT/FR98/00184  
 PRIOR FILING DATE: 1998-01-30  
 PRIOR APPLICATION NUMBER: FR 97/01005  
 PRIOR FILING DATE: 1997-01-30  
 PRIOR APPLICATION NUMBER: FR 97/11166  
 PRIOR FILING DATE: 1997-09-09  
 NUMBER OF SEQ ID NOS: 98  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 11  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Mastadenovirus, serotype 2  
 US-09-155-613A-11

Query Match 36.4% Score 4: Db 4: Length 13  
 Best Local Similarity 100.0% Pred. No. 2,400,621  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
 Db 1 NSSL 4

## RESULT 18

US-09-074,661-101  
 Sequence 101: Application US/04073661  
 Patent No. 6579854  
 GENERAL INFORMATION:  
 APPLICANT: Mitchell, William M.  
 APPLICANT: Stratton, Charles W.  
 TITLE OF INVENTION: DIAGNOSIS AND MANAGEMENT OF  
 TITLE OF INVENTION: INFECTION CAUSED BY CHLAMYDIA  
 NUMBER OF SEQUENCES: 114  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington

STATE: MA  
 COUNTRY: USA  
 ZIP: 02174  
 COMPLETE RECIPIENT: 1  
 MEDIUM TYPE: 1  
 MODIFIED: 1  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FASTSEQ 3.0  
 CURRENT FILING DATE: 1998-09-30  
 APPLICATION NUMBER: US/09/155,613A  
 FILING DATE: 1998-09-30  
 CLASSIFICATION: 1  
 PRIOR APPLICATION: 1  
 APPLICATION NUMBER: 08/911,593  
 FILING DATE: 1997-08-14  
 APPLICATION NUMBER: 60/023,921  
 FILING DATE: 1996-08-14  
 APPLICATION NUMBER: 03/275,103  
 FILING DATE: 1998-09-30  
 APPLICATION NUMBER: US/09/155,613A  
 FILING DATE: 1998-09-30  
 APPLICATION NUMBER: PCT/FR98/00184  
 FILING DATE: 1998-01-30  
 APPLICATION NUMBER: FR 97/01005  
 FILING DATE: 1997-01-30  
 APPLICATION NUMBER: FR 97/11166  
 FILING DATE: 1997-09-09  
 NUMBER OF SEQ ID NOS: 98  
 SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0  
 SEQ ID NO 11  
 LENGTH: 13  
 TYPE: PRT  
 ORGANISM: Mastadenovirus, serotype 2  
 US-09-155-613A-11  
 NAME: GILL, J. A.  
 REGISTRATION NUMBER: 38,012  
 REFERENCE/INVENTION NUMBER: 9,607,946M  
 INTERNATIONAL INFORMATION:  
 TELEPHONE: 01-617-443-1443  
 TELEFAX: 01-617-443-1443  
 TELETYPE: 01-617-443-1443  
 INVENTION FOR SEQ ID NO 11  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MEDIUM TYPE: liquid  
 US 09 025,596-103  
 Query Match 36.4% Score 4: Db 4: Length 13  
 Best Local Similarity 100.0% Pred. No. 2,400,621  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 2 KSKK 5  
 Db 7 KSKK 10  
 RESULT 19  
 US-09-074,661-101  
 Sequence 101: Application US/04073661  
 Patent No. 6579854  
 GENERAL INFORMATION:  
 APPLICANT: Mitchell, William M.  
 APPLICANT: Stratton, Charles W.  
 TITLE OF INVENTION: DIAGNOSIS AND MANAGEMENT OF  
 TITLE OF INVENTION: INFECTION CAUSED BY CHLAMYDIA  
 NUMBER OF SEQUENCES: 114  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington

STREET: Two Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/073,661  
FILING DATE: 06-MAY-1998  
CLASSIFICATION: 436

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/025,521  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: US 08/911,594  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 60/023,921  
FILING DATE: 14-AUG-1996  
APPLICATION NUMBER: US 09/025,176  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: US 09/025,174  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: US 60/045,739  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,779  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,780  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,784  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,787  
FILING DATE: 6-MAY-1997  
APPLICATION NUMBER: US 60/045,689  
FILING DATE: 6-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Carroll, Alice O  
REGISTRATION NUMBER: 33,542  
REFERENCE/DOCKET NUMBER: VDB97-09pm  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 781-861-6240  
TELEFAX: 781-861-9540  
TELEX:

INFORMATION FOR SEQ ID NO: 103:

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-073-661-103

Query Match 36.4% Score 4: 10: 4: Length 13:  
Best Local Similarity 100.0% Pred. No. 2: 3: 0: 2:  
Matches 4: Conservative 0: Mismatches 0: Labels 0: Gaps 0:

QY 2 KSRK 5  
DB 7 KSRK 10

RESULT 20  
US-08-879-565-7  
Sequence 7, Application US/08879565A  
Patent No. 6093573  
GENERAL INFORMATION:  
APPLICANT: Beamer, Lesa J  
APPLICANT: Carroll, Stephen F  
APPLICANT: Eisenberg, David  
TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF  
BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN

FILE REFERENCED: US/09/073,661  
CURRENT APPLICATION NUMBER: US/09/073,661A  
CURRENT FILING DATE: 06-MAY-1998  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent 16: 10: 1:  
SEQ ID NO: 7  
LENGTH: 14  
TYPE: PR  
ORGANISM: Human  
FEATURES:  
OTHER INFORMATION: "FastSeq" made available sequence of residues  
OTHER INFORMATION: "FASTSEQ" made available sequence of residues  
US 08-879-565-7

Query Match 36.4% Score 4: 10: 4: Length 14:  
Best Local Similarity 100.0% Pred. No. 2: 3: 0: 2:  
Matches 4: Conservative 0: Mismatches 0: Labels 0: Gaps 0:

QY 7 KSRK 5  
DB 2 KSRK 5

RESULT 21  
US 09-433-245A-10  
Sequence 10, Application US/09-433-245A  
Patent No. 6442661  
GENERAL INFORMATION:  
APPLICANT: ELFAF STEPHEN, NICHOLAS  
TITLE OF INVENTION: LEVEL DEPENDENT IN: PEANUT ALLERGEN  
FILE REFERENCED: US/09-433-245A  
CURRENT APPLICATION NUMBER: US/09-433-245A  
CURRENT FILING DATE: 09-04-1998  
PRIOR APPLICATION NUMBER: 60/104,861  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: 60/104,263  
PRIOR FILING DATE: 1998-04-13  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patent 16: 10: 1:  
SEQ ID NO: 10  
LENGTH: 14  
TYPE: PR  
ORGANISM: Unknown  
FEATURES:  
OTHER INFORMATION: "FastSeq" made available sequence of residues  
OTHER INFORMATION: "FASTSEQ" made available sequence of residues  
US 09-433-245A-10

Query Match 36.4% Score 4: 10: 4: Length 14:  
Best Local Similarity 100.0% Pred. No. 2: 3: 0: 2:  
Matches 4: Conservative 0: Mismatches 0: Labels 0: Gaps 0:

QY 7 KSRK 5  
DB 7 KSRK 10

RESULT 22  
US 09-252-404A-21  
Sequence 21, Application US/09-252-404A  
Patent No. 6455376  
GENERAL INFORMATION:  
APPLICANT: KIM PING LO  
APPLICANT: XIAO ZHEN ZHOU  
TITLE OF INVENTION: METHODS and Compositions for Regulating  
TITLE OF INVENTION: Protein-Protein Interactions  
FILE REFERENCED: 1440,134 US  
CURRENT APPLICATION NUMBER: US/09/252,404A  
CURRENT FILING DATE: 1999-02-18  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 21  
LENGTH: 14

? TYPE: PRT  
? ORGANISM: Synthetic peptide  
US-09-252-404-21

Query Match 36.4% Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2, 50, 02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
|||||  
DB 11 AKSR 14

## RESULT 23

US-08-616-844-45  
? Sequence 45, Application US/08616844  
? Patent No. 5849578  
? GENERAL INFORMATION:  
? APPLICANT: FALH, DEAN A.  
? TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
? TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
? NUMBER OF SEQUENCES: 54  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: PENNIE & EDMONDS  
? STREET: 1155 Avenue of the Americas  
? CITY: New York  
? STATE: New York  
? COUNTRY: USA  
? ZIP: 10016-2711  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? OPERATING SYSTEM: IBM PC compatible  
? SOFTWARE: Patent Release #1.0, Version #1.30  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: US/08/616,844  
? FILING DATE: 15-MAR-1996  
? CLASSIFICATION: 800  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US 08/599,654  
? FILING DATE: 09-FEB-1996  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US 08/485,573  
? FILING DATE: 07-JUN-1995  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US 08/386,844  
? FILING DATE: 10-FEB-1995  
? ATTORNEY/AGENT INFORMATION:  
? NAME: CORUZZI, LAURA A.  
? REGISTRATION NUMBER: 30,742  
? REFERENCE/DOCKET NUMBER: 7853-053  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: (212) 790-9090  
? TELEFAX: (212) 869-8864  
? INFORMATION FOR SEQ ID NO: 45:  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 15 amino acids  
? TYPE: amino acid  
? STRANDEDNESS:  
? TOPOLOGY: unknown  
? MOLECULE TYPE: peptide  
US-08-616-844-45

Query Match 36.4% Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2, 70, 02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
|||||  
DB 9 AKSR 12

RESULT 24  
US-08-650-262-10  
? Sequence 16, Application US/08650262  
? Patent No. 5866124  
? GENERAL INFORMATION:  
? APPLICANT: BORDO, NANCY ZILMAN  
? APPLICANT: PUSLAK, BOB  
? APPLICANT: MURRAY, SCOTT  
? TITLE OF INVENTION: Method for controlling antibodies  
? NUMBER OF SEQUENCES: 2  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: NANCY ZILMAN & CORPORATION  
? STREET: 60 BROAD  
? CITY: East Rutherford  
? STATE: NJ  
? COUNTRY: USA  
? ZIP: 07073-4100  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? OPERATING SYSTEM: IBM PC compatible  
? SOFTWARE: Patent Release #1.0, Version #1.30  
? CURRENT APPLICATION DATA:  
? APPLICATION NUMBER: US/08/650,262  
? FILING DATE:  
? CLASSIFICATION: 114  
? PRIOR APPLICATION DATA:  
? APPLICATION NUMBER: US/08/650,262  
? FILING DATE: 17-MAR-1996  
? ATTORNEY/AGENT INFORMATION:  
? NAME: BORDO, NANCY ZILMAN  
? REGISTRATION NUMBER: 30,742  
? REFERENCE/DOCKET NUMBER: 5, 10, 06, 06  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: 908-277-6110  
? TELEFAX: 908-277-6100  
? INFORMATION FOR SEQ ID NO: 16:  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 15 amino acids  
? TYPE: amino acid  
? STRANDEDNESS:  
? MOLECULE TYPE: peptide  
? HYDROPHATIC: NO  
US-08-650-262-10

Query Match 36.4% Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2, 70, 02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKSR 11  
|||||  
DB 11 AKSR 14

## RESULT 25

US-08-599-654-45  
? Sequence 45, Application US/08659654  
? Patent No. 5862426  
? GENERAL INFORMATION:  
? APPLICANT: FALH, DEAN A.  
? TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
? TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
? NUMBER OF SEQUENCES: 54  
? CORRESPONDENCE ADDRESS:  
? ADDRESSEE: PENNIE & EDMONDS  
? STREET: 1155 Avenue of the Americas  
? CITY: New York  
? STATE: New York  
? COUNTRY: USA  
? ZIP: 10016-2711  
? COMPUTER READABLE FORM:  
? MEDIUM TYPE: Floppy disk  
? COMPUTER: IBM PC compatible  
US-08-599-654-45

1 OPERATING SYSTEM: PC-DOS/MS-DOS  
 2 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 3 CURRENT APPLICATION DATA:  
 4 APPLICATION NUMBER: US/08/599,654  
 5 FILING DATE: 09-FEB-1995  
 6 CLASSIFICATION: 800  
 7 PRIOR APPLICATION DATA:  
 8 APPLICATION NUMBER: US 08/485,574  
 9 FILING DATE: 07-JUN-1995  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: US 08/386,844  
 12 FILING DATE: 10-FEB-1995  
 13 ATTORNEY/AGENT INFORMATION:  
 14 NAME: CORUZZI, LAURA A  
 15 REGISTRATION NUMBER: 30,742  
 16 REFERENCE/DOCKET NUMBER: 7853-641  
 17 TELEPHONE: (212) 790-9090  
 18 TELEFAX: (212) 869-8864  
 19 TELEX: 66141 PENNIE  
 20 INFORMATION FOR SEQ ID NO: 45:  
 21 SEQUENCE CHARACTERISTICS:  
 22 LENGTH: 15 amino acids  
 23 TYPE: amino acid  
 24 STRANDEDNESS:  
 25 TOPOLOGY: unknown  
 26 MOLECULE TYPE: peptide  
 27 US-08-599-654-45

Query Match 36.4% Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2 7a+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKRS 4  
 DB 9 AKRS 12

## RESULT 26

US-08-944-868A-45  
 1 Sequence 45, Application US/08944868A  
 2 Patent No. 6018025  
 3 GENERAL INFORMATION:  
 4 APPLICANT: FALB, DEAN A  
 5 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 6 TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
 7 NUMBER OF SEQUENCES: 34  
 8 CORRESPONDENCE ADDRESS:  
 9 ADDRESSEE: PENNIE & EDMONDS  
 10 STREET: 1155 Avenue of the Americas  
 11 CITY: New York  
 12 STATE: New York  
 13 COUNTRY: USA  
 14 ZIP: 10036-2711  
 15 COMPUTER READABLE FORM:  
 16 MEDIUM TYPE: Floppy disk  
 17 COMPUTER: IBM PC compatible  
 18 OPERATING SYSTEM: PC-DOS/MS-DOS  
 19 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 20 CURRENT APPLICATION DATA:  
 21 APPLICATION NUMBER: US/08/944,868A  
 22 FILING DATE:  
 23 CLASSIFICATION:  
 24 PRIOR APPLICATION DATA:  
 25 APPLICATION NUMBER: 08/599,654  
 26 FILING DATE:  
 27 PRIOR APPLICATION DATA:  
 28 APPLICATION NUMBER: US 08/386,844  
 29 FILING DATE: 10-FEB-1995  
 30 ATTORNEY/AGENT INFORMATION:  
 31 NAME: CORUZZI, LAURA A  
 32 REGISTRATION NUMBER: 30,742  
 33 REFERENCE/DOCKET NUMBER: 7853-041

1 OPERATING SYSTEM: PC-DOS/MS-DOS  
 2 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 3 CURRENT APPLICATION DATA:  
 4 APPLICATION NUMBER: US/08/599,654  
 5 FILING DATE: 09-FEB-1995  
 6 CLASSIFICATION: 800  
 7 PRIOR APPLICATION DATA:  
 8 APPLICATION NUMBER: US 08/485,574  
 9 FILING DATE: 07-JUN-1995  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: US 08/386,844  
 12 FILING DATE: 10-FEB-1995  
 13 ATTORNEY/AGENT INFORMATION:  
 14 NAME: CORUZZI, LAURA A  
 15 REGISTRATION NUMBER: 30,742  
 16 REFERENCE/DOCKET NUMBER: 7853-641  
 17 TELEPHONE: (212) 790-9090  
 18 TELEFAX: (212) 869-8864  
 19 TELEX: 66141 PENNIE  
 20 INFORMATION FOR SEQ ID NO: 45:  
 21 SEQUENCE CHARACTERISTICS:  
 22 LENGTH: 15 amino acids  
 23 TYPE: amino acid  
 24 STRANDEDNESS:  
 25 TOPOLOGY: unknown  
 26 MOLECULE TYPE: peptide  
 27 US-08-599-654-45  
 28 Query Match 36.4% Score 4; DB 2; Length 15;  
 29 Best Local Similarity 100.0%; Pred. No. 2 7a+02;  
 30 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKRS 4  
 DB 9 AKRS 12



: NAME: CORUZZI, LAURA A  
 : REGISTRATION NUMBER: 30,742  
 : REFERENCE/DOCKET NUMBER: 7853-104  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212) 790-9090  
 : TELEFAX: (212) 869-8864  
 : TELFX: 66141 PENNIE  
 : INFORMATION FOR SEQ ID NO: 45:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 15 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS:  
 : TOPOLOGY: unknown  
 : MOLECULE TYPE: peptide  
 : US-09-944-496-45

Query Match 36.4% Score 4: DB 3: Length 15:  
 Best Local Similarity 100.0% Pred. No. 2.7e+02  
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

Qy 1 AKSR 4  
 Db 9 AKSR 12

RESULT 31  
 US-09-365-530-2  
 : Sequence 2, Application US/09365530  
 : Patent No. 6440423  
 : GENERAL INFORMATION:  
 : APPLICANT: Clements, John D.  
 : APPLICANT: Dickinson, Bonny L.  
 : TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE AS A  
 : TITLE OF INVENTION: NON-TOXIC ORAL ADJUVANT  
 : NUMBER OF SEQUENCES: 5  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: PENNIE & EDMONDS LLP  
 : STREET: 1155 Avenue of the Americas  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: U.S.A.  
 : ZIP: 10036  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/365,530  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/296,848  
 : FILING DATE: 26-AUG-1994  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MISTOCK, S. Leslie  
 : REGISTRATION NUMBER: 18,872  
 : REFERENCE/DOCKET NUMBER: 5113-046  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212) 790-9090  
 : TELEFAX: (212) 869-8864/9741  
 : TELEX: 66141 PENNIE  
 : INFORMATION FOR SEQ ID NO: 2:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 15 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-09-365-530-2

Query Match 36.4% Score 4: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 2.7e+02  
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

Qy 1 AKSR 7  
 Db 4 AKSR 6  
 RESULT 32  
 US-09-365-530-5  
 : Sequence 5, Application US/09365530  
 : Patent No. 6440423  
 : GENERAL INFORMATION:  
 : APPLICANT: Clements, John D.  
 : APPLICANT: Dickinson, Bonny L.  
 : TITLE OF INVENTION: MUTANT ENTEROTOXIN EFFECTIVE AS A  
 : TITLE OF INVENTION: NON-TOXIC ORAL ADJUVANT  
 : NUMBER OF SEQUENCES:  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: PENNIE & EDMONDS LLP  
 : STREET: 1155 Avenue of the Americas  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: U.S.A.  
 : ZIP: 10036  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/365,530  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/296,848  
 : FILING DATE: 26-AUG-1994  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MISTOCK, S. Leslie  
 : REGISTRATION NUMBER: 18,872  
 : REFERENCE/DOCKET NUMBER: 5113-046  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212) 790-9090  
 : TELEFAX: (212) 869-8864/9741  
 : TELEX: 66141 PENNIE  
 : INFORMATION FOR SEQ ID NO: 5:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 15 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-09-365-530-5

Query Match 36.4% Score 4: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 2.7e+02  
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

Qy 1 AKSR 7  
 Db 4 AKSR 6

RESULT 33  
 US-09-365-530-9  
 : Sequence 9, Application US/09365530  
 : Patent No. 6440423  
 : GENERAL INFORMATION:  
 : APPLICANT: KACHAPERADZE, Arthur  
 : TITLE OF INVENTION: LOCALIZATION OF MAJOR PEPTIDE AUTOANTIGENS FOR SYSTEMIC LUPUS ERYTHEMATOSUS  
 : TITLE OF INVENTION: LOCALIZATION OF SYSTEMIC LUPUS ERYTHEMATOSUS  
 : FILE REFERENCE: 290-1007-13462-6917  
 : CURRENT APPLICATION NUMBER: US/09/365,530  
 : CURRENT FILING DATE: 2000-04-28  
 : PRIOR APPLICATION NUMBER: US 607,314,448

; PRIOR FILING DATE: 1999-04-28  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 9  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Histone fragment  
 US-09-561-490E-9

Query Match 36.4%; Score 4; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RKN 7  
 DB 2 RKN 5

RESULT 34  
 PCT-US93-06751-7  
 ; Sequence 7, Application PC/TUS9306751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: P. Keller, A. J. Conley, A. R. Shaw, B. A. Arnold  
 ; TITLE OF INVENTION: Immunological Conjugates of OMPG and  
 ; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization and Eptitopes  
 ; NUMBER OF SEQUENCES: 146  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/06751  
 ; FILING DATE: 19930719  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meredith, Roy D.  
 ; REGISTRATION NUMBER: 30,777  
 ; REFERENCE/DOCKET NUMBER: 18614  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908) 594-4678  
 ; TELEFAX: (908) 594-4720  
 ; TELEX: 138825  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; IMMEDIATE SOURCE: Random Epitope Library Alpha

PCT-US93-06751-7  
 Query Match 36.4%; Score 4; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
 DB 4 GNSS 7

RESULT 35  
 PCT-US93-06751-4  
 ; Sequence 46, Application PC/TUS9306751  
 ; GENERAL INFORMATION:  
 ; APPLICANT: P. Keller, A. J. Conley, A. R. Shaw, B. A. Arnold  
 ; TITLE OF INVENTION: Immunological Conjugates of OMPG and  
 ; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization and Eptitopes  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merck & Co., Inc.  
 ; STREET: P.O. Box 2000  
 ; CITY: Rahway  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07065  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/06751  
 ; FILING DATE: 19930719  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meredith, Roy D.  
 ; REGISTRATION NUMBER: 30,777  
 ; REFERENCE/DOCKET NUMBER: 18614  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908) 594-4678  
 ; TELEFAX: (908) 594-4720  
 ; TELEX: 138825  
 ; INFORMATION FOR SEQ ID NO: 46:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHEICAL: NO  
 ; ANTI-SENSE: NO  
 ; IMMEDIATE SOURCE: Random Epitope Library Alpha

PCT-US93-06751-46  
 Query Match 36.4%; Score 4; DB 5; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSS 9  
 DB 10 GNSS 13

RESULT 46  
 PCT-US93-06751-21  
 ; Sequence 21, Application PC/TUS9306751  
 ; Patent No. 464829  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RUPON, James  
 ; APPLICANT: 14-NOV-2004-0000  
 ; APPLICANT: FRIED, EUGENE P  
 ; TITLE OF INVENTION: SELECTED INDOLIGOS OF TISSUE KALLICREIN  
 ; NUMBER OF SEQUENCES: 141  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BAKER & POLTS, L.L.C.  
 ; STREET: 555 15th Street, N.W., Suite 500 East  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004-1109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible



```

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/079,812
? FILING DATE: 22-JUN-1993
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: Remenick, James
? REGISTRATION NUMBER: 36,902
? REFERENCE/DOCKET NUMBER: 16865-0118
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 639-7700
? TELEFAX: (202) 639-7832
? INFORMATION FOR SEQ ID NO: 21:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-079-812-21

```

```

Query Match 27.3% Score 3, DB 1, Length 8:
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 SIM 11
Db 2 SIM 4

```

## RESULT 37

```

US-08-148-910-11
? Sequence 11, Application US/08148910
? Patent No. 5466593
? GENERAL INFORMATION:
? APPLICANT: Takeshi SHIMOMURA et al.
? TITLE OF INVENTION: No. 5466593el Protein and Gene Encoding Said Protein:
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Wenderoth, Lind & Ponack
? STREET: 805 Fifteenth Street, N.W., #700
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 5.25 inch.
? MEDIUM TYPE: 500 Kb Storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: Wordperfect
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/148,910
? FILING DATE: No. 5466593ember 5, 1993
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Warren M. Cheek, Jr.
? REGISTRATION NUMBER: 33,367
? REFERENCE/DOCKET NUMBER:
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-8850
? TELEFAX: 202-371-8856
? TELEX:
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear

```

```

? MOLECULE TYPE: Protein
? ORIGINAL SOURCE:
? ORGANISM: human
? US-08-148-910-11
? Query Match 27.3% Score 3, DB 1, Length 8:
? Best Local Similarity 100.0%, Pred. No. 2.5e+05;
? Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 SIM 11
Db 2 SIM 4

```

## RESULT 38

```

US-08-082-847-7
? Sequence 7, Application US/08082847
? Patent No. 5492894
? GENERAL INFORMATION:
? APPLICANT: EILMER, ANDREW W.
? TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: THE EILMER & GAMMA COMPANY
? STREET: P.O. BOX 99763
? CITY: CINCINNATI
? STATE: OHIO
? COUNTRY: USA
? ZIP: 45249-8763
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/082,847
? FILING DATE: 1994-02-25
? CLASSIFICATION: 56
? ATTORNEY/AGENT INFORMATION:
? NAME: CYRSTAN L. BEAHM
? REGISTRATION NUMBER: 54,914
? REFERENCE/DOCKET NUMBER: 434667P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 513-627-2838
? TELEFAX: 513-627-2700
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-082-847-7

```

```

Query Match 27.3% Score 3, DB 1, Length 8:
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 SIM 1
Db 4 SIM 4

```

## RESULT 39

```

US-08-082-847-8
? Sequence 8, Application US/08082847
? Patent No. 5492894
? GENERAL INFORMATION:
? APPLICANT: EILMER, ANDREW W.
? TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
? NUMBER OF SEQUENCES: 48
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: THE EILMER & GAMMA COMPANY
? STREET: P.O. BOX 99763
? CITY: CINCINNATI
? STATE: OHIO
? COUNTRY: USA
? ZIP: 45249-8763
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/082,847
? FILING DATE: 1994-02-25
? CLASSIFICATION: 56
? ATTORNEY/AGENT INFORMATION:
? NAME: CYRSTAN L. BEAHM
? REGISTRATION NUMBER: 54,914
? REFERENCE/DOCKET NUMBER: 434667P
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 513-627-2838
? TELEFAX: 513-627-2700
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear

```

: NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082,847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 34,804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858  
 : TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 8:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-8

Query Match 27.3%, Score 3, DB 1, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2 5e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SRK 5  
 DB 4 SRK 6

RESULT 40  
 US-08-082-847-9  
 : Sequence 9, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:  
 : APPLICANT: FULMER, ANDREW W.  
 : APPLICANT: BASCOM, CHARLES C.  
 : TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 : TITLE OF INVENTION: COMPOSITING A PEPTIDE  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082,847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 34,804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858

: TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 8:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-9

Query Match 100.0%, Score 3, DB 1, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2 5e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SRK 5  
 DB 4 SRK 6

RESULT 41  
 US-08-082-847-10  
 : Sequence 1, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:  
 : APPLICANT: FULMER, ANDREW W.  
 : APPLICANT: BASCOM, CHARLES C.  
 : TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 : TITLE OF INVENTION: COMPOSITING A PEPTIDE  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082,847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 34,804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858  
 : TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 8:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-10

Query Match 100.0%, Score 3, DB 1, Length 8;  
 Best Local Similarity 100.0%, Pred. No. 2 5e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 SRK 5  
 DB 4 SRK 6

RESULT 42  
 US-08-082-847-27  
 : Sequence 27, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:

```

1 APPLICANT: FULMER, ANDREW W.
2 APPLICANT: BASCOM, CHARLES C.
3 TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
4 TITLE OF INVENTION: COMPRISING A PEPTIDE
5 NUMBER OF SEQUENCES: 38
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: THE PROCTER & GAMBLE COMPANY
8 STREET: P. O. BOX 398707
9 CITY: CINCINNATI
10 STATE: OHIO
11 COUNTRY: USA
12 ZIP: 45239-8707
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.26
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/082,847
20 FILING DATE: 19930625
21 CLASSIFICATION: 530
22 ATTORNEY/AGENT INFORMATION:
23 NAME: CORSTANJE, BRAHM J.
24 REGISTRATION NUMBER: 34,804
25 REFERENCE/DOCKET NUMBER: 4346CK
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 513-627-2858
28 TELEFAX: 513-627-0260
29 INFORMATION FOR SEQ ID NO: 27:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 8 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 MOLECULE TYPE: peptide
35 US-08-082-847-27

```

```

Query Match      27.3% Score 3: DB 1: Length 8.
Best Local Similarity 100.0% Pred. No. 2.5e+05
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0.

```

```

QY 3 SRK 5
   III
Db 3 SRK 5

```

```

RESULT 43
US-08-082 847-28
1 Sequence 28, Application US/08082847
2 Patent No. 5492894
3 GENERAL INFORMATION:
4 APPLICANT: FULMER, ANDREW W.
5 APPLICANT: BASCOM, CHARLES C.
6 TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
7 TITLE OF INVENTION: COMPRISING A PEPTIDE
8 NUMBER OF SEQUENCES: 38
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: THE PROCTER & GAMBLE COMPANY
11 STREET: P. O. BOX 398707
12 CITY: CINCINNATI
13 STATE: OHIO
14 COUNTRY: USA
15 ZIP: 45239-8707
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/082,847
23 FILING DATE: 19930625
24 CLASSIFICATION: 530
25 ATTORNEY/AGENT INFORMATION:
26 NAME: CORSTANJE, BRAHM J.

```

```

1 REGISTRATION NUMBER: 34804
2 REFERENCES/DOCKET NUMBER: 4346CK
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: 513-627-2858
5 TELEFAX: 513-627-0260
6 INFORMATION FOR SEQUENCE 38:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 8 amino acids
9 TYPE: amino acid
10 TOPOLOGY: linear
11 MOLECULE TYPE: peptide
12 US-08-082 847-28
13
14 Query Match      27.3% Score 3: DB 1: Length 8.
15 Best Local Similarity 100.0% Pred. No. 2.5e+05
16 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0.
17
18 QY 3 SRK 5
19   III
20 Db 3 SRK 5
21
22 RESULT 44
23 US-08-082-847-27
24 Sequence 27, Application US/08082847
25 Patent No. 5492894
26 GENERAL INFORMATION:
27 APPLICANT: FULMER, ANDREW W.
28 APPLICANT: BASCOM, CHARLES C.
29 TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES
30 TITLE OF INVENTION: COMPRISING A PEPTIDE
31 NUMBER OF SEQUENCES: 38
32 CORRESPONDENCE ADDRESS:
33 ADDRESSEE: THE PROCTER & GAMBLE COMPANY
34 STREET: P. O. BOX 398707
35 CITY: CINCINNATI
36 STATE: OHIO
37 COUNTRY: USA
38 ZIP: 45239-8707
39 COMPUTER READABLE FORM:
40 MEDIUM TYPE: Floppy disk
41 COMPUTER: IBM PC compatible
42 OPERATING SYSTEM: PC-DOS/MS-DOS
43 SOFTWARE: PatentIn Release #1.0, Version #1.25
44 CURRENT APPLICATION DATA:
45 APPLICATION NUMBER: US/08/082,847
46 FILING DATE: 19930625
47 CLASSIFICATION: 530
48 ATTORNEY/AGENT INFORMATION:
49 NAME: CORSTANJE, BRAHM J.
50 REGISTRATION NUMBER: 34804
51 REFERENCES/DOCKET NUMBER: 4346CK
52 INFORMATION FOR SEQUENCE 38:
53 SEQUENCE CHARACTERISTICS:
54 LENGTH: 8 amino acids
55 TYPE: amino acid
56 TOPOLOGY: linear
57 MOLECULE TYPE: peptide
58 US-08-082 847-28

```

```

Query Match      27.3% Score 3: DB 1: Length 8.
Best Local Similarity 100.0% Pred. No. 2.5e+05
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0.
17
18 QY 3 SRK 5
19   III
20 Db 3 SRK 5
21
22 RESULT 45

```

US-08-082-847-30  
 : Sequence 30, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:  
 : APPLICANT: FULMER, ANDREW W.  
 : APPLICANT: BASCOM, CHARLES C.  
 : TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 : TITLE OF INVENTION: COMPRISING A PEPTIDE  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.26  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082-847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 341804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858  
 : TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 30:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-30

Query Match 27.38; Score 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gap 0

QY 3 SRK 5  
 111  
 Db 5 SRK 7

RESULT 46  
 US-07-747-795-15  
 : Sequence 15, Application US/07747785  
 : Patent No. 549467  
 : GENERAL INFORMATION:  
 : APPLICANT: LAI, Ching-Juh  
 : APPLICANT: MEN, Ruhe  
 : APPLICANT: BRAY, Michael  
 : TITLE OF INVENTION: FLAVIVIRUS ENVELOPE PROTEINS WITH  
 : TITLE OF INVENTION: INCREASED IMMUNOREACTIVITY FOR USE IN IMMUNIZATION AGAINST  
 : NUMBER OF SEQUENCES: 15  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Cushman, Darby & Cushman  
 : STREET: 1615 L Street, N.W.  
 : CITY: Washington  
 : STATE: D.C.  
 : COUNTRY: USA  
 : ZIP: 20006-5601  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25

US-08-082-847-30  
 : SEQUENCE 30, Application US/08082847  
 : Patent No. 5492894  
 : GENERAL INFORMATION:  
 : APPLICANT: FULMER, ANDREW W.  
 : APPLICANT: BASCOM, CHARLES C.  
 : TITLE OF INVENTION: COMPOSITIONS FOR REGULATING WRINKLES  
 : TITLE OF INVENTION: COMPRISING A PEPTIDE  
 : NUMBER OF SEQUENCES: 38  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: THE PROCTER & GAMBLE COMPANY  
 : STREET: P. O. BOX 398707  
 : CITY: CINCINNATI  
 : STATE: OHIO  
 : COUNTRY: USA  
 : ZIP: 45239-8707  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.26  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/082-847  
 : FILING DATE: 19930625  
 : CLASSIFICATION: 530  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: CORSTANJE, BRAHM J.  
 : REGISTRATION NUMBER: 341804  
 : REFERENCE/DOCKET NUMBER: 4346CR  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 513-627-2858  
 : TELEFAX: 513-627-0260  
 : INFORMATION FOR SEQ ID NO: 30:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-08-082-847-30

STRANDEDNESS: UNKNOWN  
 TOPOLOGY: UNKNOWN  
 MOLECULE TYPE: PEPTIDE  
 HYPOTHETICAL: NO  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:

Query Match 27.3% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2,50,05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10  
 III  
 DB 5 SSL 7

RESULT 48  
 US-08-210-266A-7  
 Sequence 7, Application US/08210266A  
 Patent No. 5545619  
 GENERAL INFORMATION:  
 APPLICANT: Atkinson, John P.  
 APPLICANT: Hourcade, Dennis  
 APPLICANT: Kryuch, Malgorzata  
 TITLE OF INVENTION: Modified Complement System  
 TITLE OF INVENTION: Regulators  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 2800 One Atlantic Center, 1201 West Peachtree  
 STREET: Street  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: US  
 ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: DOS/MS-DOS  
 SOFTWARE: Patent No. 5545619, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/210-266A  
 FILING DATE: 19 MAR 1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/96,514  
 FILING DATE: 13 MAY 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patricia L.  
 REGISTRATION NUMBER: 41,283  
 REFERENCE/AGENT NUMBER: 8,411  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404) 373-4244  
 TELEFAX: (404) 373-8245  
 INFORMATION FOR SEQ ID NO:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Peptide  
 US-08-210-266A-7

Query Match 100.0% Score 4; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2,50,06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9  
 I I  
 DB 1 NSS 4

RESULT 49  
 US-08-097-938-41  
 Sequence 61, Application US/08093848  
 Patent No. 5929774  
 GENERAL INFORMATION:  
 APPLICANT: SUNBELT, LLC  
 APPLICANT: SUNBELT, LLC  
 TITLE OF INVENTION: RECOMBINANT 140 RECEPTOR AND ITS  
 TITLE OF INVENTION: ADRENALIN AND ANTAGONISTS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRIS & FORDER  
 STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500  
 CITY: Washington, DC  
 COUNTRY: USA  
 ZIP: 20006-1812  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: DOS/MS-DOS  
 SOFTWARE: Patent No. 5929774, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/097,938  
 FILING DATE: 26 MAR 1998  
 CLASSIFICATION: 4-3  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MORRIS & FORDER  
 REGISTRATION NUMBER: 29,039  
 REFERENCE/AGENT NUMBER: 29,039  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 867-1361  
 TELEFAX: (202) 867-1361  
 TELEX: 90-4330  
 INFORMATION FOR SEQ ID NO: 41:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 US-08-097-938-41

Search completed: September 29, 2003 1:28 PM  
 Job time: 13,947.5005

Query Match 27.3% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NSS 9  
 III  
 DB 3 NSS 5

RESULT 50  
 US-07-958-903A-53  
 : Sequence 53, Application US/07958903A  
 : Patent No 5652214  
 : GENERAL INFORMATION:  
 : APPLICANT: Lewis, Michael E.  
 : APPLICANT: Kauer, James C.  
 : APPLICANT: Smith, Kevin R.  
 : APPLICANT: Callison, Kathleen V.  
 : APPLICANT: Baldino, Frank  
 : APPLICANT: Neff, Nicola  
 : APPLICANT: Iqbal, Mohamed  
 : TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION  
 : TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND  
 : TITLE OF INVENTION: ANALOGS  
 : NUMBER OF SEQUENCES: 56  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Fish & Richardson  
 : STREET: 225 Franklin Street  
 : CITY: Boston  
 : STATE: Massachusetts  
 : COUNTRY: U.S.A.  
 : ZIP: 02110-2804  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 : COMPUTER: IBM PS/2 Model 502 or 55SX  
 : OPERATING SYSTEM: MS-DOS (Version 5.0)  
 : SOFTWARE: WordPerfect (Version 5.1)  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/07/958,903A  
 : FILING DATE: October 7, 1992  
 : CLASSIFICATION: 514  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 07/361,595  
 : FILING DATE: June 5, 1989  
 : APPLICATION NUMBER: 07/534,139  
 : FILING DATE: June 5, 1990  
 : APPLICATION NUMBER: 07/869,913  
 : FILING DATE: April 15, 1992  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Clark, Paul T.  
 : REGISTRATION NUMBER: 30,162  
 : REFERENCE/DOCKET NUMBER: 02655/003004  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 542-5070  
 : TELEFAX: (617) 542-8906  
 : TELEX: 200154  
 : INFORMATION FOR SEQ ID NO: 53:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8  
 : TYPE: amino acid  
 : STRANDEDNESS:  
 : TOPOLOGY: linear  
 : US-07-958-903A-53

Query Match 27.3% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKS 3  
 III  
 DB 5 AKS 7











? PRIOR APPLICATION NUMBER: US 60/116,673  
 ? PRIOR FILING DATE: 1999-01-21  
 ? PRIOR APPLICATION NUMBER: DK 1998 01281  
 ? PRIOR FILING DATE: 1998-10-18  
 ? PRIOR APPLICATION NUMBER: US 60/070,488  
 ? PRIOR FILING DATE: 1998-01-05  
 ? PRIOR APPLICATION NUMBER: DK 1997 01277  
 ? PRIOR FILING DATE: 1997-11-10  
 ? PRIOR APPLICATION NUMBER: US 60/044,624  
 ? PRIOR FILING DATE: 1997-04-18  
 ? PRIOR APPLICATION NUMBER: DK 1997 00376  
 ? PRIOR FILING DATE: 1997-04-02  
 ? NUMBER OF SEQ ID NOS: 174  
 ? SOFTWARE: PatentIn version 3.1  
 ? SEQ ID NO 165  
 ? LENGTH: 14  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: N-terminal sequence of IB42  
 US-10-138-473-165

Query Match 45.5%; Score 5; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNSSL 10  
 Db 2 GNSSL 6

## RESULT 2

US-09-726-470A-127  
 ? Sequence 127, Application US/09726470A  
 ? Publication No. US20030036528A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? CURRENT FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928123.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: PatentIn Ver. 2.1  
 ? SEQ ID NO 127  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? FEATURE:  
 ? NAME/KEY: SITE  
 ? LOCATION: (8)  
 ? OTHER INFORMATION: p-Fluorophenylalanine  
 US-09-726-470A-127

Query Match 36.4%; Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 Db 2 AKSR 5

## RESULT 3

US-09-726-470A-245  
 ? Sequence 235, Application US/09726470A  
 ? Publication No. US20030036528A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? CURRENT FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928123.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: PatentIn version 3.1  
 ? SEQ ID NO 245  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: Peptide  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 US-09-726-470A-245

Query Match 46.4%; Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 Db 2 AKSR 5

## RESULT 4

US-10-231-894-19  
 ? Sequence 19, Application US/09726470A  
 ? Publication No. US20030036528A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? TITLE OF INVENTION: Compositions and Methods of Treatment of Diabetes  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/10/231,894  
 ? CURRENT FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928123.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 64  
 ? SOFTWARE: PatentIn Ver. 2.1  
 ? SEQ ID NO 19  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Homo Sapiens  
 US-10-231-894-19

Query Match 66.4%; Score 4; DB 12; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSKR 5  
 Db 1 KSKR 4

RESULT 5  
 US-10-112-527-7



Query Match 36.48; Score 4; Pos 1; Location 0;  
Best Local Similarity 100.0%; Prod. No. 50-08;  
Matches 4; Conservative 0; Mismatches 0; Indels

Qy	6	GNSS	9
Dy	5	GNSS	8

## 6. CONCLUSION

```

US-10-040-862 9765
: Sequence 9765, Application US/10040862
: Publication NO. US20030078396A1
: GENERAL INFORMATION:
: APPLICANT: Gaiger, Alexander
: APPLICANT: Alqate, Paul A.
: APPLICANT: Mannion, Jane
: APPLICANT: Retter, Marc
: APPLICANT: Corixa Corporation
: TITLE OF INVENTION: Compositions and Methods
: FILE REFERENCE: 014058-013520UG
: CURRENT APPLICATION NUMBER: US/10/040-862

```

```

; NUMBER OF SEQ ID NOS: 10487
; SOFTWARE: FASTSEQ for Windows Version 1.0
; SEQ ID NO 9765
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-9765

```

Query Match 36.4%; Score 4; IP 15; Length 17;  
Best Local Similarity 100.0%; Prod. No. 62-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0

Qy	6 GNSS	9 GNSS
Db	5 GNSS <td>11 GNSS </td>	11 GNSS

## RESULT 10

US-10-040-862-9811  
; Sequence 9811, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:

```

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,103
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,774
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,599
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,261
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 05/796,652
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ. ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9987
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862 5987

```

Query Match: 36.4%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

QY 6 GNSS 9
   11111
DB 6 GNSS 9

```

## RESULT 12

```

US-10-040-862-10270
; Sequence 10270, Application US/10040842
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galquer, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Reiter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/230,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,803
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,774
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,994
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,291
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03

```

```

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,103
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,774
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,599
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,261
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 05/796,652
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ. ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9987
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862 10270

```

Query Match: 36.4%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

QY 6 GNSS 9
   11111
DB 6 GNSS 9

```

## RESULT 13

```

US-10-040-862-10270
; Sequence 10270, Application US/10040842
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galquer, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Reiter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/230,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,803
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,774
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,994
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,291
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03

```

Query Match: 36.4%; Score 4; DB 15; Length 9;

```

US-10-040-862-10270
; Sequence 10270, Application US/10040842
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Galquer, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Reiter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-0135200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/230,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,803
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,774
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,994
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,291
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; SEQ ID NO 9987
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862 10270

```

Query Match: 36.4%; Score 4; DB 15; Length 9;







Query Match 36.4% Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSR 4  
 ||||  
 DB 3 AKSR 6

## RESULT 23

US-09-876-904A-83  
 ; Sequence 83, Application US/09876904A  
 ; Publication No. US2003007279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDENES TM) AND THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PUSOGENIC PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPIDOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876.904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210.925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 83  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic T-DNA-linked VIRT2  
 ; OTHER INFORMATION: endonuclease of the Agrobacterium tumefaciens tumor-inducing  
 ; OTHER INFORMATION: plasmid  
 US-09-876-904A-83

Query Match 36.4% Score 4; DB 11; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRKG 6  
 ||||  
 DB 4 SRKG 7

## RESULT 24

US-10-211-088-246  
 ; Sequence 246, Application US/10211088  
 ; Publication No. US20030104479A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bright, Gary R.  
 ; APPLICANT: Premkumar, D. David  
 ; APPLICANT: Chen, Yih-Tai  
 ; TITLE OF INVENTION: No. US20030104479A1e1 Fusion Proteins And Assays For Molecular Hu  
 ; FILE REFERENCE: 01-1022-US  
 ; CURRENT APPLICATION NUMBER: US/10/211.088  
 ; CURRENT FILING DATE: 2002-10-15  
 ; PRIOR APPLICATION NUMBER: 60/309,395  
 ; PRIOR FILING DATE: 2001-08-01  
 ; PRIOR APPLICATION NUMBER: 60/341,589  
 ; PRIOR FILING DATE: 2001-12-13  
 ; NUMBER OF SEQ ID NOS: 366  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 246  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Nuclear localization signal  
 US-10-211-088-246

Query Match 36.4% Score 4; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SRKG 6  
 ||||  
 DB 4 SRKG 7

## RESULT 25

US-09-880-748-2774  
 ; Sequence 2774, Application US/0980748  
 ; Publication No. US2003007279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert et al  
 ; TITLE OF INVENTION: Antidotes that immunospecifically bind to  
 ; FILE REFERENCE: 1F503  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; CURRENT FILING DATE: 2003-06-10  
 ; PRIOR APPLICATION NUMBER: 60/210,925  
 ; PRIOR FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: 60/225,846  
 ; PRIOR FILING DATE: 2001-06-12  
 ; PRIOR APPLICATION NUMBER: 60/226,248  
 ; PRIOR FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: 60/277,479  
 ; PRIOR FILING DATE: 2003-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,549  
 ; PRIOR FILING DATE: 2001-06-25  
 ; NUMBER OF SEQ ID NOS: 4249  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2774  
 ; LENGTH: 12  
 ; TYPE: PRI  
 ; ORGANISM: Homo Sapiens  
 US-09-880-748-2774

Query Match 36.4% Score 4; DB 12; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSIM 11  
 ||||  
 DB 3 SSIM 7

## RESULT 26

US-09-880-748-4015  
 ; Sequence 4015, Application US/0980748  
 ; Publication No. US2003007279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert et al  
 ; TITLE OF INVENTION: Antidotes that immunospecifically bind to  
 ; FILE REFERENCE: 1F503  
 ; CURRENT APPLICATION NUMBER: 60/226,248  
 ; CURRENT FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: 60/277,479  
 ; PRIOR FILING DATE: 2003-03-21  
 ; PRIOR APPLICATION NUMBER: 60/240,874  
 ; PRIOR FILING DATE: 2001-06-12  
 ; PRIOR APPLICATION NUMBER: 60/226,248  
 ; PRIOR FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: 60/277,479  
 ; PRIOR FILING DATE: 2003-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,549  
 ; NUMBER OF SEQ ID NOS: 4249  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4015  
 ; LENGTH: 12  
 ; TYPE: PRI  
 ; ORGANISM: Homo Sapiens  
 US-09-880-748-4015

Query Match 36.4% Score 4; DB 11; Length 12;

Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSLM 11  
||||  
Db 3 SSLM 6

## RESULT 27

US-09-880-748-3016  
; Sequence 3016, Application US/99880748  
; Publication No. US2003005937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind H-Ys  
; FILE REFERENCE: PFS23  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3016  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-3016

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSLM 11  
||||  
Db 3 SSLM 6

## RESULT 28

US-10-190-082-538  
; Sequence 538, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Heid, Heike A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: P1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/303,644  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO 538  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-538

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKSR 4

Qy 2 AKSR 1  
|

US-10-190-082-538  
; Sequence 538, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Heid, Heike A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: P1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; PRIOR APPLICATION NUMBER: US/01/303,644  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO 580  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-538

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AKSR 1  
|

US-10-286-457-095  
; Sequence 457, Application US/10286457  
; Publication No. US2003006004A1  
; GENERAL INFORMATION:  
; APPLICANT: JEN CYBERNETICS, INC.  
; TITLE OF INVENTION: IN-CYTOPLASMIC PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: P095R1  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/338,224  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 344  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 457  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Isolated from random peptide library and  
; OTHER INFORMATION: secreted by a secretory plasmid to endoplasmic reticulum  
US-10-286-457-095

Query Match 36.4%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5,8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NKS 11  
|

US-10-254-444-157  
; Sequence 157, Application US/1025444A  
; Publication No. US2003011071A1  
; GENERAL INFORMATION:  
US-10-254-444-157

1 APPLICANT: Belcher, Angela M  
2 APPLICANT: Smalley, Richard E.  
3 APPLICANT: Ryan, Esther  
4 APPLICANT: Lee, Seung-Wuk  
5 TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES  
6 FILE REFERENCE: 11927-1066  
7 CURRENT APPLICATION NUMBER: US/10/254.445A  
8 PRIOR FILING DATE: 2003-02-19  
9 PRIOR APPLICATION NUMBER: 60/125,664  
10 PRIOR FILING DATE: 2001-09-28  
11 NUMBER OF SEQ ID NOS: 245  
12 SOFTWARE: PatentIn version 3.1  
13 SEQ ID NO 157  
14 LENGTH: 12  
15 TYPE: PRI  
16 ORGANISM: artificial sequence  
17 FEATURE:  
18 OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage library  
19 US-10-254-446A-157

Query Match 36.4% Score 47 DB 157 Length 12  
Best Local Similarity 100.0% Pred. No. 5, de-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 SSLM 11  
DB 6 SSLM 9

RESULT 32  
US-09-851-138-164  
1 Sequence 164, Application US/09851138  
2 Publication No. US20020183508A1  
3 GENERAL INFORMATION:  
4 APPLICANT: MAERTENS, GERT  
5 STUYVER, LIEVEN  
6 TITLE OF INVENTION: NEW SEQUENCES OF HERPESVIRUS GENOTYPES  
7 AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
8 AGENTS  
9 NUMBER OF SEQUENCES: 207  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: ARNOLD, WHITE & DURKEE  
12 STREET: P.O. BOX 4433  
13 CITY: HOUSTON  
14 STATE: TEXAS  
15 COUNTRY: USA  
16 ZIP: 77210-4433  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Floppy disk  
19 COMPUTER: IBM PC compatible  
20 OPERATING SYSTEM: PC-DOS/MS-DOS  
21 SOFTWARE: MICROSOFT WORD 6.0 / ASCII text format  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/09/851,138  
24 FILING DATE: 09-May-2001  
25 PRIOR APPLICATION DATA:  
26 APPLICATION NUMBER: 08/816,075  
27 FILING DATE: <unknown>  
28 APPLICATION NUMBER: EP 94870166.4  
29 FILING DATE: 21 Oct 1994  
30 APPLICATION NUMBER: EP 95870076.7  
31 FILING DATE: 28 Jun 1995  
32 ATTORNEY/AGENT INFORMATION:  
33 NAME: KAMMERER, PATRICIA A.  
34 REGISTRATION NUMBER: 29,775  
35 REFERENCE/DOCKET NUMBER: INNS-004  
36 INFORMATION FOR SEQ ID NO: 164:  
37 SEQUENCE CHARACTERISTICS:  
38 LENGTH: 13 amino acids  
39 TYPE: amino acid  
40 TOPOLOGY: linear  
41 MOLECULE TYPE: peptide  
42 SEQUENCE DESCRIPTION: SEQ ID NO: 164:

US-09-851-138-164  
1 Query Match 36.4% Score 47 DB 157 Length 12  
2 Best Local Similarity 100.0% Pred. No. 5, de-02:  
3 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 SSSLM 11  
DB 6 SSSLM 9

RESULT 33  
US-10-254-444-157  
1 Sequence 164, Application US/10/254.444  
2 Publication No. US20020183508A1  
3 GENERAL INFORMATION:  
4 APPLICANT: MAERTENS, GERT  
5 STUYVER, LIEVEN  
6 TITLE OF INVENTION: NEW SEQUENCES OF HERPESVIRUS GENOTYPES  
7 AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
8 AGENTS  
9 NUMBER OF SEQUENCES: 207  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: ARNOLD, WHITE & DURKEE  
12 STREET: P.O. BOX 4433  
13 CITY: HOUSTON  
14 STATE: TEXAS  
15 COUNTRY: USA  
16 ZIP: 77210-4433  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Floppy disk  
19 COMPUTER: IBM PC compatible  
20 OPERATING SYSTEM: PC-DOS/MS-DOS  
21 SOFTWARE: MICROSOFT WORD 6.0 / ASCII text format  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/10/254.444  
24 FILING DATE: 09-May-2001  
25 PRIOR APPLICATION DATA:  
26 APPLICATION NUMBER: 08/816,075  
27 FILING DATE: <unknown>  
28 APPLICATION NUMBER: EP 94870166.4  
29 FILING DATE: 21 Oct 1994  
30 APPLICATION NUMBER: EP 95870076.7  
31 FILING DATE: 28 Jun 1995  
32 ATTORNEY/AGENT INFORMATION:  
33 NAME: KAMMERER, PATRICIA A.  
34 REGISTRATION NUMBER: 29,775  
35 REFERENCE/DOCKET NUMBER: INNS-004  
36 INFORMATION FOR SEQ ID NO: 164:  
37 SEQUENCE CHARACTERISTICS:  
38 LENGTH: 13 amino acids  
39 TYPE: amino acid  
40 TOPOLOGY: linear  
41 MOLECULE TYPE: peptide  
42 SEQUENCE DESCRIPTION: SEQ ID NO: 164:

## RESULT 35

US-10-153-244-173  
 : Sequence 173, Application US/10153244  
 : Publication No. US20030144191A1

## GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company  
 : TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER  
 : FILE REFERENCE: D0144 NP  
 : CURRENT APPLICATION NUMBER: US/10/153,244  
 : PRIOR FILING DATE: 2002-05-22  
 : PRIOR APPLICATION NUMBER: US 60/292,599  
 : PRIOR FILING DATE: 2001-05-22  
 : PRIOR APPLICATION NUMBER: US 60/362,944  
 : PRIOR FILING DATE: 2002-03-08  
 : NUMBER OF SEQ ID NOS: 335  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 173  
 : LENGTH: 13  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-153-244-173

Query Match 36.4%, Score 4; bp 12; length 13;

Best local Similarity 100.0%, Pred. No. 6, 2+0+2;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5

Db 111

Db 5 KSRK 8

## RESULT 36

US-10-153-244-223  
 : Sequence 223, Application US/10153244  
 : Publication No. US20030144191A1

## GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company  
 : TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER  
 : FILE REFERENCE: D0144 NP  
 : CURRENT APPLICATION NUMBER: US/10/153,244  
 : CURRENT FILING DATE: 2002-05-22  
 : PRIOR FILING DATE: 2001-05-22  
 : PRIOR APPLICATION NUMBER: US 60/292,599  
 : PRIOR FILING DATE: 2001-05-22  
 : PRIOR APPLICATION NUMBER: US 60/362,944  
 : NUMBER OF SEQ ID NOS: 335  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 223  
 : LENGTH: 13  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-153-244-223

Query Match 36.4%, Score 4; bp 12; length 13;

Best local Similarity 100.0%, Pred. No. 6, 2+0+2;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5

Db 111

Db 5 KSRK 8

## RESULT 37

US-10-100-785-101  
 : Sequence 101, Application US/10100785  
 : Publication No. US20030171348A1

## GENERAL INFORMATION:

APPLICANT: Mitchell, William W.  
 : Stratton, Charles W.

US-10-100-785-101  
 : Sequence 101, Application US/10100785  
 : Publication No. US20030171348A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mitchell, William W.  
 : Stratton, Charles W.  
 : TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER  
 : FILE REFERENCE: D0144 NP  
 : CURRENT APPLICATION NUMBER: US/10/153,244  
 : PRIOR FILING DATE: 2002-05-22  
 : PRIOR APPLICATION NUMBER: US 60/292,599  
 : PRIOR FILING DATE: 2001-05-22  
 : PRIOR APPLICATION NUMBER: US 60/362,944  
 : NUMBER OF SEQ ID NOS: 335  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 101  
 : LENGTH: 13  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-100-785-101

Query Match 36.4%, Score 4; bp 12; length 13;

Best local Similarity 100.0%, Pred. No. 6, 2+0+2;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KSRK 5

Db 111

Db 5 KSRK 8

## RESULT 38

US-10-100-785-101

```

: Sequence 103, Application US/10100785
: Publication No. US20030171348A1
: GENERAL INFORMATION:
: APPLICANT: Mitchell, William M.
:           Stratton, Charles W.
: TITLE OF INVENTION: DIAGNOSIS AND MANAGEMENT OF
: INFECTION CAUSED BY CHLAMYDIA
: NUMBER OF SEQUENCES: 114
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
: STREET: Two Millitia Drive
: CITY: Lexington
: STATE: MA
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0E
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/100,785
: FILING DATE: 19-Mar-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/073,661
: FILING DATE: 06-MAY-1998
: APPLICATION NUMBER: US 09/025,521
: FILING DATE: 18-FEB-1998
: APPLICATION NUMBER: US 08/911,593
: FILING DATE: 14-AUG-1997
: APPLICATION NUMBER: US 60/023,921
: FILING DATE: 14-AUG-1996
: APPLICATION NUMBER: US 09/025,176
: FILING DATE: 18-FEB-1998
: APPLICATION NUMBER: US 09/025,174
: FILING DATE: 18-FEB-1998
: APPLICATION NUMBER: US 60/045,739
: FILING DATE: 6-MAY-1997
: APPLICATION NUMBER: US 60/045,779
: FILING DATE: 6-MAY-1997
: APPLICATION NUMBER: US 60/045,780
: FILING DATE: 6-MAY-1997
: APPLICATION NUMBER: US 60/045,784
: FILING DATE: 6-MAY-1997
: APPLICATION NUMBER: US 60/045,787
: FILING DATE: 6-MAY-1997
: APPLICATION NUMBER: US 60/045,589
: FILING DATE: 6-MAY-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Carroll, Alice O
: REGISTRATION NUMBER: 33,542
: REFERENCE/DOCKET NUMBER: VDB97 09PM
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 781-861-6240
: TELEFAX: 781-861-9540
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 103:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-100-785-103

```

```

Query Match      36.4%   Score 4;   DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 6,2e-02;
Matches 4; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 KSRK 5
      ||||

```

```

1b      2 KSRK 10
      ||||
RESULT 49
US-10-020-269-101
: Sequence 101, Application US/10-020-269
: Publication No. US2003017540A1
: GENERAL INFORMATION:
: APPLICANT: Mitchell, William M.
:           Stratton, Charles W.
: TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
: TITLE OF INVENTION: SEQUENCES
: FILE REFERENCE: VDB97 1
: CURRENT APPLICATION NUMBER: US/10/020-269
: CURRENT FILING DATE: 2002-12-14
: PRIOR APPLICATION NUMBERS: EARLIER APPLICATION NUMBERS: 09/025,596
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBERS: EARLIER APPLICATION NUMBERS: 60/023,921
: PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 2.0
: SEQ ID NO: 101
: TYPE: PPT
: ORGANISM: Chlamydia pneumoniae
: US-10-020-269-101

```

```

Query Match      66.1%   Score 4;   DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 6,2e-02;
Matches 4; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 KSRK 5
      ||||
1b      7 KSRK 10

```

```

RESULT 49
US-10-020-269-103
: Sequence 103, Application US/10-020-269
: Publication No. US2003017540A1
: GENERAL INFORMATION:
: APPLICANT: Mitchell, William M.
:           Stratton, Charles W.
: TITLE OF INVENTION: IDENTIFICATION OF ANTIGENIC PEPTIDE
: TITLE OF INVENTION: SEQUENCES
: FILE REFERENCE: VDB97 1
: CURRENT APPLICATION NUMBER: US/10/020-269
: CURRENT FILING DATE: 2002-12-14
: PRIOR APPLICATION NUMBERS: EARLIER APPLICATION NUMBERS: 09/025,596
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBERS: EARLIER APPLICATION NUMBERS: 60/023,921
: PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-14
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 2.0
: SEQ ID NO: 103
: TYPE: PPT
: ORGANISM: Chlamydia pneumoniae
: US-10-020-269-103

```

```

Query Match      66.1%   Score 4;   DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 6,2e-02;
Matches 4; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 KSRK 5
      ||||
1b      7 KSRK 10

```

```

RESULT 41
US-10-108-445-89
: Sequence 89, Application US/10168445
: Publication No. US20030177518A1

```

```

? GENERAL INFORMATION:
? APPLICANT: Osbourn, Anne E
? APPLICANT: Haralampidis, Kosmas
? APPLICANT: Bryan, Gregory T
? TITLE OF INVENTION: Plant Gene
? FILE REFERENCE: 0380-P02892US0
? CURRENT APPLICATION NUMBER: US/10/168.445
? CURRENT FILING DATE: 2002-10-30
? PRIOR APPLICATION NUMBER: PCT/GB00/04508
? PRIOR FILING DATE: 2000-12-20
? PRIOR APPLICATION NUMBER: GB 9930394.3
? PRIOR FILING DATE: 1999-12-22
? PRIOR APPLICATION NUMBER: GB 0020217.6
? PRIOR FILING DATE: 2000-08-16
? NUMBER OF SEQ ID NOS: 219
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 89
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Avena sativa
US-10-168-445-89

```

```

Query Match          36.4%   Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 NSSL 10
    ||||
Db 3 NSSL 6

```

```

RESULT 42
US-10-156-820-11
? Sequence 11; Application US/10156820
? Publication No. US20020150558A1
? GENERAL INFORMATION:
? APPLICANT: Boulanger, Pierre
? APPLICANT: Hong, Saw See
? APPLICANT: Karayan, Lucie
? TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
? FILE REFERENCE: 032751-036
? CURRENT APPLICATION NUMBER: US/10/156.820
? CURRENT FILING DATE: 2002-06-30
? PRIOR APPLICATION NUMBER: PCT/FR98/00184
? PRIOR FILING DATE: 1998-01-30
? PRIOR APPLICATION NUMBER: FR 97/01005
? PRIOR FILING DATE: 1997-01-30
? PRIOR APPLICATION NUMBER: FR 97/11166
? PRIOR FILING DATE: 1997-09-09
? NUMBER OF SEQ ID NOS: 98
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 11
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Mastadenovirus, serotype 2
US-10-156-820-11

```

```

Query Match          36.4%   Score 4; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 NSSL 10
    ||||
Db 1 NSSL 4

```

```

RESULT 43
US-10-256-865-21
? Sequence 21; Application US/10256865
? Publication No. US20030049672A1
? GENERAL INFORMATION:
? APPLICANT: Kun Ping Lu
? APPLICANT: Xiao Zhen Zhou

```

```

? TITLE OF INVENTION: Methods and compositions for detection
? FILE REFERENCE: 0445-1041-01
? CURRENT APPLICATION NUMBER: US/10/256.865
? CURRENT FILING DATE: 2003-09-26
? PRIOR APPLICATION NUMBER: FR 00/052,484
? PRIOR FILING DATE: 1999-09-18
? NUMBER OF SEQ ID NOS: 42
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 21
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Synthetic Peptide
US-10-256-865-21

```

```

Query Match          47.4%   Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 ASSE 1
    |
Db 1 ASSE 1

```

```

RESULT 44
US-10-123-604-27
? Sequence 27; Application US/1020004
? Publication No. US200201647A1
? GENERAL INFORMATION:
? APPLICANT: Bristol-Myers Squibb Company

```

```

? TITLE OF INVENTION: Polymorphs, Uses and Formulation of Two Novel Human G Protein-Coupled Receptors
? FILE REFERENCE: 0014-001
? CURRENT APPLICATION NUMBER: US/10/123.604
? CURRENT FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 60/225,519
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 60/225,519
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 60/225,519
? PRIOR FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 60/225,519
? PRIOR FILING DATE: 2001-04-11
? NUMBER OF SEQ ID NOS: 226
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 27
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-123-604-27

```

```

Query Match          47.4%   Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 NSSL 1
    |
Db 1 NSSL 1

```

```

RESULT 45
US-10-120-604-29
? Sequence 29; Application US/1020004
? Publication No. US200201647A1
? GENERAL INFORMATION:
? APPLICANT: Bristol-Myers Squibb Company

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? TITLE OF INVENTION: Polymorphs, Uses and Formulation of Two Novel Human G Protein-Coupled Receptors
? FILE REFERENCE: 0014-001
? CURRENT APPLICATION NUMBER: US/10/120.604
? CURRENT FILING DATE: 2001-04-11
? PRIOR APPLICATION NUMBER: US 60/225,519
? PRIOR FILING DATE: 2001-04-11

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1 PRIOR APPLICATION NUMBER: US 60/283,161  
2 PRIOR FILING DATE: 2001-04-11  
3 PRIOR APPLICATION NUMBER: US 60/288,458  
4 PRIOR FILING DATE: 2001-05-03  
5 PRIOR APPLICATION NUMBER: US 60/300,619  
6 PRIOR FILING DATE: 2001-06-25  
7 NUMBER OF SEQ ID NOS: 226  
8 SOFTWARE: PatentIn version 3.0  
9 SEQ ID NO 28  
10 LENGTH: 14  
11 TYPE: PRT  
12 ORGANISM: Homo sapiens  
13 US-10-120-604-28

Query Match 36.4% Score 4: DB 15: Length 14:  
Best Local Similarity 100.0% Pred. No. 6,600,025  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 6 NSSL 9

## RESULT 46

US-10-120-604-70  
1 Sequence 70: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:

4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR FILING DATE: 2001-04-11  
13 PRIOR APPLICATION NUMBER: US 60/286,458  
14 PRIOR FILING DATE: 2001-05-03  
15 PRIOR APPLICATION NUMBER: US 60/300,619  
16 PRIOR FILING DATE: 2001-06-25  
17 NUMBER OF SEQ ID NOS: 226  
18 SOFTWARE: PatentIn version 3.0  
19 SEQ ID NO 70  
20 LENGTH: 14  
21 TYPE: PRT  
22 ORGANISM: Homo sapiens  
23 US-10-120-604-70

Query Match 36.4% Score 4: DB 15: Length 14:  
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Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 7 NSSL 10

## RESULT 47

US-10-120-604-71  
1 Sequence 71: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:

4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR APPLICATION NUMBER: US 60/283,161

1 PRIOR FILING DATE: 2001-04-11  
2 PRIOR APPLICATION NUMBER: US 60/288,458  
3 PRIOR FILING DATE: 2001-05-03  
4 PRIOR APPLICATION NUMBER: US 60/300,619  
5 PRIOR FILING DATE: 2001-06-25  
6 NUMBER OF SEQ ID NOS: 226  
7 SOFTWARE: PatentIn version 3.0  
8 SEQ ID NO 71  
9 LENGTH: 14  
10 TYPE: PRT  
11 ORGANISM: Homo sapiens  
12 US-10-120-604-71

Query Match 36.4% Score 4: DB 15: Length 14:  
Best Local Similarity 100.0% Pred. No. 6,600,025  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 6 NSSL 9

## RESULT 48

US-10-120-604-86  
1 Sequence 86: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:

4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR FILING DATE: 2001-04-11  
13 PRIOR APPLICATION NUMBER: US 60/286,458  
14 PRIOR FILING DATE: 2001-05-03  
15 PRIOR APPLICATION NUMBER: US 60/300,619  
16 PRIOR FILING DATE: 2001-06-25  
17 NUMBER OF SEQ ID NOS: 226  
18 SOFTWARE: PatentIn version 3.0  
19 SEQ ID NO 86  
20 LENGTH: 14  
21 TYPE: PRT  
22 ORGANISM: Homo sapiens  
23 US-10-120-604-86

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Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 NSSL 10  
1111  
DB 7 NSSL 10

## RESULT 49

US-10-120-604-87  
1 Sequence 87: Application US/10120604  
2 Publication No. US20030096347A1  
3 GENERAL INFORMATION:

4 APPLICANT: Bristol-Myers Squibb Company  
5 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR  
6 FILE REFERENCE: D0143NP  
7 CURRENT APPLICATION NUMBER: US/10/120,604  
8 CURRENT FILING DATE: 2002-04-11  
9 PRIOR APPLICATION NUMBER: US 60/283,145  
10 PRIOR FILING DATE: 2001-04-11  
11 PRIOR APPLICATION NUMBER: US 60/283,161  
12 PRIOR APPLICATION NUMBER: US 60/283,161

; PRIOR APPLICATION NUMBER: US 60/288,458
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-87

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Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 7 NSSL 10
DB 6 NSSL 9

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; Sequence 10, Application US/00d6816A
; Publication No. US20030106075A1
; GENERAL INFORMATION:
; APPLICANT: CILILAR, TOMAS
; TITLE OF INVENTION: NOVEL GENE ENCODING HEMANIN ANION TRANSFER
; FILE REFERENCE: 240,1PCD
; CURRENT APPLICATION NUMBER: US/10/086,816A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/330,245
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/112,267
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: 60/088,864
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Immunogenic peptide
US-10-086-816A-10

Query Match 36.4%; Score 4; LH 15; Length 14;
Best Local Similarity 100.0%; Pos. 1; End 27
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DB 7 SRKG 10

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Job time : 23.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 ; Search time 41.08 sec. Records  
(without aliases) 42 459 Million cell updates/sec

Title: US-09-787-443-22

perfect score:

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Searched: 1107863 seqs, 158726573 residues

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Minimum DB seq length: 8

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Post-processing: Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

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2	11	100.0	11	23	ABG69350 Human neural cell
3	5	45.5	8	23	ABB74692 Transcription fact
4	5	45.5	8	23	ABB74740 Transcription fact
5	5	45.5	8	23	ABB74743 Transcription fact
6	5	45.5	8	23	ABB74756 Transcription fact
7	5	45.5	14	22	AAW97433 Human peptide #708
8	15	36.4	8	15	AAW72176 Hepatitis C Virus
9	4	36.4	8	15	AAW72177 Hepatitis C Virus

83	4	36.4	14	23	ABB07294	Human histone H3 F	156	8	27.3	8	27	AA012109	HIV A02 super motif
84	4	36.4	15	17	AAR97895	Japan cedar pollen	157	8	27.3	8	27	AA012100	HIV A02 super motif
85	4	36.4	15	17	AAR97896	Japan cedar pollen	158	8	27.3	8	27	AA012102	HIV A02 super motif
86	4	36.4	15	20	AA030406	New noctuides ana	159	8	27.3	8	27	AA012029	HIV A02 super motif
87	4	36.4	15	21	RAY66773	T cell antigen rec	160	8	27.3	8	27	AA012029	HIV A02 super motif
88	4	36.4	15	21	RAY66773	T cell antigen rec	161	8	27.3	8	27	AA012029	HIV A02 super motif
89	4	36.4	15	22	AAG67887	Human Kazal type I	162	8	27.3	8	27	AA012029	HIV A02 super motif
90	4	36.4	15	22	AAG66997	Human phospholipase	163	8	27.3	8	27	AA012029	HIV A02 super motif
91	4	36.4	15	22	AAU06693	Interleukin 2 rece	164	8	27.3	8	27	AA012029	HIV A02 super motif
92	4	36.4	15	22	AAR70498	Antigenesis prote	165	8	27.3	8	27	AA012029	HIV A02 super motif
93	4	36.4	15	22	AAB65553	Immunogenic peptid	166	8	27.3	8	27	AA012029	HIV A02 super motif
94	4	36.4	15	23	ABO09896	N-terminal of reov	167	8	27.3	8	27	AA012029	HIV A02 super motif
95	4	36.4	15	23	AAU78983	Histone H3 dist act	168	8	27.3	8	27	AA012029	HIV A02 super motif
96	4	36.4	15	23	AAE13706	198 kDa glucan-displa	169	8	27.3	8	27	AA012029	HIV A02 super motif
97	4	36.4	15	23	ABB74422	Karyophilin peptid	170	8	27.3	8	27	AA012029	HIV A02 super motif
98	4	36.4	15	24	ABR30373	Human cancer relat	171	8	27.3	8	27	AA012029	HIV A02 super motif
99	4	36.4	15	24	ABR30501	Human cancer relat	172	8	27.3	8	27	AA012029	HIV A02 super motif
100	4	36.4	15	24	ABR30502	Human cancer relat	173	8	27.3	8	27	AA012029	HIV A02 super motif
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102	4	36.4	15	24	ABR30685	Human cancer relat	175	8	27.3	8	27	AA012029	HIV A02 super motif
103	4	36.4	15	24	ABR30685	Human cancer relat	176	8	27.3	8	27	AA012029	HIV A02 super motif
104	4	36.4	15	24	ABR31261	Human cancer relat	177	8	27.3	8	27	AA012029	HIV A02 super motif
105	4	36.4	15	24	ABR31262	Human cancer relat	178	8	27.3	8	27	AA012029	HIV A02 super motif
106	4	36.4	15	24	ABR31314	Human cancer relat	179	8	27.3	8	27	AA012029	HIV A02 super motif
107	3	27.3	8	7	AAP60494	Peptide with Fe re	180	8	27.3	8	27	AA012029	HIV A02 super motif
108	3	27.3	8	13	AAR33141	Selectin-dectived F	181	8	27.3	8	27	AA012029	HIV A02 super motif
109	3	27.3	8	14	AAR33077	Human cytomegalov	182	8	27.3	8	27	AA012029	HIV A02 super motif
110	3	27.3	8	14	AAR35999	Hepatitis C virus	183	8	27.3	8	27	AA012029	HIV A02 super motif
111	3	27.3	8	14	AAR36000	Hepatitis C virus	184	8	27.3	8	27	AA012029	HIV A02 super motif
112	3	27.3	8	14	AAR36001	Hepatitis C virus	185	8	27.3	8	27	AA012029	HIV A02 super motif
113	3	27.3	8	14	AAR36002	Hepatitis C virus	186	8	27.3	8	27	AA012029	HIV A02 super motif
114	3	27.3	8	14	AAR36003	Hepatitis C virus	187	8	27.3	8	27	AA012029	HIV A02 super motif
115	3	27.3	8	14	AAR36004	Hepatitis C virus	188	8	27.3	8	27	AA012029	HIV A02 super motif
116	3	27.3	8	14	AAR34367	Se/SSA epitope 285	189	8	27.3	8	27	AA012029	HIV A02 super motif
117	3	27.3	8	15	AAR72179	Hepatitis C Virus	190	8	27.3	8	27	AA012029	HIV A02 super motif
118	3	27.3	8	15	AAR72173	Hepatitis C Virus	191	8	27.3	8	27	AA012029	HIV A02 super motif
119	3	27.3	8	15	AAR58338	Hypotensive polype	192	8	27.3	8	27	AA012029	HIV A02 super motif
120	3	27.3	8	15	AAR61039	Dynorphin-like po	193	8	27.3	8	27	AA012029	HIV A02 super motif
121	3	27.3	8	16	AAW21334	Carcinogen precursor	194	8	27.3	8	27	AA012029	HIV A02 super motif
122	3	27.3	8	16	AAW73354	Human TSH receptor	195	8	27.3	8	27	AA012029	HIV A02 super motif
123	3	27.3	8	16	AAW73355	Human TSH receptor	196	8	27.3	8	27	AA012029	HIV A02 super motif
124	3	27.3	8	16	AAW73356	Human TSH receptor	197	8	27.3	8	27	AA012029	HIV A02 super motif
125	3	27.3	8	16	AAW77244	C-peptide 1/2 June	198	8	27.3	8	27	AA012029	HIV A02 super motif
126	3	27.3	8	16	AAR64595	PF-1 peptide 4.3.11	199	8	27.3	8	27	AA012029	HIV A02 super motif
127	3	27.3	8	17	AAR96814	N-glycanase Iga	200	8	27.3	8	27	AA012029	HIV A02 super motif
128	3	27.3	8	17	AAR96815	Human laminin b2	201	8	27.3	8	27	AA012029	HIV A02 super motif
129	3	27.3	8	18	AAW30602	CAEV immunogen	202	8	27.3	8	27	AA012029	HIV A02 super motif
130	3	27.3	8	19	AAW20217	Human beta-amyloid	203	8	27.3	8	27	AA012029	HIV A02 super motif
131	3	27.3	8	19	AAW64273	mhc.p.7 peptide sub	204	8	27.3	8	27	AA012029	HIV A02 super motif
132	3	27.3	8	19	AAW56994	Enzyme inhibitor p	205	8	27.3	8	27	AA012029	HIV A02 super motif
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136	3	27.3	8	20	AAW25226	HIV gag protein gp	209	8	27.3	8	27	AA012029	HIV A02 super motif
137	3	27.3	8	20	AAW16056	Human keratin K5	210	8	27.3	8	27	AA012029	HIV A02 super motif
138	3	27.3	8	20	AAW03877	Predicted binding	211	8	27.3	8	27	AA012029	HIV A02 super motif
139	3	27.3	8	20	AAW03884	Predicted binding	212	8	27.3	8	27	AA012029	HIV A02 super motif
140	3	27.3	8	20	AAW10144	1 cell epitope/MHC	213	8	27.3	8	27	AA012029	HIV A02 super motif
141	3	27.3	8	21	AAW08137	Peptide monomer	214	8	27.3	8	27	AA012029	HIV A02 super motif
142	3	27.3	8	21	AAW08138	Peptide derived fr	215	8	27.3	8	27	AA012029	HIV A02 super motif
143	3	27.3	8	21	AAW03780	Fibrinogen fragmen	216	8	27.3	8	27	AA012029	HIV A02 super motif
144	3	27.3	8	21	AAW03781	Fibrinogen fragmen	217	8	27.3	8	27	AA012029	HIV A02 super motif
145	3	27.3	8	21	AAW01920	Peptide sequence	218	8	27.3	8	27	AA012029	HIV A02 super motif
146	3	27.3	8	21	AAW84390	N-terminal peptide	219	8	27.3	8	27	AA012029	HIV A02 super motif
147	3	27.3	8	21	AAW85203	Human IgE mutant	220	8	27.3	8	27	AA012029	HIV A02 super motif
148	3	27.3	8	21	AAW85220	Human IgE mutant	221	8	27.3	8	27	AA012029	HIV A02 super motif
149	3	27.3	8	21	AAW82893	Antigenic peptide	222	8	27.3	8	27	AA012029	HIV A02 super motif
150	3	27.3	8	21	AAW85421	Ornithine decarboxyl	223	8	27.3	8	27	AA012029	HIV A02 super motif
151	3	27.3	8	21	AAW67468	Pro70 peptide-havin	224	8	27.3	8	27	AA012029	HIV A02 super motif
152	3	27.3	8	21	AAW89404	Core polypeptide	225	8	27.3	8	27	AA012029	HIV A02 super motif
153	3	27.3	8	21	AAW89405	Core polypeptide	226	8	27.3	8	27	AA012029	HIV A02 super motif
154	3	27.3	8	21	AAW66381	HLA-B8-binding HIV	227	8	27.3	8	27	AA012029	HIV A02 super motif
155	3	27.3	8	22	ABP11993	HIV A02 super motif	228	8	27.3	8	27	AA012029	HIV A02 super motif

229	3	27.3	8	22	AAB01182	Human gene 2 encod	322	3	27.3	4	21	AAV40742	Active motif sequen
230	3	27.3	8	22	AAB72647	Mammalian interfeu	323	3	27.3	4	21	AAV26747	beta 1 globulin clon
231	3	27.3	8	22	AAB72649	Mammalian interfeu	324	3	27.3	4	21	AAV26748	beta 1 globulin clon
232	3	27.3	8	22	AAB72650	Mammalian interfeu	325	3	27.3	4	21	AAV26749	HIV Env gp120 prote
233	3	27.3	8	22	AAB72651	Mammalian interfeu	326	3	27.3	4	21	AAV26750	PCR AB1 gp120 prote
234	3	27.3	8	22	AAB77805	Core polypeptide 1	327	3	27.3	4	21	AAV40871	HIV gp120 gp120 cl
235	3	27.3	8	22	AAB77806	Core polypeptide 1	328	3	27.3	4	21	AAV40872	HIV gp120 gp120 cl
236	3	27.3	8	22	AAB77807	Core polypeptide 1	329	3	27.3	4	21	AAV40873	HIV gp120 gp120 cl
237	3	27.3	8	22	AAB76079	Tumor associated	330	3	27.3	4	21	AAV40874	Anti-HIV gp120/RN
238	3	27.3	8	22	AAB55198	Anti-RSV F1 gp178	331	3	27.3	4	21	AAV40875	HIV class 1 motif
239	3	27.3	8	22	AB060424	Protease binding p	332	3	27.3	4	21	AAV40876	Tyrosine kinase BL
240	3	27.3	8	23	AB060426	Protease binding p	333	3	27.3	4	21	AAV40877	Human CASp19 prot
241	3	27.3	8	23	AB060427	Yeast GPAL amino t	334	3	27.3	4	21	AAV40878	Human CASp19 prot
242	3	27.3	8	23	AB060428	MHC class 1 molecu	335	3	27.3	4	21	AAV40879	Human CASp19 prot
243	3	27.3	8	23	AB060429	West Nile virus ca	336	3	27.3	4	21	AAV40880	Epitope derived fr
244	3	27.3	8	23	AB060430	Synthetic vascular	337	3	27.3	4	21	AAV40881	Human MHC class 1
245	3	27.3	8	23	AB060431	Human albumin fusi	338	3	27.3	4	21	AAV40882	Epitope derived fr
246	3	27.3	8	23	AB060432	Her2/neu derived H	339	3	27.3	4	21	AAV40883	Human MHC class 1
247	3	27.3	8	23	AB060433	Human prostate can	340	3	27.3	4	21	AAV40884	Epitope derived fr
248	3	27.3	8	23	AB060434	HIV gp120 gp120 cl	341	3	27.3	4	21	AAV40885	Human MHC class 1
249	3	27.3	8	23	AB060435	Desmoglein-2 CAR s	342	3	27.3	4	21	AAV40886	Epitope derived fr
250	3	27.3	8	23	AB060436	Desmoglein-2 CAR s	343	3	27.3	4	21	AAV40887	Human MHC class 1
251	3	27.3	8	23	AB060437	Transcription fact	344	3	27.3	4	21	AAV40888	Epitope derived fr
252	3	27.3	8	24	AB060438	Motif-specific and	345	3	27.3	4	21	AAV40889	Human MHC class 1
253	3	27.3	8	24	AB060439	MHC binding peptid	346	3	27.3	4	21	AAV40890	Epitope derived fr
254	3	27.3	8	24	AB060440	Proteome analysis	347	3	27.3	4	21	AAV40891	Human MHC class 1
255	3	27.3	9	10	AB060441	Proposed 1 cell ep	348	3	27.3	4	21	AAV40892	Epitope derived fr
256	3	27.3	9	12	AB060442	Native HIV core pr	349	3	27.3	4	21	AAV40893	Human MHC class 1
257	3	27.3	9	12	AB060443	CMV gB epitope 559	350	3	27.3	4	21	AAV40894	Epitope derived fr
258	3	27.3	9	13	AB060444	Anti histamine and	351	3	27.3	4	21	AAV40895	Human MHC class 1
259	3	27.3	9	14	AB060445	Tryptic peptide #1	352	3	27.3	4	21	AAV40896	Epitope derived fr
260	3	27.3	9	14	AB060446	Lactoferrin p60 pepi	353	3	27.3	4	21	AAV40897	Human MHC class 1
261	3	27.3	9	14	AB060447	CAD tryptic peptid	354	3	27.3	4	21	AAV40898	Epitope derived fr
262	3	27.3	9	14	AB060448	TRAP-41 Synthe	355	3	27.3	4	21	AAV40899	Human MHC class 1
263	3	27.3	9	15	AB060449	Hepatitis B virus	356	3	27.3	4	21	AAV40900	Epitope derived fr
264	3	27.3	9	15	AB060450	HIV-derived HIV-bi	357	3	27.3	4	21	AAV40901	Human MHC class 1
265	3	27.3	9	15	AB060451	Peptide fragment (	358	3	27.3	4	21	AAV40902	Epitope derived fr
266	3	27.3	9	15	AB060452	Peptide fragment (	359	3	27.3	4	21	AAV40903	Human MHC class 1
267	3	27.3	9	16	AB060453	HSV 2 glycoprotein	360	3	27.3	4	21	AAV40904	Epitope derived fr
268	3	27.3	9	16	AB060454	RapB (72-180) pe	361	3	27.3	4	21	AAV40905	Human MHC class 1
269	3	27.3	9	16	AB060455	N. alata arabinoga	362	3	27.3	4	21	AAV40906	Epitope derived fr
270	3	27.3	9	16	AB060456	A. alternata allerq	363	3	27.3	4	21	AAV40907	Human MHC class 1
271	3	27.3	9	16	AB060457	C-epsilon-1/2 jun	364	3	27.3	4	21	AAV40908	Epitope derived fr
272	3	27.3	9	16	AB060458	Peptide neutralisi	365	3	27.3	4	21	AAV40909	Human MHC class 1
273	3	27.3	9	16	AB060459	PF-1 peptide 41 ir	366	3	27.3	4	21	AAV40910	Epitope derived fr
274	3	27.3	9	16	AB060460	Human leucocyte an	367	3	27.3	4	21	AAV40911	Human MHC class 1
275	3	27.3	9	17	AB060461	Human leucocyte ac	368	3	27.3	4	21	AAV40912	Epitope derived fr
276	3	27.3	9	17	AB060462	Human leucocyte an	369	3	27.3	4	21	AAV40913	Human MHC class 1
277	3	27.3	9	17	AB060463	Human leucocyte an	370	3	27.3	4	21	AAV40914	Epitope derived fr
278	3	27.3	9	17	AB060464	Human leucocyte an	371	3	27.3	4	21	AAV40915	Human MHC class 1
279	3	27.3	9	18	AB060465	Autocrine mobility	372	3	27.3	4	21	AAV40916	Epitope derived fr
280	3	27.3	9	18	AB060466	HIV peptide #1 sup	373	3	27.3	4	21	AAV40917	Human MHC class 1
281	3	27.3	9	18	AB060467	HIV 1 psi peptide	374	3	27.3	4	21	AAV40918	Epitope derived fr
282	3	27.3	9	18	AB060468	Specific human leu							
283	3	27.3	9	18	AB060469	Immunomodulatory p							
284	3	27.3	9	18	AB060470	Immunogenic peptid							
285	3	27.3	9	18	AB060471	Immunogenic peptid							
286	3	27.3	9	18	AB060472	Antibiotic potent							
287	3	27.3	9	19	AB060473	Human neurofilamen							
288	3	27.3	9	19	AB060474	Human neurofilamen							
289	3	27.3	9	19	AB060475	Denque virus type							
290	3	27.3	9	19	AB060476	Denque virus type							
291	3	27.3	9	19	AB060477	Nuclear localisat							
292	3	27.3	9	19	AB060478	Amino-terminal pro							
293	3	27.3	9	20	AB060479	CAL4 activation do							
294	3	27.3	9	20	AB060480	Bcr-Abi epitope (a							
295	3	27.3	9	20	AB060481	Immunogenic peptid							
296	3	27.3	9	20	AB060482	Immunogenic peptid							
297	3	27.3	9	20	AB060483	Immunogenic peptid							
298	3	27.3	9	20	AB060484	Immunogenic peptid							
299	3	27.3	9	20	AB060485	Immunogenic peptid							
300	3	27.3	9	20	AB060486	Immunogenic peptid							
301	3	27.3	9	20	AB060487	Immunogenic peptid							



XX OS Synthetic.

XX PN WO200018801-A2.

XX PD 06-APR-2000.

XX PF 23 SEP-1999; 99WO-DK00500.

XX PR 29-SEP-1998; 98DK-0001232.

XX PR 29-APR-1999; 99DK-0000592.

XX PA (RONN/) RONN I C B.

XX PA (BOCK/) BOCK E.

XX PA (HOLM/) HOLM A.

XX PA (OLSE/) OLSEN M.

XX PA (OSTE/) OSTERGAARD S.

XX PA (JENSEN) JENSEN P H.

XX PA (POUL/) POULSEN F H.

XX PA (SORO/) SOROKA V.

XX PA (RALE/) RALETS I.

XX PA (BERE/) BEREZIN V.

XX PI Ronn ICh, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH,

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX WIPI: 2000-293111/25.

XX PT Compositions that bind neural cell adhesion molecules useful for

PT treating disorders of the nervous system and muscles e.g. Alzheimer's

PT and Parkinson's diseases.

XX PS Example 4: Page 25; 119pp; English.

XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule

CC NCAM is found in three forms, two of which are transmembrane forms, while

CC the third is attached via a lipid anchor to the cell membrane. All three

CC NCAM forms have an extracellular structure consisting five immunoglobulin

CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the

CC N-terminal. The present sequence represents a peptide which binds to the

CC NCAM Ig1 domain. The peptide can be used in a compound which binds to the

CC NCAM Ig1/Ig2 domains, and is capable of stimulating or promoting neurite

CC outgrowth from NCAM presenting cells, and is also capable of promoting

CC the proliferation of NCAM presenting cells. The compound may be used in

CC the treatment of normal, degenerated or damaged NCAM presenting cells.

CC The compound may in particular be used to treat diseases of the central

CC and peripheral nervous systems such as post operative nerve damage,

CC traumatic nerve damage, impaired myelination of nerve fibres, conditions

CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,

CC demetias, sclerosis, nerve degeneration associated with diabetes,

CC mellitus, disorders affecting the circadian clock or neuro-muscular

CC transmission and schizophrenia. Conditions affecting the muscles may also

CC be treated with the compound, such as conditions associated with impaired

CC function of neuromuscular connections (e.g. genetic or traumatic shock or

CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas

CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,

CC liver and bowel may also be treated using the compound. The compound is

CC used in a prosthetic nerve guide, and also to stimulate the ability to

CC learn, and to stimulate the memory of a subject.

XX SQ Sequence 11 AA:

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 8 5e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 ARKSRDMTA1K 11

Db 1 ARKSRDMTA1K 11

RESULT 2

ABC69350

XX AA: 2000-293111/25; 119pp; English.

XX PF 23 SEP-1999; 99WO-DK00500.

XX PR 29-SEP-1998; 98DK-0001232.

XX PR 29-APR-1999; 99DK-0000592.

XX PA (RONN/) RONN I C B.

XX PA (BOCK/) BOCK E.

XX PA (HOLM/) HOLM A.

XX PA (OLSE/) OLSEN M.

XX PA (OSTE/) OSTERGAARD S.

XX PA (JENSEN) JENSEN P H.

XX PA (POUL/) POULSEN F H.

XX PA (SORO/) SOROKA V.

XX PA (RALE/) RALETS I.

XX PA (BERE/) BEREZIN V.

XX PI Ronn ICh, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH,

PI Poulsen FM, Soroka V, Ralets I, Berezin V;

XX WIPI: 2000-293111/25.

XX PT Compositions that bind neural cell adhesion molecules useful for

PT treating disorders of the nervous system and muscles e.g. Alzheimer's

PT and Parkinson's diseases.

XX PS Example 4: Page 25; 119pp; English.

XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule

CC NCAM is found in three forms, two of which are transmembrane forms, while

CC the third is attached via a lipid anchor to the cell membrane. All three

CC NCAM forms have an extracellular structure consisting five immunoglobulin

CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the

CC N-terminal. The present sequence represents a peptide which binds to the

CC NCAM Ig1 domain. The peptide can be used in a compound which binds to the

CC NCAM Ig1/Ig2 domains, and is capable of stimulating or promoting neurite

CC outgrowth from NCAM presenting cells, and is also capable of promoting

CC the proliferation of NCAM presenting cells. The compound may be used in

CC the treatment of normal, degenerated or damaged NCAM presenting cells.

CC The compound may in particular be used to treat diseases of the central

CC and peripheral nervous systems such as post operative nerve damage,

CC traumatic nerve damage, impaired myelination of nerve fibres, conditions

CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,

CC demetias, sclerosis, nerve degeneration associated with diabetes,

CC mellitus, disorders affecting the circadian clock or neuro-muscular

CC transmission and schizophrenia. Conditions affecting the muscles may also

CC be treated with the compound, such as conditions associated with impaired

CC function of neuromuscular connections (e.g. genetic or traumatic shock or

CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas

CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,

CC liver and bowel may also be treated using the compound. The compound is

CC used in a prosthetic nerve guide, and also to stimulate the ability to

CC learn, and to stimulate the memory of a subject.

XX SQ Sequence 11 AA:

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 8 5e-06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 ARKSRDMTA1K 11

Db 1 ARKSRDMTA1K 11

RESULT 2

ABC69350



```

XX 18-APR-2002 (first entry)
XX Transcription factor nuclear localisation signal peptide SEQ ID NO:507.
DE FUSOGENIC: nuclear localisation signal; NLS; encapsulation; liposome;
XX liposome; micelle; karyophilic; cytosolic; antitumour; solid tumour;
XX peptide-lipid-poly-nucleotide complex; neoplastic disease; gene therapy;
XX breast carcinoma; prostate carcinoma.
OS Rattus sp.
XX W0200193836-A2.
XX PN W0200193836-A2.
XX PD 13-DEC-2001.
XX PF 08-JUN-2001; 2001WO-US18657.
XX PR 09-JUN-2000; 2000US-210925P.
XX PA (BOUL/) BOULIKAS T.
XX Boulikas T.
XX WIPI: 2002-164295/21.
XX DR Encapsulation of plasmid DNA (Liponenes) and therapeutic agents with
XX PT nuclear localisation signal/fusogenic peptide conjugates into targeted
XX PT liposome complexes -
XX PS Claim 14; Page 81; 107pp; English.
XX CC The present invention describes a method for producing micelles with
XX CC entrapped therapeutic agents. The method comprises: (1) combining
XX CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
XX CC of the negatively charged atoms are neutralised by positive charges on
XX CC lipid molecules to form an electrostatic micelle complex in 20-80 %
XX CC ethanol; and (2) combining the micelle complex of (1) with fusogenic
XX CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
XX CC micelles with entrapped therapeutic agents. Also described is a method
XX CC for delivering a therapeutic agent in vivo, comprising the administration
XX CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
XX CC nuclear localisation signal (NLS) peptides for use in the method as the
XX CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
XX CC and antitumour activities. The peptide-lipid-poly-nucleotide complexes
XX CC produced are useful for inhibiting the progression of neoplastic
XX CC diseases. The invention relates to the field of gene therapy and is
XX CC directed toward methods for producing peptide-lipid-poly-nucleotide
XX CC complexes suitable for delivery of polynucleotides. The encapsulated
XX CC molecules display therapeutic efficacy in eradicating solid tumors
XX CC including but not limited to breast carcinoma or prostate carcinoma.
XX CC ABB74235 to ABB74255 are used in the exemplification of the present
XX CC invention.
XX SQ Sequence 8 AA;
XX Query Match 45.5%; Score 5; DB 23; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9; Seq. 5;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 RKSRD 6
Db 2 RKSRD 6
|||||
RESULT 6
ABB74756
1D ABB74756 standard; Peptide: 8 AA.
XX ID
XX AC ABB74756;
XX DT 18-APR-2002 (first entry)
XX XX

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DE Transcription factor nuclear localisation signal peptide SEQ ID NO: 507.
XX FUSOGENIC: nuclear localisation signal; NLS; encapsulation; liposome;
XX liposome; micelle; karyophilic; cytosolic; antitumour; solid tumour;
XX peptide-lipid-poly-nucleotide complex; neoplastic disease; gene therapy;
XX breast carcinoma; prostate carcinoma.
XX Rattus sapiens
XX W 200193836-A2.
XX IN 03072001.
XX PF 08-JUN-2001; 2001WO-US18657.
XX PR 09-JUN-2000; 2000US-210925P.
XX PA (BOUL/) BOULIKAS T.
XX Boulikas T.
XX WIPI: 2002-164295/21.
XX DR Encapsulation of plasmid DNA (Liponenes) and therapeutic agents with
XX PT nuclear localisation signal/fusogenic peptide conjugates into targeted
XX PT liposome complexes
XX Claim 14; Page 81; 107pp; English
XX The present invention describes a method for producing micelles with
XX CC entrapped therapeutic agents. The method comprises: (1) combining
XX CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
XX CC of the negatively charged atoms are neutralised by positive charges on
XX CC lipid molecules; (2) combining the micelle complex of (1) with fusogenic
XX CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
XX CC micelles with entrapped therapeutic agents. Also described is a method
XX CC for delivering a therapeutic agent in vivo, comprising the administration
XX CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
XX CC nuclear localisation signal (NLS) peptides for use in the method as the
XX CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
XX CC and antitumour activities. The peptide-lipid-poly-nucleotide complexes
XX CC produced are useful for inhibiting the progression of neoplastic
XX CC diseases. The invention relates to the field of gene therapy and is
XX CC directed toward methods for producing peptide-lipid-poly-nucleotide
XX CC complexes suitable for delivery of polynucleotides. The encapsulated
XX CC molecules display therapeutic efficacy in eradicating solid tumors
XX CC including but not limited to breast carcinoma or prostate carcinoma.
XX CC ABB74235 to ABB74255 are used in the exemplification of the present
XX CC invention.
XX SQ Sequence 8 AA;
XX Query Match 45.5%; Score 5; DB 23; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9; Seq. 5;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 RKSRD 6
Db 2 RKSRD 6
|||||
RESULT 7
AAM74743
1D AAM74743 standard; Peptide: 11 AA.
XX AC
XX AC AAM74743;
XX DT 24-JAN-2002 (first entry);
XX DE Human peptide #708 encoded by a 580 cDNA clone;
XX XX immunosuppressive; immunostimulatory; anti-inflammatory; cytostatic;

```

KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.  
XX  
OS Homo sapiens.  
XX  
XX WO200147944-A2.  
XX  
XX 05-JUL-2001.  
XX  
XX 28-DEC-2000; 2000WO-US35498.  
XX  
XX 28-DEC-1999; 99US-0173419.  
XX  
XX 27-DEC-2000; 2000US-0173419.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach M;  
XX WPI; 2001-465210/50.  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polykerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -  
XX  
XX Disclosure; Page 3823; 4143pp; English.  
XX  
XX The present invention relates to oligonucleotides (see AA:26754:AA14655)  
XX encoding polymorphic variants of proteins related to amylases, amyloid  
XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
XX complement, oncogenes, histones, kinases, colony stimulating factors,  
XX complement related proteins, cytochromes, kinesins, cytokines,  
XX interferons, interleukins, G-protein coupled receptors and thioesterases.  
XX The present sequence is a peptide encoded by one such oligonucleotide.  
XX The oligonucleotides and the peptides encoded by them may be used in the  
XX prevention, diagnosis and treatment of diseases associated with  
XX inappropriate expression of the proteins listed above. Disorders that may  
XX be prevented, diagnosed and/or treated include multifactorial diseases  
XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus,  
XX CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
XX brain, breast, colon and kidney, leukaemia), diseases of the nervous  
XX system and an infection of pathogenic organisms.  
XX  
XX Sequence 14 AA:  
Query Match 45.5%; Score 5; LH 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 RKSRD 6  
DB IIIII  
5 RKSRD 9  
RESULT 8  
AAR72176  
ID AAR72176 standard; peptide; 8 AA.  
XX  
XX AAR72176;  
XX  
XX 25-MAR-2003 (updated)  
XX 28-JUN-1995 (first entry)  
XX  
XX Hepatitis C Virus NS5a octapeptide for epitope mapping.  
XX  
XX Hepatitis C Virus; HCV; non-structural protein; NS5a;  
XX dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.  
XX

US Synthetic  
XX EP424547-A1  
XX  
XX 17-NOV-1994.  
XX  
XX 02 MAY-1994; 94EP 000204  
XX  
XX 12-MAY-1994; 94EP 000204  
XX  
XX (S881) SEFIN POLYMORPHIC NS5A  
XX  
XX Bonelli E, Gurevitz E, Gurevitz S, Rosa C;  
XX WPI; 1994-45749/44.  
XX  
XX New peptides (S881) related to hepatitis C virus epitopes of non-  
XX structural proteins, for some time and selected to detect and  
XX antibodies in body fluids.  
XX  
XX Example 1: E47-494-44-44.  
XX  
XX 62 overlapping octapeptides (AA:26754:AA14655) were synthesised to  
XX cover the more hydrophobic domain of the hepatitis C virus NS5a  
XX non-structural protein (100-1100) between 900-1100 amino acids (2250-  
XX 2307). The peptides were analysed in an ELISA in order to map the  
XX immunodominant epitope of NS5a based on the assay results and  
XX highly immunoreactive peptides was synthesised (AAR72176) which is  
XX useful for in vitro detection of HCV.  
XX (Updated on 25-MAR-2003 to correct PW field.)  
XX  
XX Sequence 8 AA:  
Query Match 45.5%; Score 4; LH 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 RKSR 5  
DB IIIII  
5 RKSR 6  
RESULT 9  
AAR72177  
ID AAR72177 standard; peptide; 8 AA.  
XX  
XX AAR72177;  
XX  
XX 25-MAR-2003 (updated)  
XX 28-JUN-1995 (first entry)  
XX  
XX Hepatitis C Virus NS5a octapeptide for epitope mapping.  
XX  
XX Hepatitis C Virus; HCV; non-structural protein; NS5a;  
XX dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.  
XX  
XX Synthetic.  
XX  
XX EP424547-A1  
XX  
XX 17-NOV-1994.  
XX  
XX 02 MAY-1994; 94EP 000204  
XX  
XX 12-MAY-1994; 94EP 000204  
XX  
XX (S881) SEFIN POLYMORPHIC NS5A  
XX  
XX Bonelli E, Gurevitz E, Gurevitz S, Rosa C;  
XX WPI; 1994-45749/44.  
XX



PT New peptide(s) contg hepatitis C virus dominant epitopes - of non-  
PT structural proteins, for sensitive and selective detection of  
PT antibodies in body fluids

PS Example 1; Fig 3; 39pp; English.

XX 52 overlapping octapeptides (AAR72158-R72209) were synthesised to  
CC cover the more hydrophobic domain of the hepatitis C virus NS5a  
CC non-structural polypeptide (i.e. between HCV amino acids 2256-  
CC 2307). The peptides were analysed in an ELISA in order to map the  
CC immunodominant epitope of NS5a. Based on the assay results, a  
CC highly immunoreactive peptide was synthesised (AAR72156) which is  
CC useful for in vitro detection of HCV.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 3e-05;  
Matches 4; Conservative 0; Mismatches 0; Index 0;

QY 2 RKSR 5  
DB IIII  
2 RKSR 5

RESULT 10

AAR72178  
ID AAR72178 standard; peptide: 8 AA.

XX AC AAR72178;

XX 25-MAR-2003 (updated)

DT 28-JUN-1995 (first entry)

DE Hepatitis C Virus NS5a octapeptide for epitope mapping.

XX Hepatitis C Virus; HCV; non-structural protein; NS5a;

KW dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.

XX Synthetic.

XX EP624597-A1.

XX 17-NOV-1994.

XX 02-MAY-1994; 94EP-0830208.

XX 12-MAY-1993; 93IT-RM00309.

XX (SORI-) SORIN BIOMEDICA SPA.

XX Bonelli F, Garetto F, Griva S, Osborne SJ, Rosa C.

DR WPI; 1994-350745/44.

XX New peptide(s) contg hepatitis C virus dominant epitopes - of non-  
PT structural proteins, for sensitive and selective detection of  
PT antibodies in body fluids

PS Example 1; Fig 3; 39pp; English.

XX 52 overlapping octapeptides (AAR72158-R72209) were synthesised to  
CC cover the more hydrophobic domain of the hepatitis C virus NS5a  
CC non-structural polypeptide (i.e. between HCV amino acids 2256-  
CC 2307). The peptides were analysed in an ELISA in order to map the  
CC immunodominant epitope of NS5a. Based on the assay results, a  
CC highly immunoreactive peptide was synthesised (AAR72156) which is  
CC useful for in vitro detection of HCV.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 4e-05;  
Matches 4; Conservative 0; Mismatches 0; Index 0;

QY 2 RKSR 5  
DB IIII  
2 RKSR 4

RESULT 11

AAR72174  
ID AAR72174 standard; peptide: 8 AA.

XX AC AAR72174;

XX 25-MAR-2003 (updated)

DT 28-JUN-1995 (first entry)

DE Hepatitis C Virus NS5a octapeptide for epitope mapping

XX Hepatitis C Virus; HCV; non-structural protein; NS5a;

KW dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.

XX Synthetic.

XX EP624597-A1.

XX 17-NOV-1994.

XX 02-MAY-1994; 94EP-0830208.

XX 12-MAY-1993; 93IT-RM00309.

XX (SORI-) SORIN BIOMEDICA SPA.

XX Bonelli F, Garetto F, Griva S, Osborne SJ, Rosa C.

DR WPI; 1994-350745/44.

XX New peptide(s) contg hepatitis C virus dominant epitopes - of non-  
PT structural proteins, for sensitive and selective detection of  
PT antibodies in body fluids

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XX 52 overlapping octapeptides (AAR72158-R72209) were synthesised to  
CC cover the more hydrophobic domain of the hepatitis C virus NS5a  
CC non-structural polypeptide (i.e. between HCV amino acids 2256-  
CC 2307). The peptides were analysed in an ELISA in order to map the  
CC immunodominant epitope of NS5a. Based on the assay results, a  
CC highly immunoreactive peptide was synthesised (AAR72156) which is  
CC useful for in vitro detection of HCV.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9; 4e-05;  
Matches 4; Conservative 0; Mismatches 0; Index 0;

QY 2 RKSR 5  
DB IIII  
5 RKSR 8

RESULT 12

AAR72175  
ID AAR72175 standard; peptide: 8 AA.

XX AC AAR72175;

```

XX 25-MAR-2003 (updated)
DT 28-JUN-1995 (first entry)
XX
DE Hepatitis C Virus NS5a octapeptide for epitope mapping.
KW Hepatitis C Virus; HCV; non-structural protein; NS5a;
KW dominant epitope; non-A, non-B hepatitis virus; immunodiagnosis.
XX
OS Synthetic.
XX
XX EP624597-A1.
XX
XX 17-NOV-1994.
XX
XX 02-MAY-1994; 94EP-0830208.
XX
XX 12-MAY-1993; 93IT-RM00309.
XX
XX (SORI-) SORIN BIOMEDICA SPA.
XX
XX Bonelli F, Garetto F, Griva S, Osborne SM, Bessa G.
XX
XX WPI: 1994-350745/44.
XX
XX New peptide(s) contg hepatitis C virus dominant epitopes of the
PT structural proteins, for sensitive and selective detection of
PT antibodies in body fluids
XX
XX Example 1: Fig 3; 39pp; English.
XX
XX 52 overlapping octapeptides (AAR72158-W72205) were synthesised to
CC cover the more hydrophobic domain of the hepatitis C virus NS5a
CC non-structural polypeptide (i.e. between HCV amino acids 2456
CC 2307). The peptides were analysed in an ELISA in order to map the
CC immunodominant epitope of NS5a. Based on the assay results, a
CC highly immunoreactive peptide was synthesised (AAR72156) which is
CC useful for in vitro detection of HCV.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 8 AA:
SQ
Query Match 36.4%; Score 4; DR 1%; Length 8;
Best local Similarity 100.0%; Pred. No. 4 to 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 RKSR 5
DB 4 RKSR 7
XX
RESULT 13
AAQ21641
ID AAQ21641 standard; Peptide: 8 AA.
XX
XX AAQ21641;
XX
XX 05-SEP-2002 (first entry)
XX
XX Histone acetyltransferase inhibitor related peptide; SEQ ID NO: 1.
XX
XX Cytostatic; amide derivative; coenzyme A: CoA; acetyltransferase; cancer
KW gene therapy; enzyme inhibitor.
XX
XX Unidentified.
XX
XX US6369030-B1.
XX
XX 09-APR-2002.
XX
XX 29-NOV-1999; 99US-0451034.
XX

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DE 26-NOV-2000 (first entry)
XX
XX (USP6369030-B1)
XX
XX Palo PA, Garavito RM, Khandan SM, Konda RK, Reader PG.
XX
XX WPI: 2002-5690754
XX
XX New amide derivatives of histone coenzyme A are histone
XX acetyltransferase inhibitors useful in the treatment of cancers
XX and gene therapy.
XX
XX Histone related peptide 4 (AAR72156-54).
XX
XX The invention relates to a novel peptide derivatives comprising coenzyme A
XX (CoA), the derivative of which is the invention can be used in inhibiting
XX acetyltransferase in cancer cells and treating e.g. cancer, and also
XX for use in gene therapy. The sequence represents a peptide which is part
XX of a synthetic molecule and which is an enzyme inhibitor relating to the
XX invention.
XX
XX Sequences 8 AA.
XX
XX Query Match 36.4%; Score 4; DR 1%; Length 8;
XX Best local Similarity 100.0%; Pred. No. 4 to 65;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 RKSR 5
DB 4 RKSR 7
XX
RESULT 14
AAQ21641
ID AAQ21641 standard; Peptide: 8 AA.
XX
XX AAR72156.
XX
XX AAR72156.
XX
XX 11-JAN-1999 (first entry)
XX
XX Peptide specific antigen (PSA) substrates.
XX
XX Human prostate specific antigen (PSA) substrates; prostate cancer;
XX metastatic prostate cancer; PSA inhibitor.
XX
XX Synthesis.
XX
XX W04040744-23.
XX
XX 10-SEP-1998.
XX
XX 05-MAR-1998; 98W-304902.
XX
XX 11-MAR-1997; 97US-046234.
XX
XX (SEQ ID NO: 1) KEEFFIN (NS) PARTS: HPS
XX
XX Biogen, Inc., Boston, MA, USA.
XX
XX WPI: 1998-520900/44
XX
XX Engineered histone prostatic inhibitor substrates useful in
XX e.g. measure prostate specific antigen activity, identify
XX therapeutically used, inhibit use of glucose metabolism or state
XX cancer.
XX
XX Claim 1: Page 10; 14pp; English.
XX
XX AAR72156-54 represent substrates for human prostate specific antigen
XX (PSA). The PSA substrates are used in assays which measure PSA
XX activity. Such assays may provide a clinical evaluation of patients
XX suffering from at risk for, prostate cancer. Elevated levels of PSA
XX in serum are widely used as a marker of prostate cancer, and the

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XX DE Human MHC class I molecule HLA-A3 binding 103p2b6 peptide #46.
XX KW 103p2b6: PCR primer; DNA adaptor; prostate; testis; foetal tissue.
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytotaxin;
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.
XX OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US05996.
XX PR 24-FEB-2000; 2000US-0184558.
XX PR 13-JUL-2000; 2000US-0218856.
XX PA (UROS-1) UROXENESYS INC.
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SR, Suker AS;
XX PI Challita-old PM, Paris M, Jakobovits A;
XX DR WPI; 2001-557705/62.
XX PT New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103p2b6 gene which encodes for 103p2b6 related proteins.
XX PS Example 15: Page 87; 132pp; English.
XX CC Sequences AAU23815-AAU24515 represent the 103p2b6 related protein and
XX CC peptide fragments of the polypeptide. 103p2b6 is not expressed in normal
XX CC adult tissue but is aberrantly expressed in some foetal tissues and many
XX CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX CC ovary, breast, pancreas, colon and lung. The 103p2b6 polynucleotide, its
XX CC related protein and also peptide fragments of the protein are therefore
XX CC useful for diagnosing and treating cancer. A vector comprising a
XX CC polynucleotide which encodes a single chain monoclonal antibody, that
XX CC immunospecifically binds to an 103p2b6 related protein, and a ribozyme
XX CC capable of cleaving a polynucleotide having the 103p2b6 coding sequence,
XX CC are both useful in the preparation of a composition for treating a
XX CC patient with a cancer that expresses 103p2b6. The sequences can be used
XX CC in diagnostic methods to monitor the level of 103p2b6 gene products in
XX CC serum, blood, urine and tissue and to thereby detect the presence of
XX CC cancerous cells.
XX SQ Sequence 9 AA:
    Query Match 36.4%; Score 4; D6 226; Length 9;
    Best Local Similarity 100.0%; Prod. No. 9; 4005;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 RRSR 5
DB 111
6 RRSR 9
RESULT 18
AAU24130
ID AAU24130 standard; Peptide; 9 AA.
AC AAU24130;
XX 17-DEC-2001 (first entry)
XX Human MHC molecule HLA-A11 binding 103p2b6 peptide #15.
XX DE 103p2b6: PCR primer; DNA adaptor; prostate; testis; foetal tissue.
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytotaxin;
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.

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XX H 80084002
XX W 200162925-A2.
XX 30-AUG-2001
XX 26-FEB-2001; 2001WO-US05996
XX 24-FEB-2000; 2000US-0184558
XX 13-JUL-2000; 2000US-0218856
XX (UROS-1) UROXENESYS INC
XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SR, Suker AS;
XX Challita-old PM, Paris M, Jakobovits A;
XX WPI; 2001-557705/62
XX New polynucleotide for treating and diagnosing prostate cancer is the
XX 103p2b6 gene which encodes for 103p2b6 related proteins
XX Example 15: Page 87; 132pp; English
XX Sequences AAU23815-AAU24515 represent the 103p2b6 related protein and
XX peptide fragments of the polypeptide. 103p2b6 is not expressed in normal
XX adult tissue but is aberrantly expressed in some foetal tissues and many
XX cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX ovary, breast, pancreas, colon and lung. The 103p2b6 polynucleotide, its
XX related protein and also peptide fragments of the protein are therefore
XX useful for diagnosing and treating cancer. A vector comprising a
XX polynucleotide which encodes a single chain monoclonal antibody, that
XX immunospecifically binds to an 103p2b6 related protein, and a ribozyme
XX capable of cleaving a polynucleotide having the 103p2b6 coding sequence,
XX are both useful in the preparation of a composition for treating a
XX patient with a cancer that expresses 103p2b6. The sequences can be used
XX in diagnostic methods to monitor the level of 103p2b6 gene products in
XX serum, blood, urine and tissue and to thereby detect the presence of
XX cancerous cells.
XX SQ Sequence 9 AA:
    Query Match 36.4%; Score 4; D6 226; Length 9;
    Best Local Similarity 100.0%; Prod. No. 9; 4005;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 RRSR 5
DB 111
6 RRSR 9
RESULT 19
AAU24224
ID AAU24224 standard; Peptide; 9 AA.
AC AAU24224;
XX 17-DEC-2001 (first entry)
XX Human MHC molecule HLA-A23 binding 103p2b6 peptide #16.
XX DE 103p2b6: PCR primer; DNA adaptor; prostate; testis; foetal tissue.
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytotaxin;
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.
XX OS Homo sapiens.
XX PN WO200162925-A2
XX PD 30-AUG-2001
XX PF 26-FEB-2001; 2001WO-US05996

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DR WPI: 2002-329578/36.  
 XX Detecting enzyme activity in immunoassay involves incubating  
 PT protein/peptide/derivative comprising sequence motif with enzyme to  
 PT modify protein/peptide/derivative, adding antibody, and detecting  
 PT enzyme activity.  
 XX  
 PS Example 11; Page 33; 61pp; English.  
 XX  
 CC The invention describes a method of detecting enzyme activity in an  
 CC immunoassay comprising incubating a protein/peptide or its derivative  
 CC (1) as a substrate for an enzyme with the enzyme that modifies (1). An  
 CC antibody is added to discriminate a modified position from the unmodified  
 CC position of (1), where the discrimination is mediated by the presence of  
 CC an enhancer. The method is useful for detecting enzyme activity such as  
 CC kinase, carboxylase, decarboxylase, acylase, deacetylase, hydroxylase,  
 CC dehydroxylase, amylase, and deamylase, in particular phosphatase,  
 CC acetylase or deacetylase activity in an immunoassay. In addition, the  
 CC method is useful for screening compound libraries in order to locate  
 CC molecules which inhibit or activate phosphatases, and these molecules are  
 CC promising candidates for designing drugs for the treatment of e.g.,  
 CC Parkinson's disease, Alzheimer's disease, cancer, diabetes mellitus and  
 CC other metabolic disorders. The method is highly reliable and simple  
 CC to perform. When used for detecting phosphatase activity, the method does  
 CC not require the need to develop specific high affinity  
 CC anti-phospho-serine/-phospho-threonine antibodies. This sequence  
 CC represents a synthetic peptide that can be used as a substrate to  
 CC identify acetyltransferase or deacetylase activity in an immunoassay.  
 XX  
 SQ Sequence 9 AA:  
 Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKS 4  
 Db IIII  
 1 AKKS 4  
 RESULT 22  
 AAU78978  
 ID AAU78978 standard; Peptide; 9 AA.  
 AC AAU78978;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Histone H3 antigenic fragment #2.  
 XX  
 KW Histone; antibody; antigen; methyllysine; gene activation;  
 KW gene repression; heterochromatin; euchromatin; histone methylation;  
 KW genetic imprinting; gene silencing; Prader-Willi syndrome;  
 KW Angelman syndrome.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 5 /note- "lys is methylated"  
 FT  
 XX  
 XX WO200218418-A1.  
 PN  
 XX 07-MAR-2002.  
 PD  
 XX 23-AUG-2001; 2001WO-US26283.  
 XX  
 XX 25-AUG-2000; 2000US-227767P.  
 PR  
 XX 03-JUL-2001; 2001US-302747P.  
 XX  
 XX (UYVI-) UNIV VIRGINIA PATENT FOUND.  
 PA  
 XX Allis CD, Strahl BD;  
 PI

XX WPI: 2002-415547/15  
 XX New methyllysine specific antibody useful for as diagnostic tool  
 PT screening tools, as well as in identifying regions of heterochromatin  
 PT or euchromatin  
 XX  
 PS Claim 1; Page 4; 61pp; English.  
 XX  
 CC This invention relates to methyllysine histone antibodies which  
 CC specifically bind to histones H3 and H4. The present invention is  
 CC directed to post-translational modifications of histones, in particular  
 CC the methylation of lysine residues. Methylation of histones has been  
 CC shown to be important for gene activation and repression. The antibodies  
 CC are useful in identifying regions of heterochromatin or euchromatin. The  
 CC antibodies are also useful as diagnostic or screening tools. The  
 CC antibodies may also be used to analyse chromosomes for regions of  
 CC transcriptional activity according to differential methylation and also  
 CC to studies of gene expression and gene silencing. The antibodies may  
 CC also be useful for clinical assays aimed to identify such as Prader-  
 CC Willi syndrome or Angelman syndrome. The present sequence represents the  
 CC histone antibodies which specifically bind to the N-terminal histone H3  
 CC used to generate the above sequence with loss of the invention  
 XX  
 SQ Sequence 9 AA:  
 Query Match 36.4%; Score 4; DB 21; Length 9;  
 Best local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKKS 4  
 Db IIII  
 1 AKKS 4  
 RESULT 22  
 AAU78978  
 ID AAU78978 standard; Peptide; 9 AA.  
 AC AAU78978;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Histone H3 antigenic fragment #2.  
 XX  
 KW Histone; antibody; antigen; methyllysine; gene activation;  
 KW gene repression; heterochromatin; euchromatin; histone methylation;  
 KW genetic imprinting; gene silencing; Prader-Willi syndrome;  
 KW Angelman syndrome.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 5 /note- "lys is methylated"  
 FT  
 XX  
 XX WO200218418-A1  
 PN  
 XX 07-MAR-2002  
 PD  
 XX 23-AUG-2001; 2001WO-US26283  
 XX  
 XX 25-AUG-2000; 2000US-227767P  
 PR  
 XX 03-JUL-2001; 2001US-302747P  
 XX  
 XX (UYVI-) UNIV VIRGINIA PATENT FOUND  
 PA  
 XX Allis CD, Strahl BD;  
 PI  
 XX New methyllysine specific antibodies useful for as diagnostic tool  
 PT screening tools, as well as in identifying regions of heterochromatin  
 PT or euchromatin

PS Claim 1; Page 8; 60pp; English.

XX This invention relates to novel methyllysine histone antibodies which

XX specifically bind to histones H3 and H4. The present invention is

CC directed to post translational modifications of histones, in particular

CC the methylation of lysine residues. Methylation of histones has been

CC shown to be important for gene activation and repression. The antibodies

CC are useful in identifying regions of heterochromatin or euchromatin. The

CC antibodies are also useful as diagnostic or screening tools. The

CC antibodies may also be used to analyse chromosomes for regions of

CC transcriptional activity according to differential methylation and also

CC in studies of genetic imprinting and gene silencing. The antibodies may

CC also be useful for studying diseases linked to imprinting such as Prader-

CC Willi syndrome or Angelman syndrome. The present sequence represents the

CC histone antigenic fragment #3 specific for the N terminal of histone H3

XX used to generate anti histone antibodies of the invention.

XX Sequence 9 AA:

Query Match 36.48; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Prod. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARKS 4

Db 3 ARKS 6

RESULT 24

ABR04917

ID ABR04917 standard; Peptide: 9 AA.

XX ABR04917;

XX 19 MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 H1A peptide #252.

DE Human; cytostatic; vaccine; cancer; immune response; H1A;

KW human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

PN 24-OCT-2002.

PD 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Eid PM, Faris M, Go W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI: 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prophylactic and

PT diagnostic reagents for eliciting cellular or humoral immune response

PT in cancer patients.

XX Claim 13; Page 161; 1021pp; English.

PS The present invention relates to novel human cancer-related genes and

XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the proteins as tools for modulation of

CC inhibiting the expression of the proteins as tools for modulation of

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prophylactic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX from the invention.

SQ Sequence 9 AA:

Query Match 36.48; Score 4; DB 24; Length 9;

Best Local Similarity 100.0%; Prod. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARKS 4

Db 4 ARKS 7

RESULT 25

ABR04917

ID ABR04917 standard; Peptide: 9 AA.

XX ABR04917;

XX 19 MAY-2003 (first entry)

XX Human cancer-related protein 83P4B8 H1A peptide #294

DE Human; cytostatic; vaccine; cancer; immune response; H1A;

KW human leukocyte antigen

XX Homo sapiens

OS WO200283921-A2.

PN 24-OCT-2002

PR 10-APR-2002; 2002WO-US11654

XX 10-APR-2001; 2001US-282739P.

PR 10-APR-2001; 2001US-283112P.

PR 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

PA Jakobovits A, Challita-Eid PM, Faris M, Go W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI: 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prophylactic and

PT diagnostic reagents for eliciting cellular or humoral immune response

PT in cancer patients.

XX Claim 13; Page 161; 1021pp; English.

PS The present invention relates to novel human cancer-related genes and

XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the proteins as tools for modulation of

CC inhibiting the expression of the proteins and/or translation of translated

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prophylactic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

XX from the invention.

SQ Sequence 9 AA:

Query Match 35.4%; Score 4; DB 24; Description:  
 Best Local Similarity 100.0%; Pred. Max. 4,000.5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 ARKS 4  
 IIII  
 DB 5 ARKS 8

## RESULT 26

AA01246  
 ID AAY01246 standard; peptide: 10 AA.

XX AC AAY01246;

DT 27-MAY 1999 (first entry)

DE Internalising peptide ligand FL5.

XX Internalising ligand; bacteriophage; receptor; gene therapy; osteoarthritis;  
 KW hyperproliferative disorder; smooth muscle cell disease; ovarian cancer;  
 KW tumour; melanoma; neuroblastoma; pterygia; secondary bone cancer; burn;  
 KW angiofibroma; arteriovenous malformation; arthritis; wound healing;  
 KW atherosclerotic plaque; corneal graft neovascularisation; retinopathy;  
 KW hemangioma; hemophilic joint; hypertrophic scar; neovascular glaucoma;  
 KW fracture; Osier-Weber syndrome; psoriasis; pyogenic granuloma; trachea;  
 KW scleroderma; retrorenal fibroplasia; vascular adhesion.

XX OS Mammalia.

XX XX WC9910485-A1.

XX PD 04-MAR-1999.

XX PF 28-AUG-1998; 98WC-US17949.

XX PR 29-AUG-1997; 97US-0057067.

XX XX (SELE-) SELECTIVE GENETICS INC.

XX PA Larocca D;

XX PI WPI: 1999 190616/16.

XX OR Selection method for internalizing ligands using bacteriophage  
 PT which express peptides and a detectable product and cells which  
 PT comprise a receptor for internalization

XX PS Claim 20, Page 30; 45pp; English.

XX The invention relates to new selection methods for internalising  
 CC ligands. The method comprises (a) contacting a library of bacteriophages  
 CC expressing peptides with a cell, where the bacteriophage carries a gene  
 CC encoding a detectable product; and (b) detecting the product; thereby  
 CC identifying a bacteriophage expressing a heterologous peptide that binds  
 CC to a cell surface receptor and internalises. The methods can be used to  
 CC select cDNAs, fabs, SVF, or random peptides. for the discovery of new  
 CC ligands. They can also be used to detect mutated and gene-shuffled  
 CC versions of known ligands for targeting ability. The ligands identified  
 CC by the methods may be used as targeting agents for delivering  
 CC therapeutic agents to cells or tissues. The bacteriophages provided are  
 CC useful for treating and preventing various diseases, syndromes,  
 CC hyperproliferative disorders, such as restenosis, other smooth muscle  
 CC cell diseases, tumours, such as melanomas, ovarian cancers,  
 CC neuroblastomas, pterygia, or secondary lens clouding, and strabismus.  
 CC arteriovenous malformations, arthritis, atherosclerotic plaques, retinal  
 CC graft neovascularisation, delayed wound healing, diabetic retinopathy,  
 CC granulations due to burns, hemangiomas, hemophilic joints, hypertrophic  
 CC scars, neovascular glaucoma, nonunion fractures, Osier-Weber syndrome,  
 CC psoriasis, pyogenic granuloma, retrorenal fibroplasia, scleroderma,  
 CC solid tumors, trachea or vascular adhesions. Sequences AAY01246-48  
 CC represent internalising ligands identified by the method of the  
 CC invention.

XX SC sequence 1 AA.  
 XX Query Match:  
 Best Local Similarity 100.0%; Pred. Max. 4,000.5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 ARKS 1

DB 3 ARKS 1

## RESULT 27

AA01246  
 ID AAY01246 standard; peptide: 10 AA.

XX AC AAY01246;

XX Y 11 SEP 2000

XX SC sequence 1 AA.

XX Query Match:  
 Best Local Similarity 100.0%; Pred. Max. 4,000.5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

XX QY 2 ARKS 1

XX DB 3 ARKS 1

XX Internalising ligand; bacteriophage; receptor; gene therapy; osteoarthritis;  
 KW hyperproliferative disorder; smooth muscle cell disease; ovarian cancer;  
 KW tumour; melanoma; neuroblastoma; pterygia; secondary bone cancer; burn;  
 KW angiofibroma; arteriovenous malformation; arthritis; wound healing;  
 KW atherosclerotic plaque; corneal graft neovascularisation; retinopathy;  
 KW hemangioma; hemophilic joint; hypertrophic scar; neovascular glaucoma;  
 KW fracture; Osier-Weber syndrome; psoriasis; pyogenic granuloma; trachea;  
 KW scleroderma; retrorenal fibroplasia; vascular adhesion.

XX OS Mammalia.

XX XX WC9910485-A1.

XX PD 04-MAR-1999.

XX PF 28-AUG-1998; 98WC-US17949.

XX PR 29-AUG-1997; 97US-0057067.

XX XX (SELE-) SELECTIVE GENETICS INC.

XX PA Larocca D;

XX PI WPI: 1999 190616/16.

XX OR Selection method for internalizing ligands using bacteriophage  
 PT which express peptides and a detectable product and cells which  
 PT comprise a receptor for internalization

XX PS Claim 20, Page 30; 45pp; English.

XX The invention relates to new selection methods for internalising  
 CC ligands. The method comprises (a) contacting a library of bacteriophages  
 CC expressing peptides with a cell, where the bacteriophage carries a gene  
 CC encoding a detectable product; and (b) detecting the product; thereby  
 CC identifying a bacteriophage expressing a heterologous peptide that binds  
 CC to a cell surface receptor and internalises. The methods can be used to  
 CC select cDNAs, fabs, SVF, or random peptides. for the discovery of new  
 CC ligands. They can also be used to detect mutated and gene-shuffled  
 CC versions of known ligands for targeting ability. The ligands identified  
 CC by the methods may be used as targeting agents for delivering  
 CC therapeutic agents to cells or tissues. The bacteriophages provided are  
 CC useful for treating and preventing various diseases, syndromes,  
 CC hyperproliferative disorders, such as restenosis, other smooth muscle  
 CC cell diseases, tumours, such as melanomas, ovarian cancers,  
 CC neuroblastomas, pterygia, or secondary lens clouding, and strabismus.  
 CC arteriovenous malformations, arthritis, atherosclerotic plaques, retinal  
 CC graft neovascularisation, delayed wound healing, diabetic retinopathy,  
 CC granulations due to burns, hemangiomas, hemophilic joints, hypertrophic  
 CC scars, neovascular glaucoma, nonunion fractures, Osier-Weber syndrome,  
 CC psoriasis, pyogenic granuloma, retrorenal fibroplasia, scleroderma,  
 CC solid tumors, trachea or vascular adhesions. Sequences AAY01246-48  
 CC represent internalising ligands identified by the method of the  
 CC invention.



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QY      2 RKSR 5
Db      7 RKSR 10

RESULT 28
AAU24177
1D  AAU24177 standard; Peptide; 10 AA.
AC  AAU24177;
XX
XX
DT  17-DEC-2001 (first entry)
DE  Human MHC molecule HLA-A*01:01 binding 103P206 peptide #62.
XX
XX  103P206; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
KW  tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
KW  gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
KW  single chain monoclonal antibody; cervix; human.
XX
OS  Homo sapiens.
PN  WO200162925-A2.
XX
XX  30-AUG-2001.
XX
XX  26-FEB-2001; 2001WO-US05956.
XX
XX  24-FEB-2000; 2000US-0184558.
PR  13-JUL-2000; 2000US-0218856.
XX
XX  (UROC-) UROGENESYS INC.
XX
XX  Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
PI  Challita-eid PM, Faris M, Jakobovits A;
XX
XX  WPI; 2001-557705/62.
XX
XX  New polynucleotide for treating and diagnosing prostate cancer is the
PT  103P206 gene which encodes for 103P206-related proteins.
PS
PS  Example 15; Page 90; 132pp; English.
XX
XX  Sequences AAU23815-AAU24515 represent the 103P206 related protein and
CC  peptide fragments of the polypeptide. 103P206 is not expressed in normal
CC  adult tissue but is aberrantly expressed in some foetal tissues and many
CC  cancers including tumours of the prostate, testis, bladder, bone, cervix,
CC  ovary, breast, pancreas, colon and lung. The 103P206 polynucleotide, its
CC  related protein and also peptide fragments of the protein are therefore
CC  useful for diagnosing and treating cancer. A vector comprising a
CC  polynucleotide which encodes a single chain monoclonal antibody, that
CC  immunospecifically binds to an 103P206-related protein, and a ribozyme
CC  capable of cleaving a polynucleotide having the 103P206 coding sequence,
CC  are both useful in the preparation of a composition for treating a
CC  patient with a cancer that expresses 103P206. The sequences can be used
CC  in diagnostic methods to monitor the level of 103P206 gene products in
CC  serum, blood, urine and tissue and to thereby detect the presence of
CC  cancerous cells.
XX
SQ  Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4062;
Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY      2 RKSR 5
Db      6 RKSR 9

RESULT 29
AAU24202

```

```

1D  AAU24202 standard; Peptide; 10 AA.
AC  AAU24202.
XX
XX  17-DEC-2001 (first entry)
XX
XX  Human MHC molecule HLA-A*01:01 binding 103P206 peptide #62.
XX
XX  103P206; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
KW  tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
KW  gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
KW  single chain monoclonal antibody; cervix; human.
XX
OS  Homo sapiens.
PN  WO200162925-A2.
XX
XX  30-AUG-2001.
XX
XX  26-FEB-2001; 2001WO-US05956.
XX
XX  24-FEB-2000; 2000US-0184558.
PR  13-JUL-2000; 2000US-0218856.
XX
XX  (UROC-) UROGENESYS INC.
XX
XX  Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
PI  Challita-eid PM, Faris M, Jakobovits A;
XX
XX  WPI; 2001-557705/62.
XX
XX  New polynucleotide for treating and diagnosing prostate cancer is the
PT  103P206 gene which encodes for 103P206-related proteins.
PS
PS  Example 15; Page 90; 132pp; English.
XX
XX  Sequences AAU23815-AAU24515 represent the 103P206 related protein and
CC  peptide fragments of the polypeptide. 103P206 is not expressed in normal
CC  adult tissue but is aberrantly expressed in some foetal tissues and many
CC  cancers including tumours of the prostate, testis, bladder, bone, cervix,
CC  ovary, breast, pancreas, colon and lung. The 103P206 polynucleotide, its
CC  related protein and also peptide fragments of the protein are therefore
CC  useful for diagnosing and treating cancer. A vector comprising a
CC  polynucleotide which encodes a single chain monoclonal antibody, that
CC  immunospecifically binds to an 103P206-related protein, and a ribozyme
CC  capable of cleaving a polynucleotide having the 103P206 coding sequence,
CC  are both useful in the preparation of a composition for treating a
CC  patient with a cancer that expresses 103P206. The sequences can be used
CC  in diagnostic methods to monitor the level of 103P206 gene products in
CC  serum, blood, urine and tissue and to thereby detect the presence of
CC  cancerous cells.
XX
SQ  Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4062;
Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY      2 RKSR 5
Db      6 RKSR 9

RESULT 30
AAU24274
1D  AAU24274 standard; Peptide; 10 AA.
XX
XX  AAU24274;
AC
XX
XX  17-DEC-2001 (first entry)
XX
XX  Human MHC molecule HLA-A*01:01 binding 103P206 peptide #64.
XX

```

KW 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 OS Homo sapiens.  
 XX WO200162925-A2.  
 PN 30-AUG-2001.  
 PD  
 XX 26-FEB-2001: 2001WO-US05996.  
 PF  
 XX 24-FEB-2000: 2000US-0184558.  
 PR  
 XX 13-JUL-2000: 2000US-0218856.  
 PR  
 XX (UROC-) UROGENESYS INC.  
 PA  
 XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SG, Hubert RS;  
 PI Challita-eid PM, Paris M, Jakobovits A;  
 PI WPI: 2001-557705/62.  
 DR  
 XX  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins.  
 PT  
 XX Example 15; page 93; 132pp; English.  
 PS  
 XX Sequences AAU23815-AAU24515 represent the 103P2D6 related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 SQ Sequence: 10 AA:  
 Query Match 36.4%; Score 4; Bb 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RKSR 5  
 Db IIII  
 4 RKSR 7  
 RESULT 31  
 AAU24369  
 ID AAU24369 standard; Peptide: 10 AA.  
 XX  
 AC AAU24369;  
 XX  
 DT 17-DEC-2001 (first entry)  
 XX  
 XX Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #54.  
 DE  
 KW 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 OS Homo sapiens.  
 XX WO200162925-A2.  
 PN

XX  
 CL 09-AUG-2001.  
 XX  
 PF 26-FEB-2001: 2001WO-US05996.  
 XX  
 PR 24-FEB-2000: 2000US-0184558.  
 PR 13-JUL-2000: 2000US-0218856.  
 XX  
 XX (UROC-) UROGENESYS INC.  
 XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SG, Hubert RS;  
 PI Challita-eid PM, Paris M, Jakobovits A;  
 PI WPI: 2001-557705/62.  
 DR  
 XX  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins.  
 PT  
 XX Example 15; page 93; 132pp; English.  
 PS  
 XX Sequences AAU23815-AAU24515 represent the 103P2D6 related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody that  
 CC immunospecifically binds to a 103P2D6 related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 SQ Sequence: 10 AA.  
 Query Match 36.4%; Score 4; Bb 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 RKSR 5  
 Db IIII  
 4 RKSR 7  
 RESULT 31  
 AAU24369  
 ID AAU24369 standard; Peptide: 10 AA.  
 XX  
 AC AAU24369;  
 XX  
 DT 17-DEC-2001 (first entry)  
 XX  
 XX Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #54.  
 DE  
 KW 103P2D6: PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 OS Homo sapiens.  
 XX WO200162925-A2.  
 PN

PA (UOOG-) UKOGENESYS INC.  
 XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid PM, Farris M, Jakobovits A;  
 XX WPI: 2001-557705/62.  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins .  
 XX  
 XX Example 15; Page 100; 132pp; English.  
 XX  
 XX Sequences AAU23015-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.  
 XX  
 SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HKSR 5  
 IIII  
 Db 4 RKSR 7

RESULT 33  
 AAU43146  
 ID AAU43146 standard; Peptide: 10 AA.  
 AC AAU43146;  
 XX  
 XX 22-OCT-2001 (first entry)  
 XX  
 DE Mycoplasma genitalium intermolecular complementary peptide, SPO ID 455.  
 XX  
 KW Mycoplasma genitalium; complementary peptide; ligand;  
 KW protein-protein interaction; drug design; intermolecular;  
 KW intramolecular.  
 XX

XX Mycoplasma genitalium.  
 OS WO200142278-A2.  
 XX  
 XX 14-JUN-2001.  
 XX  
 PF 13-DEC-2000; 2000WO-GB04778.  
 XX  
 PR 13-DEC-1999; 99GB-0029466.  
 XX  
 PA (PROT-) PROTEOM LTD.  
 XX  
 PI Roberts GW, Heal JR;  
 XX  
 DR WPI: 2001-514238/56.  
 XX  
 XX Complementary peptide ligands as reagents and drugs for drug discovery  
 PT programs and as lead ligands to facilitate drug design and development,  
 PT are generated from microbial genome sequences .

XX Example 2; Page 112; 21pp; English  
 PS The present sequence is one of a large number of complementary peptide  
 XX ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or assisting specific interaction of a protein with  
 CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of both the target screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming  
 CC sampling problems. The set of complementary peptides includes both  
 CC intermolecular (between proteins) and intramolecular (within a  
 CC protein) sequences  
 XX  
 SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKRS 4  
 IIII  
 Db 2 AKRS 5

RESULT 34  
 AAU43147  
 ID AAU43147 standard; Peptide: 10 AA.  
 AC AAU43147;  
 XX  
 XX 22-OCT-2001 (first entry)  
 XX

DE Mycoplasma genitalium intermolecular complementary peptide, SPO ID 455.  
 XX  
 KW Mycoplasma genitalium; complementary peptide; ligand;  
 KW protein-protein interaction; drug design; intermolecular;  
 KW intramolecular.  
 XX

XX Mycoplasma genitalium.  
 OS WO200142278-A2.  
 XX  
 XX 14-JUN-2001.  
 XX  
 PF 13-DEC-2000; 2000WO-GB04778.  
 XX  
 PR 13-DEC-1999; 99GB-0029466.  
 XX  
 PA (PROT-) PROTEOM LTD.  
 XX  
 PI Roberts GW, Heal JR;  
 XX  
 DR WPI: 2001-514238/56.  
 XX  
 XX Complementary peptide ligands as reagents and drugs for drug discovery  
 PT programs and as lead ligands to facilitate drug design and development,  
 PT are generated from microbial genome sequences .

Example 2; Page 112; 21pp; English.

XX The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or assisting specific interaction of a protein with

CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of high-throughput screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming  
 CC sampling problems. The set of complementary peptides includes both  
 CC intermolecular (between proteins) and intramolecular (within a  
 CC protein) sequences.  
 XX  
 SQ Sequence 10 AA:

Query Match 36.4% Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 40+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 IIII  
 DB 2 ARKS 5

#### RESULT 35

AAM43468

ID AAM43468 standard; Peptide: 10 AA.

XX

AC AAM43468;

XX

DT 22-OCT-2001 (first entry)

XX

DE Mycoplasma genitalium intramolecular complementary peptide, SEQ ID 777.

XX

KW Mycoplasma genitalium; complementary peptide; ligand;

KW protein-protein interaction; drug design; intermolecular;

KW intramolecular;

XX

XX

OS Mycoplasma genitalium.

XX

XX WO200142278-A2.

PN

PD 14-JUN-2001.

XX

PF 13-DEC-2000; 2000WO-GB04778.

XX

PR 13-DEC-1999; 99GB-0029466.

XX

PA (PROT-) PROTEOM LTD.

XX

PI Roberts GW, Heal JR;

XX

PS WPI; 2001-514238/56.

XX

PT Complementary peptide ligands as reagents and drugs for drug discovery  
 PT programs and as lead ligands to facilitate drug design and development,  
 PT are generated from intermolecular genome sequences.

XX

PS Example 4; Page 157; 161pp; English.

XX

CC The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or agonising specific interaction of a protein with  
 CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of high-throughput screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming

CC sampling problems. The set of complementary peptides includes both  
 CC intermolecular (between proteins) and intramolecular (within a  
 CC protein) sequences.

XX Sequence 10 AA:

Query Match 36.4% Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 40+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 I  
 DB 2 ARKS 5

#### RESULT 36

AAM43469

ID AAM43469 standard; Peptide: 10 AA.

XX

AC AAM43469;

XX

DT 22-OCT-2001 (first entry)

XX

DE Mycoplasma genitalium intramolecular complementary peptide, SEQ ID 778.

XX

KW Mycoplasma genitalium; complementary peptide; ligand;

KW protein-protein interaction; drug design; intermolecular;

KW intramolecular;

XX

XX

OS Mycoplasma genitalium.

XX

XX WO200142278-A2.

PN

PD 14-JUN-2001.

XX

PF 13-DEC-2000; 2000WO-GB04778.

XX

PR 13-DEC-1999; 99GB-0029466.

XX

PA (PROT-) PROTEOM LTD.

XX

PI Roberts GW, Heal JR;

XX

PS WPI; 2001-514238/56.

XX

PT Complementary peptide ligands as reagents and drugs for drug discovery  
 PT programs and as lead ligands to facilitate drug design and development,  
 PT are generated from intermolecular genome sequences.

XX

PS Example 4; Page 157; 161pp; English.

XX

CC The present sequence is one of a large number of complementary peptide  
 CC ligands generated from Mycoplasma genitalium genome sequences. These  
 CC specific complementary peptides interact with their relevant target  
 CC proteins encoded by the microbial genome. They are capable of  
 CC antagonising or agonising specific interaction of a protein with  
 CC another protein or receptor and are thus useful as reagents and drugs,  
 CC and as lead ligands to facilitate drug design and development. They  
 CC are useful as tools for functional genomic studies, reagents for the  
 CC configuration of high-throughput screens, as a starting point for  
 CC medicinal chemistry manipulation, for peptide mimetics and as  
 CC therapeutic agents. The analysis and acquisition of peptide sequences  
 CC facilitates understanding of protein-protein interactions. The method  
 CC allows for analysis of an entire database at a time, thus overcoming  
 CC sampling problems. The set of complementary peptides includes both  
 CC intermolecular (between proteins) and intramolecular (within a  
 CC protein) sequences.

XX Sequence 10 AA:

QY

Query Match 36.4% Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 40+02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 1 ARKS 4  
DB 1111  
2 ARKS 5

## RESULT 17

AAG94948  
ID AAG94948 standard; Peptide: 10 AA.

XX AC AAG94948;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 1142.

XX KW Human; complementary peptide; ligand; drug discovery; drug design

XX OS Homo sapiens.

XX PN WO200142277 A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04776.

XX PR 13-DEC-1999; 99GB-0029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Robertis GW, Heal JR;

XX DR WPI: 2001-408419/43.

XX PT A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.

XX PS Example 4; Page 203; 646pp; English.

XX CC The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as novel ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.

XX SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 46+02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 1 ARKS 4  
DB 1111  
3 ARKS 6

## RESULT 18

AAG94950  
ID AAG94950 standard; Peptide: 10 AA.

XX AC AAG94950;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 1144.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX KW WO200142277 A2.

XX DT 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04776.

XX PR 13-DEC-1999; 99GB-0029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Robertis GW, Heal JR;

XX DR WPI: 2001-408419/43.

XX PT A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.

XX PS Example 4; Page 203; 646pp; English.

XX CC The invention relates to a set of complementary peptide ligands generated from the human genome. The complementary peptides interact with their relevant target proteins encoded in the human genome. They can be used as reagents in drug discovery and as novel ligands to facilitate drug design and development. The present sequence is a complementary peptide provided in the specification.

XX SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 46+02;

Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 1 ARKS 4  
DB 1111  
4 ARKS 7

## RESULT 19

AAG94950  
ID AAG94950 standard; Peptide: 10 AA.

XX AC AAG94950;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 2944

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX PN WO200142277 A2

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04776.

XX PR 13-DEC-1999; 99GB-0029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Robertis GW, Heal JR;

XX DR WPI: 2001-408419/43

XX PT A set of peptide ligands consisting of specific complementary peptides to proteins encoded by genes of the human genome, useful in an assay for screening and identifying of one or more novel peptides which are drug candidates or pro-drugs.

XX

```

PS Example 4: Page 472; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
SQ Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 RKSR 5
DB 1111
2 RKSR 5

RESULT 40
AAG97695
ID AAG97695 standard; Peptide; 10 AA.
XX
AC AAG97695;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide; ligand; drug discovery; drug design
XX
KW Human: complementary peptide; ligand; drug discovery; drug design
XX
OS Homo sapiens.
XX
PN WQ200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04776.
XX
PR 13-DEC-1999; 99GB-0029464.
XX
PA (PROT-) PROTEUM LTD.
XX
PI Roberts GW, Heai JR;
XX
DR WPI: 2001-438419/43.
XX
PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs.
XX
PS Example 6: Page 591; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
SQ Sequence 10 AA;
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ARKS 4
DB 1111
1 ARKS 4

```

```

RESULT 41
AAG97696
ID AAG97696 standard; Peptide; 10 AA.
XX
AC AAG97696;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide; ligand; drug discovery; drug design
XX
KW Human: complementary peptide; ligand; drug discovery; drug design
XX
OS Homo sapiens.
XX
PN WQ200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04776.
XX
PR 13-DEC-1999; 99GB-0029464.
XX
PA (PROT-) PROTEUM LTD.
XX
PI Roberts GW, Heai JR;
XX
DR WPI: 2001-438419/43.
XX
PT A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs.
XX
PS Example 8: Page 601; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
SQ Sequence 10 AA.
Query Match 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ARKS 4
DB 1111
1 ARKS 4

RESULT 42
AAG97697
ID AAG97697 standard; Peptide; 10 AA.
XX
AC AAG97697;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide; ligand; drug discovery; drug design
XX
KW Human: complementary peptide; ligand; drug discovery; drug design
XX
OS Homo sapiens.
XX
PN WQ200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04776.

```

PR 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides  
PT to proteins encoded by genes of the human genome, useful in an assay  
PT for screening and identifying of one or more novel peptides which are  
PT drug candidates or pro-drugs -

XX Example 6; Page 591; 646pp; English.

XX The invention relates to a set of complementary peptide ligands  
CC generated from the human genome. The complementary peptides  
CC interact with their relevant target proteins encoded in the human  
CC genome. They can be used as reagents in drug discovery and as lead  
CC ligands to facilitate drug design and development. The present  
CC sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 40-62;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 ARKS 4

DB 2 ARKS 5

#### RESULT 43

AAG97700

ID AAG97700 standard; Peptide: 10 AA.

XX AAC97700;

XX 18-SEP-2001 (first entry)

XX Human complementary peptide, SEQ ID NO: 3895.

XX Human; complementary peptide; ligand; drug discovery; drug design.

XX Homo sapiens.

XX WO200142277-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB04776.

XX 13-DEC-1999; 99GB-0029464.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides  
PT to proteins encoded by genes of the human genome, useful in an assay  
PT for screening and identifying of one or more novel peptides which are  
PT drug candidates or pro-drugs -

XX Example 6; Page 592; 646pp; English.

XX The invention relates to a set of complementary peptide ligands  
CC generated from the human genome. The complementary peptides  
CC interact with their relevant target proteins encoded in the human  
CC genome. They can be used as reagents in drug discovery and as lead  
CC ligands to facilitate drug design and development. The present

CC Sequence is a complementary peptide provided in the specification  
XX Sequence 10 AA

Query Match 36.4%; Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 40-62;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 ARKS 4

DB 2 ARKS 5

#### RESULT 44

AAG97946

ID AAG97946 standard; Peptide: 10 AA.

XX AAC97946;

XX 18-SEP-2001 (first entry)

XX Human complementary peptide; ligand; drug discovery; drug design.

XX Homo sapiens.

XX WO200142277-A2.

XX 14-JUN-2001.

XX 13-SEP-2000; 2000WO-GB04776.

XX 13-SEP-2001 (first entry)

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides  
PT to proteins encoded by genes of the human genome, useful in an assay  
PT for screening and identifying of one or more novel peptides which are  
PT drug candidates or pro-drugs -

XX Example 6; Page 592; 646pp; English.

XX The invention relates to a set of complementary peptide ligands  
CC generated from the human genome. The complementary peptides  
CC interact with their relevant target proteins encoded in the human  
CC genome. They can be used as reagents in drug discovery and as lead  
CC ligands to facilitate drug design and development. The present  
CC sequence is a complementary peptide provided in the specification.

XX Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 40-62;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 ARKS 4

DB 2 ARKS 5

#### RESULT 45

AAG97946

ID AAG97946 standard; Peptide: 10 AA.

XX AAC97946;

XX 18-SEP-2001 (first entry)

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XX DE Human complementary peptide, SEQ ID NO: 431.
XX KW Human: complementary peptide; ligand; drug discovery; drug action.
XX OS Homo sapiens.
XX PN W0200142277-A2.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB04776.
XX PR 13-DEC-1999; 99GB-0029464.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX DR WPI: 2001-408419/43.
XX A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, used in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs.
XX Example 6; Page 625; 646pp; English.
XX The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX Sequence 10 AA;
  Query Match 36.4%; Score 4; Db 22; Length 10;
  Best Local Similarity 100.0%; Pred. No. 4e-02;
  Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;
QY 1 ARKS 4
DB 1111
  6 ARKS 9
  RESULT 46
  AAG84101
  ID AAG84101 standard; Peptide: 10 AA.
  AC AAG84101;
  DT 11-SEP-2001 (first entry)
  DE Arabidopsis thaliana peptide ligand #741.
  KW Plant: peptide pesticide; peptide herbicide; agricultural research.
  OS Arabidopsis thaliana.
  PN W0200142279-A2.
  PD 14-JUN-2001.
  PF 13-DEC-2000; 2000WO-GB04781.
  PR 13-DEC-1999; 99GB-0029469.
  PA (PROT-) PROTEOM LTD.
  PI Roberts GW, Heal JR;
  XX WPI: 2001-381629/40.

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XX A set of peptide ligands for agricultural research and development of
PT therapeutic agents or pesticides specific complementary peptides to proteins
XX encoded by genes of plant genomes.
XX Example 4; Page 134; 211pp; English.
XX The present invention relates to a set of peptide ligands consisting of
CC specific complementary peptides to proteins encoded by genes of plant
CC genomes. The present sequence is such a complementary peptide from Arabidopsis
CC thaliana. The peptide of the present invention are useful in an assay to
CC identify a peptide, especially a peptide pesticide or herbicide. The
CC peptides are also useful for tools for agricultural research and
CC development.
XX Sequence 10 AA;
  Query Match 36.4%; Score 4; Db 22; Length 10;
  Best Local Similarity 100.0%; Pred. No. 4e-02;
  Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;
QY 1 ARKS 4
DB 1111
  6 ARKS 9
  RESULT 47
  AAG84105
  ID AAG84105 standard; Peptide: 1 AA.
  AC AAG84105;
  DT 11-SEP-2001 (first entry)
  DE Arabidopsis thaliana peptide ligand #745.
  KW Plant: peptide pesticide; peptide herbicide; agricultural research.
  OS Arabidopsis thaliana.
  PN W0200142279-A2.
  PD 14-JUN-2001.
  PF 13-DEC-2000; 2000WO-GB04781.
  PR 13-DEC-1999; 99GB-0029469.
  PA (PROT-) PROTEOM LTD.
  PI Roberts GW, Heal JR;
  XX WPI: 2001-381629/40.
  A set of peptide ligands for agricultural research and development of
PT therapeutic agents or pesticides specific complementary peptides to proteins
XX encoded by genes of plant genomes.
XX Example 4; Page 134; 211pp; English.
XX The present invention relates to a set of peptide ligands consisting of
CC specific complementary peptides to proteins encoded by genes of plant
CC genomes. The present sequence is such a peptide from Arabidopsis
CC thaliana. The peptide of the present invention are useful in an assay to
CC identify a peptide, especially a peptide pesticide or herbicide. The
CC peptides are also useful for tools for agricultural research and
CC development.
XX Sequence 10 AA;
  Query Match 36.4%; Score 4; Db 22; Length 10;
  Best Local Similarity 100.0%; Pred. No. 4e-02;
  Matches 4; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

```





OS Homo sapiens.  
XX WO200283921-A2.  
XX 24-OCT-2002.  
XX 10-APR-2002; 2002WO-US11654.  
XX 10-APR-2001; 2001US-282739P.  
XX 10-APR-2001; 2001US-283112P.  
XX 25-APR-2001; 2001US-286630P.  
XX (AGEN-) AGENSYS INC.  
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Roberts RS;  
PI Morrison K, Morrison RK, Raitano AH;  
XX WPI; 2003-075555/07.  
XX New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response  
PT in cancer patients.  
XX  
PS Claim 13: Page 160; 1021pp; English.  
XX  
CC The present invention relates to novel human cancer related genes and  
CC proteins (AB278120-AB278168 and AB278169-AB278186), the genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
XX from the invention.  
XX  
SQ Sequence 10 AA;  
  
Query Match 36.4%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 40+32;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ARKS 4  
DB 4 ARKS 7  
  
Search completed: September 30, 2003, 10:25:45  
Job time : 46.1667 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 11.3333 seconds  
(without alignments)  
93,340 Million cell updates/sec

Title: US-09-787-443-22

Perfect score: 11

Sequence: 1 AKKSRDMTAK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2062

Minimum DB seq length: 8  
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : PIR76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	8	1 LFSAME	Proteobacterium
2	3	27.3	10	2 H28027	protein p11, cell
3	3	27.3	10	2 PN0165	triose-phosphate
4	3	27.3	11	2 PH0919	1 cell receptor
5	3	27.3	12	2 A44874	phospholipid
6	3	27.3	12	2 S43013	hypothetical prote
7	3	27.3	13	2 A53608	neuriteless, quic
8	3	27.3	13	2 PN0122	cell protein - vac
9	3	27.3	13	2 PC4055	hypothetical 14 p
10	3	27.3	13	2 S61798	1 cell specific
11	3	27.3	14	2 A49018	myosin heavy chain
12	3	27.3	14	2 A35377	GTP binding prote
13	3	27.3	14	2 B34135	RNA binding prote
14	3	27.3	14	2 PH1471	1 cell receptor
15	3	27.3	15	2 PA0053	nucleoside-diphos
16	3	27.3	15	2 A41338	isocitrate lyase
17	3	27.3	15	2 PA0075	fructose biphosph
18	3	27.3	15	2 PA0102	fructose biphosph
19	3	27.3	15	2 A47628	serine receptor
20	3	27.3	15	2 G49255	1 cell receptor
21	3	27.3	15	2 PH1590	14 heavy chain V
22	2	18.2	8	2 PH1407	14 heavy chain V
23	2	18.2	8	2 A31570	anion-chloride-con
24	2	18.2	8	2 S43971	tumor-associated
25	2	18.2	8	2 S43972	tumor-associated
26	2	18.2	8	2 T10077	hypothetical prote
27	2	18.2	8	2 PC4131	hypothetical prote
28	2	18.2	8	2 S37141	rp5A protein, 25w
29	2	18.2	8	2 S21273	cellulase (EC 3.2.

1	2	18.2	8	2 S21273	cellulase (EC 3.2.
2	2	18.2	8	2 S21273	cellulase (EC 3.2.
3	2	18.2	8	2 S21273	cellulase (EC 3.2.
4	2	18.2	8	2 S21273	cellulase (EC 3.2.
5	2	18.2	8	2 S21273	cellulase (EC 3.2.
6	2	18.2	8	2 S21273	cellulase (EC 3.2.
7	2	18.2	8	2 S21273	cellulase (EC 3.2.
8	2	18.2	8	2 S21273	cellulase (EC 3.2.
9	2	18.2	8	2 S21273	cellulase (EC 3.2.
10	2	18.2	8	2 S21273	cellulase (EC 3.2.
11	2	18.2	8	2 S21273	cellulase (EC 3.2.
12	2	18.2	8	2 S21273	cellulase (EC 3.2.
13	2	18.2	8	2 S21273	cellulase (EC 3.2.
14	2	18.2	8	2 S21273	cellulase (EC 3.2.
15	2	18.2	8	2 S21273	cellulase (EC 3.2.
16	2	18.2	8	2 S21273	cellulase (EC 3.2.
17	2	18.2	8	2 S21273	cellulase (EC 3.2.
18	2	18.2	8	2 S21273	cellulase (EC 3.2.
19	2	18.2	8	2 S21273	cellulase (EC 3.2.
20	2	18.2	8	2 S21273	cellulase (EC 3.2.
21	2	18.2	8	2 S21273	cellulase (EC 3.2.
22	2	18.2	8	2 S21273	cellulase (EC 3.2.
23	2	18.2	8	2 S21273	cellulase (EC 3.2.
24	2	18.2	8	2 S21273	cellulase (EC 3.2.
25	2	18.2	8	2 S21273	cellulase (EC 3.2.
26	2	18.2	8	2 S21273	cellulase (EC 3.2.
27	2	18.2	8	2 S21273	cellulase (EC 3.2.
28	2	18.2	8	2 S21273	cellulase (EC 3.2.
29	2	18.2	8	2 S21273	cellulase (EC 3.2.



249	2	18.2	13	2	S23638	Ig kappa chain J s	322	2	18.2	11	2	S23639	Ig kappa chain J s
250	2	18.2	13	2	S23640	Ig kappa chain J s	323	2	18.2	11	2	S23641	T cell receptor alpha
251	2	18.2	13	2	B61458	Ig kappa chain V-I	324	2	18.2	11	2	S23642	T cell receptor beta
252	2	18.2	13	2	B61458	Ig kappa chain V-I	325	2	18.2	11	2	S23643	T cell receptor gamma
253	2	18.2	13	2	PL0157	Ig kappa chain V-I	326	2	18.2	11	2	S23644	T cell receptor delta
254	2	18.2	13	2	B61458	Ig kappa chain V-I	327	2	18.2	11	2	S23645	T cell receptor epsilon
255	2	18.2	13	2	B61458	Ig kappa chain V-I	328	2	18.2	11	2	S23646	T cell receptor zeta
256	2	18.2	13	2	S47359	Ig kappa chain V-I	329	2	18.2	11	2	S23647	T cell receptor eta
257	2	18.2	13	2	S47377	T-cell antigen rec	330	2	18.2	11	2	S23648	T cell receptor theta
258	2	18.2	13	2	S47384	T-cell antigen rec	331	2	18.2	11	2	S23649	T cell receptor iota
259	2	18.2	13	2	S47388	T-cell antigen rec	332	2	18.2	11	2	S23650	T cell receptor kappa
260	2	18.2	13	2	S23372	T-cell receptor alpha	333	2	18.2	11	2	S23651	T cell receptor lambda
261	2	18.2	13	2	S56046	urinary tract ston	334	2	18.2	11	2	S23652	T cell receptor mu
262	2	18.2	13	2	S10562	zona pellucida-bi	335	2	18.2	11	2	S23653	T cell receptor nu
263	2	18.2	13	2	A39836	aggrexin - bevine	336	2	18.2	11	2	S23654	T cell receptor xi
264	2	18.2	13	2	C53275	Ig kappa chain J	337	2	18.2	11	2	S23655	T cell receptor omicron
265	2	18.2	13	2	E53275	Ig kappa chain J	338	2	18.2	11	2	S23656	T cell receptor tau
266	2	18.2	13	2	H25448	Ig kappa chain J	339	2	18.2	11	2	S23657	T cell receptor phi
267	2	18.2	13	2	PC2240	heat shock protein	340	2	18.2	11	2	S23658	T cell receptor chi
268	2	18.2	13	2	PH1636	Ig H chain V-D-J	341	2	18.2	11	2	S23659	T cell receptor psi
269	2	18.2	13	2	PH1620	Ig H chain V-D-J	342	2	18.2	11	2	S23660	T cell receptor omega
270	2	18.2	13	2	PH1593	Ig H chain V-D-J	343	2	18.2	11	2	S23661	T cell receptor sigma
271	2	18.2	13	2	PH1595	Ig H chain V-D-J	344	2	18.2	11	2	S23662	T cell receptor theta
272	2	18.2	13	2	PH1596	Ig H chain V-D-J	345	2	18.2	11	2	S23663	T cell receptor iota
273	2	18.2	13	2	PH1585	Ig H chain V-D-J	346	2	18.2	11	2	S23664	T cell receptor kappa
274	2	18.2	13	2	D37267	Ig heavy chain C	347	2	18.2	11	2	S23665	T cell receptor lambda
275	2	18.2	13	2	A33933	Ig kappa chain J	348	2	18.2	11	2	S23666	T cell receptor mu
276	2	18.2	13	2	B26406	Ig kappa chain J	349	2	18.2	11	2	S23667	T cell receptor nu
277	2	18.2	13	2	PH0799	Ig kappa chain J	350	2	18.2	11	2	S23668	T cell receptor xi
278	2	18.2	13	2	PH0805	T-cell receptor alpha	351	2	18.2	11	2	S23669	T cell receptor omicron
279	2	18.2	13	2	D47630	Ig kappa chain J	352	2	18.2	11	2	S23670	T cell receptor tau
280	2	18.2	13	2	H85575	hypothetical prote	353	2	18.2	11	2	S23671	T cell receptor phi
281	2	18.2	13	2	S01043	glutamate-ammonia	354	2	18.2	11	2	S23672	T cell receptor chi
282	2	18.2	13	2	S54344	glyoxaldehyde-3-P	355	2	18.2	11	2	S23673	T cell receptor psi
283	2	18.2	13	2	AB0764	his operon leader	356	2	18.2	11	2	S23674	T cell receptor omega
284	2	18.2	13	4	170075	glycophorin B (mis	357	2	18.2	11	2	S23675	T cell receptor sigma
285	2	18.2	14	1	NYR614	hypothalamic tetra	358	2	18.2	11	2	S23676	T cell receptor theta
286	2	18.2	14	1	QWVHM	mastoparan M - hor	359	2	18.2	11	2	S23677	T cell receptor iota
287	2	18.2	14	1	LFECF	trp operon leader	360	2	18.2	11	2	S23678	T cell receptor kappa
288	2	18.2	14	1	LFECFS	trp operon leader	361	2	18.2	11	2	S23679	T cell receptor lambda
289	2	18.2	14	2	A60622	somatostatin - spu	362	2	18.2	11	2	S23680	T cell receptor mu
290	2	18.2	14	2	B61309	nitrophenyl beta-ch	363	2	18.2	11	2	S23681	T cell receptor nu
291	2	18.2	14	2	JN0389	histamine-releasin	364	2	18.2	11	2	S23682	T cell receptor xi
292	2	18.2	14	2	PH1677	Ig heavy chain V	365	2	18.2	11	2	S23683	T cell receptor omicron
293	2	18.2	14	2	PH1705	Ig heavy chain V	366	2	18.2	11	2	S23684	T cell receptor tau
294	2	18.2	14	2	S51430	hemoglobin beta ch	367	2	18.2	11	2	S23685	T cell receptor phi
295	2	18.2	14	2	S50900	calyculin A/B-inh	368	2	18.2	11	2	S23686	T cell receptor chi
296	2	18.2	14	2	A42473	crmk leader peptid	369	2	18.2	11	2	S23687	T cell receptor psi
297	2	18.2	14	2	A44515	Trp EG leader pept	370	2	18.2	11	2	S23688	T cell receptor omega
298	2	18.2	14	2	JH0328	prolactin tetradec	371	2	18.2	11	2	S23689	T cell receptor sigma
299	2	18.2	14	2	E90858	trp operon leader	372	2	18.2	11	2	S23690	T cell receptor theta
300	2	18.2	14	2	B38222	excinuclease ABC c	373	2	18.2	11	2	S23691	T cell receptor iota
301	2	18.2	14	2	I56388	Kmr(r) protein - Es	374	2	18.2	11	2	S23692	T cell receptor kappa
302	2	18.2	14	2	B44854	1,2,4-diaminobuty	375	2	18.2	11	2	S23693	T cell receptor lambda
303	2	18.2	14	2	A60158	disaggregatase - M	376	2	18.2	11	2	S23694	T cell receptor mu
304	2	18.2	14	2	PA0111	protein QA10054 -	377	2	18.2	11	2	S23695	T cell receptor nu
305	2	18.2	14	2	PN0147	omega-3-linolenic a	378	2	18.2	11	2	S23696	T cell receptor xi
306	2	18.2	14	2	PN0151	omega-3-linolenic a	379	2	18.2	11	2	S23697	T cell receptor omicron
307	2	18.2	14	2	PS0255	20K protein 5503 -	380	2	18.2	11	2	S23698	T cell receptor tau
308	2	18.2	14	2	PS0249	porin - rics (stra	381	2	18.2	11	2	S23699	T cell receptor phi
309	2	18.2	14	2	PQ0698	unidentified 6.9/5	382	2	18.2	11	2	S23700	T cell receptor chi
310	2	18.2	14	2	S35267	acetyl-CoA carboxy	383	2	18.2	11	2	S23701	T cell receptor psi
311	2	18.2	14	2	A39239	actin B - slime mo	384	2	18.2	11	2	S23702	T cell receptor omega
312	2	18.2	14	2	S14336	mastoparan B - hor	385	2	18.2	11	2	S23703	T cell receptor sigma
313	2	18.2	14	2	B39111	Ig heavy chain V r	386	2	18.2	11	2	S23704	T cell receptor theta
314	2	18.2	14	2	PT0223	Ig heavy chain CDR	387	2	18.2	11	2	S23705	T cell receptor iota
315	2	18.2	14	2	PT0294	Ig heavy chain CDR	388	2	18.2	11	2	S23706	T cell receptor kappa
316	2	18.2	14	2	PH1347	Ig heavy chain D2	389	2	18.2	11	2	S23707	T cell receptor lambda
317	2	18.2	14	2	PH1327	Ig heavy chain DJ	390	2	18.2	11	2	S23708	T cell receptor mu
318	2	18.2	14	2	PH1311	Ig heavy chain DJ	391	2	18.2	11	2	S23709	T cell receptor nu
319	2	18.2	14	2	PH1321	Ig heavy chain DJ	392	2	18.2	11	2	S23710	T cell receptor xi
320	2	18.2	14	2	PH1305	Ig heavy chain DJ	393	2	18.2	11	2	S23711	T cell receptor omicron
321	2	18.2	14	2	PH1306	Ig heavy chain DJ	394	2	18.2	11	2	S23712	T cell receptor tau









FEBS Lett. 260, 57-61, 1990  
 A:Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan *Crithidia fascicularis*  
 A:Reference number: A34135  
 A:Accession: B34135  
 A:Molecule type: protein  
 A:Residues: 1-14 <IT>  
 A:Genetics:  
 A:Genome: mitochondrion  
 A:Genetic code: SGC6  
 C:Keywords: mitochondrion

Query Match: 27.3%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.60000;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4

DB 11 RKS 13

#### RESULT 14

PHI471  
 T-cell receptor beta chain (clone A24/PEF4) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
 C:Accession: PHI471  
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Hilla, C.; Pannuelier, C.; Renard, A.; K...  
 J. Exp. Med. 177, 811-820, 1993  
 A:Title: T cell receptor selection by and recognition of two class I major histocompat...  
 A:Reference number: PHI430; MUID:93171621; PMID:943641  
 A:Accession: PHI471  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <CAS>  
 A:Experimental source: cytolytic T-lymphocyte  
 A:Superfamily: immunoglobulin homology  
 C:Keywords: receptor; T-cell

Query Match: 27.3%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.60000;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6

DB 4 SRD 6

#### RESULT 15

PA0003  
 nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 18-Nov-1994 #sequence\_revision 06-Jan-1995 #text\_change 15-Mar-1996  
 C:Accession: PA0003  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
 A:Reference number: PA0001  
 A:Accession: PA0003  
 A:Molecule type: protein  
 A:Residues: 1-15 <KAM>  
 A:Experimental source: leaf and callus  
 C:Superfamily: nucleoside-diphosphate kinase  
 C:Keywords: phosphotransferase

Query Match: 27.3%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.80000;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AIK 11

DB 9 AIK 11

#### RESULT 16

A:Title: Inositol 1,4,5-trisphosphate 3-kinase (EC 2.7.1.37) - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 28-May-1992 #sequence\_revision 06-May-1992 #text\_change 24-Jul-1994  
 C:Accession: A1444  
 R:Boyd, J.C.; Delzon, S.; Boeckmann, J.  
 J. Biochem. J. 299, 443-449, 1994  
 A:Title: Purification and characterization of Arabidopsis inositol 1,4,5-trisphosphate 3-kinase  
 A:Reference number: A1444; MUID:91021101; PMID:1518844  
 A:Accession: A1444  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-17 H Y  
 C:Keywords: inositol 1,4,5-trisphosphate 3-kinase

Query Match: 27.0%; Score 3; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.90000;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6

DB 4 SRD 6

#### RESULT 17

PA0075  
 fructose-bisphosphate phosphatase (EC 3.1.3.17) - human (human spermatozoal vesicles)  
 A:Title: Human fructose-bisphosphate phosphatase (FBPase) from spermatozoal vesicles  
 C:Species: HOMO SAPIENS (human)  
 C:Date: 21-Jul-1995 #sequence\_revision 23-Jul-1995 #text\_change 23-Jul-2001  
 C:Accession: I1A\_76; PA0075  
 R:Gawron, J.P.; Fagan, M.; Saitou, N.; Kato, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, Oct 4, 1994  
 A:Description: FBPase, a cytosolic fructose-bisphosphate phosphatase of human spermatozoal vesicles  
 A:Reference number: PA0075  
 A:Accession: PA0075  
 A:Molecule type: protein  
 A:Residues: 1-133  
 A:Status: preliminary  
 A:Experimental source: (1) and (2) human spermatozoal vesicles and an electric point of  
 A:Residues: 1-133  
 A:Keywords: fructose-bisphosphate phosphatase

Query Match: 27.0%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.90000;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6

DB 4 SRD 6

#### RESULT 18

PA0102  
 fructose-bisphosphate phosphatase (EC 3.1.3.17) - human (human spermatozoal vesicles)  
 C:Species: HOMO SAPIENS (human)  
 C:Date: 21-Jul-1995 #sequence\_revision 23-Jul-1995 #text\_change 23-Jul-2001  
 C:Accession: PA0102  
 R:Gawron, J.P.; Fagan, M.; Saitou, N.; Kato, Y.; Tabuchi, K.; Tsutsumi, A.  
 submitted to JIPID, Oct 4, 1994  
 A:Description: FBPase, a cytosolic fructose-bisphosphate phosphatase of human spermatozoal vesicles  
 A:Reference number: PA0102  
 A:Accession: PA0102  
 A:Molecule type: protein  
 A:Residues: 1-133  
 A:Status: preliminary  
 C:Keywords: fructose-bisphosphate phosphatase

Query Match: 27.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.90000;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4  
III  
DB 8 RKS 10

## RESULT 19

A47628

Fc gamma receptor II (CD32) - human (fragments)

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07 May 1994

C:Accession: A47628

R:Warmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, E.J.; Copel, P.J.A.

J. Exp. Med. 172, 19-25, 1990

A:Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).

A:Reference number: A47628; MUID:90293679; PMID:2141627

A:Accession: A47628

A&gt;Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-15 &lt;WAR&gt;

C:Keywords: immunoglobulin receptor

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Rev: 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MTA 9

III

DB 1 MTA 3

## RESULT 20

G49255

T-cell receptor beta chain V-D-J-C region (V beta 24, J beta 2.1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30 May 1997

C:Accession: G49255

R:Rosenberg, W.M.; Moss, P.A.; Bell, J.L.

Eur. J. Immunol. 22, 541-549, 1992

A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A:Reference number: A49039; MUID:92164737; PMID:1311263

A:Accession: G49255

A&gt;Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-15 &lt;ROS&gt;

A&gt;Note: sequence extracted from NCBI backbone (NCBI:90728)

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Rev: 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6

III

DB 4 SRD 6

## RESULT 21

PH1590

Ig H chain V-D-J region (wild-type clone 141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1994

C:Accession: PH1590

R:Levinson, D.A.; Campos-Torres, J.; Leber, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-28 mice

A:Reference number: PH1580; MUID:93301609; PMID:8415367

A:Accession: PH1590

A:Molecule type: DNA

A:Residues: 1-15 &lt;LEV&gt;

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2; Rev: 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RKM 7

III

DB 3 RKM 5

## RESULT 22

PH1449

Ig heavy chain V region (pre-B cell clone 14.4.17R) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 01-Dec-1993 #sequence\_revision 01-Dec-1993 #text\_change 12-Mar-1995

C:Accession: PH1449

R:Shirasaka, T.; Miyazawa, H.; Kikuchi, S.; Kimoto, H.; Sakemura, K.; Taniuchi, M.

J. Exp. Med. 176, 209-214, 1992

A:Title: Heavy chain of the V(H) region: diversity generated by V(D)J recombination

A:Accession: PH1449

A:Reference number: PH1449; MUID:90134265

A:Accession: PH1449

A:Accession: PH1449

A:Accession: PH1449

A:Accession: PH1449

A:Accession: PH1449

A:Accession: PH1449

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A:Accession: PH1449

A:Accession: PH1449

A:Accession: PH1449

A:Accession: PH1449

A:Accession: PH1449

A:Residues: 1-8 <MAN>

C:Superfamily: unassigned animal peptides

Query Match 18.2% Score 2: DB 2: Length 8:

Best Local Similarity 100.0% Pred. No. 2.8e+05:

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 TA 9

DB 5 TA 6

RESULT 25

S43972

tumor-associated antigen MUT2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000

C:Accession: S43972

R:Mandelblat, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.

Nature 369, 67-71, 1994

A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine

A:Reference number: S43971; MUID:94217811; PMID:8164742

A:Accession: S43972

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAN>

C:Superfamily: unassigned animal peptides

Query Match

Best Local Similarity 100.0% Pred. No. 2.8e+05:

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 TA 9

DB 5 TA 6

RESULT 26

T10077

hypothetical protein N - Methylophilus methylotrophus (fragment)

C:Species: Methylophilus methylotrophus

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000

C:Accession: T10077

R:Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.

J. Bacteriol. 176, 4073-4080, 1994

A:Title: Organization of the methylanine utilization (mau) genes in Methylophilus methyl-

A:Reference number: T10077; MUID:94292427; PMID:8021188

A:Accession: T10077

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <CHT>

A:CROSS-references: EMBL:L26407; NID:9561931; PID:AA846955.1; PID:q561944

A:Experimental source: strain W3A1

C:Genetics:

A:Gene: mauN

Query Match

Best Local Similarity 100.0% Pred. No. 2.8e+05:

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 9 A1 10

DB 6 A1 7

RESULT 27

PC4131

hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: PC4131

R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.

Gene 167, 87-91, 1995

A:Title: Sequencing and characterization of the downstream region of the genes involved in the biosynthesis of gamma-D-glutamate. PMID:8566817

A:Reference number: S47141; MUID:0144154; PMID:8566817

A:Accession: S47141

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <KAW>

A:CROSS-references: EMBL:054474; K:0127354

A:Note: This ORF is not annotated in Genbank entry F58187, release 113.0

Query Match

Best Local Similarity 100.0% Pred. No. 2.8e+05:

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 KS 5

DB 5 SR 5

RESULT 28

S47141

tpsa protein - Escherichia coli

C:Species: Escherichia coli

C:Date: 06-Jan-1994 #sequence\_revision 06-Jan-1994 #text\_change 08-Jul-1999

C:Accession: S47141

R:Douville, A.; Tessier, A.; Lacombe, M.

submitted to the EMBL Data Library, August 1993

A:Description: Identification of the information host factor genes of Escherichia coli

A:Reference number: S47141

A:Accession: S47141

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <KAW>

A:CROSS-references: EMBL:X74749; K:0199669; PID:CAA52769.1; EMBL:541108

Query Match

Best Local Similarity 100.0% Pred. No. 2.8e+05:

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KS 4

DB 3 KS 4

RESULT 29

S21274

cellulase (EC 3.2.1.4) - Clostridium thermocellum (fragment)

N:Alternate names: endo-1,4-beta-D-glucanase

C:Species: Clostridium thermocellum

C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 22-Nov-1999

C:Accession: S21274

R:Romaniuk, M.F.M.; Barth, D.; Kojima, T.; Haskisson, N.S.; Barker, R.L.; Demain, J.

Biotechnol. J. 283, 69-73, 1992

A:Title: Purification and characterization of a new endoglucanase from Clostridium t

A:Reference number: S21274; MUID:0204850; PMID:1567379

A:Accession: S21274

A:Molecule type: protein

A:Residues: 1-8 <KAW>

C:Function:

A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as

A:Pathway: cellulase degradation

C:Keywords: alycosidase, hydrolase, polysaccharide degradation

Query Match

Best Local Similarity 100.0% Pred. No. 2.8e+05:

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 TA 9

DB 7 TA 8

RESULT 30

```

Tl0952
hypothetical protein 1 - spring vetch
C:Species: Vicia sativa (spring vetch, tare)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: Tl0952
R:Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgaard, N.; Larsen, K.; Yang, W.; Hiss,
submitted to the EMBL Data Library, December 1995
A:Description: A novel type of DNA binding protein interacts with a conserved sequence
A:Reference number: 217228
A:Accession: Tl0952
A>Status: preliminary; translated from GB/EMBL/DDRJ
A:Molecule type: mRNA
A:Residues: 1-8 <CHR>
A:Cross-references: EMBL:X95995; NID:g1360633; PIR:025824

Query Match      18.2%  Score 2:  Db 2:  Length 8:
Best Local Similarity 100.0%: Pred. No. 2.8e+05:
Matches 2:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY      7 MT 8
Db      3 MT 4

RESULT 31
S22428
chitin-binding protein - potato (fragment)
C:Species: Solanum tuberosum (potato)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Nov-1998
C:Accession: S22428
R:Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.P.; Redwood, G.F.
Biochem. J. 283, 813-821, 1992
A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A:Reference number: S21288; MUID:92272683; PML0:1523771
A:Accession: S22428
A:Molecule type: protein
A:Residues: 1-8 <MIL>
C:Function:
A:Description: may be involved in plant defence
C:Keywords: glycoprotein; hydroxyproline

Query Match      18.2%  Score 2:  Db 2:  Length 8:
Best Local Similarity 100.0%: Pred. No. 2.8e+05:
Matches 2:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY      6 DM 7
Db      3 DM 4

RESULT 32
P10162
paramyosin - northern quahog (fragment)
C:Species: Mercenaria mercenaria (northern quahog)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-May-2000
C:Accession: P10162
R:Watabe, S.; Tsuchiya, T.; Hartshorne, D.J.
Comp. Biochem. Physiol. B 94, 813-821, 1989
A:Title: Phosphorylation of paramyosin.
A:Reference number: P10162; MUID:90107385; PML0:2542591
A:Accession: P10162
A:Molecule type: protein
A:Residues: 1-8 <WAT>
A:Experimental source: white adductor muscle
A:Note: The sequence is the phosphorylated tryptic peptide
C:Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-par
om the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by
C:Keywords: muscle; phosphoprotein
F:5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match      18.2%  Score 2:  Db 2:  Length 8:
Best Local Similarity 100.0%: Pred. No. 2.8e+05:
Matches 2:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

```

```

QY      4 SA 5
Db      1 SA 2

RESULT 33
P45800
serum albumin - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 03-Jul-1993 #sequence_revision 03-Jul-1993 #text_change 31-Dec-1993
C:Accession: P45800
R:Partridge, R.L.; Gostomski, E.; Bowness, W.; Mitra, S.P.
J. Immunol. 153, 176-180, 1994
A:Title: Structures of histidine residues in dog albumin peptides formed by the action of gold pr
A:Reference number: A45800; MUID:9244111; PML0:2474609
A:Accession: P45800
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <PAR>

```

```

Query Match      18.2%  Score 2:  Db 2:  Length 8:
Best Local Similarity 100.0%: Pred. No. 2.8e+05:
Matches 2:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

```

```

QY      1 AR 2
Db      4 AR 4

```

```

RESULT 34
P16138
beta chain V-DJ region (rat brain testis)
C:Species: Mus musculus (house mouse)
C:Date: 02-Mar-1994 #sequence_revision 2-Mar-1994 #text_change 17-May-1999
C:Accession: P16138
R:Levenson, D.A.; Cui, S.; Levenson, J.; Levent, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of a rat V-gene induced immunoglobulin heavy chain N terminu
A:Reference number: P16138; MUID:9244111; PML0:435487
A:Accession: P16138
A:Molecule type: DNA
A:Residues: 1-8 <LEV>
A:Experimental source: brain testis from 6 lymphocyte
C:Keywords: immunoglobulin

```

```

Query Match      18.2%  Score 2:  Db 2:  Length 8:
Best Local Similarity 100.0%: Pred. No. 2.8e+05:
Matches 2:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

```

```

QY      1 AR 2
Db      2 AR 3

```

```

RESULT 35
P10049
beta chain receptor beta chain V-DJ region (rat brain testis)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jul-1992 #sequence_revision 19-Jul-1992 #text_change 04-May-1992
C:Accession: P10049
R:Penney, A.J.
J. Exp. Med. 174, 115-121, 1991
A:Title: Functional sequences of rat beta chain receptor beta chains have low N terminu
A:Reference number: P10049; MUID:9277601; PML0:171556
A:Accession: P10049
A>Status: translation not done
A:Molecule type: mRNA
A:Residues: 1-8 <PEN>
A:Experimental source: brain testis from 6 lymphocyte
C:Keywords: T cell receptor

```

```

Query Match      18.2%  Score 2:  Db 2:  Length 8:

```

Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Labels 0; Caps 0

QY 1 AR 2  
DB 7 AR 8

#### RESULT 36

A47618  
beta-galactosidase (EC 3.2.1.23) lacZ - Streptococcus bovis (Tramont)  
C:Species: Streptococcus bovis  
C>Date: 01-Feb-1994 #sequence\_revision 03 Feb 1994 #text\_change 05 Nov 1994  
C:Accession: A47618  
R:Gilbert, H.J.; Hall, J.  
J. Gen. Microbiol. 133, 2285-2293, 1987  
A:Title: Molecular cloning of Streptococcus bovis lactose catabolic genes.  
A:Reference number: A47618  
A:Accession: A47618  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 18 <GIL>  
A:Cross-references: GB:M35285; NID:q154682; PIDN:AAA7412; PII:q154682  
C:Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Labels 0; Caps 0

Matches 2; Conservative 0; Mismatches 0; Labels 0; Caps 0

QY 9 AI 10  
DB 7 AI 8

#### RESULT 37

T13818  
cytochrome oxidase subunit 1 - Atlantic hagfish mitochondrial (Tramont)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Jul-2000  
C:Accession: T13818  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the NID and the CIL  
A:Reference number: 217775; MUID:97398704; PMID:9254918  
A:Accession: T13818  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 18 <DEL>  
A:Cross-references: EMBL:Y09527; NID:q2345619; PIDN:CAA70718; PII:q2345622  
C:Genetics:  
A:Genome: mitochondrion  
A>Note: COI  
C:Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Labels 0; Caps 0

Matches 2; Conservative 0; Mismatches 0; Labels 0; Caps 0

QY 4 SR 5  
DB 4 SR 5

#### RESULT 38

S66296  
Na<sup>+</sup>-transporting ATP synthase (EC 3.6.1.3) chain c Acetobacterium woodii (Tramont)  
N:Alternate names: ATPase chain c  
C:Species: Acetobacterium woodii  
C>Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07 May 1999  
C:Accession: S66296  
R:Reidlinger, J.; Mueller, V.  
Eur. J. Biochem. 223, 275-283, 1994  
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a

A:Accession: S66296  
A:Molecule type: Protein  
A:Residues: 18 <GIL>  
A:Experimental status: submitted  
C:Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Labels 0; Caps 0

Matches 2; Conservative 0; Mismatches 0; Labels 0; Caps 0

QY 9 AI 10  
DB 7 AI 8

#### RESULT 39

A47618  
beta-galactosidase (EC 3.2.1.23) lacZ - Streptococcus bovis (Tramont)  
C:Species: Streptococcus bovis  
C>Date: 01-Feb-1994 #sequence\_revision 03 Feb 1994 #text\_change 05 Nov 1994  
C:Accession: A47618  
R:Gilbert, H.J.; Hall, J.  
J. Gen. Microbiol. 133, 2285-2293, 1987  
A:Title: Molecular cloning of Streptococcus bovis lactose catabolic genes.  
A:Reference number: A47618  
A:Accession: A47618  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 18 <GIL>  
A:Cross-references: GB:M35285; NID:q154682; PIDN:AAA7412; PII:q154682  
C:Keywords: glycosidase; hydrolase

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Labels 0; Caps 0

Matches 2; Conservative 0; Mismatches 0; Labels 0; Caps 0

QY 9 AI 10  
DB 7 AI 8

#### RESULT 40

T13818  
cytochrome oxidase subunit 1 - Atlantic hagfish mitochondrial (Tramont)  
C:Species: mitochondrion Myxine glutinosa (Atlantic hagfish)  
C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Jul-2000  
C:Accession: T13818  
R:Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
Mol. Biol. Evol. 14, 807-813, 1997  
A:Title: The main features of the craniate mitochondrial DNA between the NID and the CIL  
A:Reference number: 217775; MUID:97398704; PMID:9254918  
A:Accession: T13818  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 18 <DEL>  
A:Cross-references: EMBL:Y09527; NID:q2345619; PIDN:CAA70718; PII:q2345622  
C:Genetics:  
A:Genome: mitochondrion  
A>Note: COI  
C:Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Labels 0; Caps 0

Matches 2; Conservative 0; Mismatches 0; Labels 0; Caps 0

QY 9 AI 10  
DB 7 AI 8

#### RESULT 41

T48646  
hypothetical protein, uncharacterized Streptomyces coelicolor (Tramont)  
C:Species: Streptomyces coelicolor  
C>Date: 22-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20 Jun 2000  
C:Accession: T48646

Query Match 18.2%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0; Labels 0; Caps 0

Matches 2; Conservative 0; Mismatches 0; Labels 0; Caps 0

QY 9 AI 10  
DB 7 AI 8

R:Matsumoto, A.; Hata, S.; Ishizuka, H.; Horinouchi, S.; Beppu, T.  
 Gene 146, 47-56, 1994  
 A:Title: Phosphorylation of the AfSR protein involved in secondary metabolism in Streptomyces  
 A:Reference number: 224852; MUID:94341568; PMID:8061134  
 A:Accession: T48890  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <MAT>  
 A:Cross-references: EMBL:D15062; PDB:BAW4035.1  
 A:Experimental source: Strain M130

Query Match 18.28; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 MT 8  
 DB 1 MT 2

RESULT 42  
 154017  
 granulocyte-colony stimulating factor precursor - synthetic (fragment)  
 C:Species: synthetic  
 A:Note: human gene engineered and expressed in Escherichia coli  
 A:Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
 C:Accession: 154017  
 R:Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, L.F.; Watt, K.W.; Devlin, P.E.  
 Gene 65, 23-22, 1988  
 A:Title: Alteration of amino-terminal codons of human granulocyte colony stimulating factor  
 1.  
 A:Reference number: 154017; MUID:88284374; PMID:2456269  
 A:Accession: 154017  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <DEV>  
 A:Cross-references: GB:M20922; NID:q806638; PDB:AAA66454.1; PDB:1m04

Query Match 18.28; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 MT 8  
 DB 1 MT 2

RESULT 43  
 155411  
 hypothetical histone H2A.X (mistranslated) - human (fragment)  
 C:Species: Homo sapiens (man)  
 A:Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
 C:Accession: 155411  
 R:Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.  
 J. Biol. Chem. 269, 24189-24194, 1994  
 A:Title: Characterization of the human histone H2A.X gene: comparison of its promoter with  
 A:Reference number: 155411; MUID:9501456; PMID:7923675  
 A:Accession: 155411  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <IVA>  
 A:Cross-references: GB:S73863; NID:q76525; PDB:AAA1414.1; PDB:1q451-451  
 A:Note: this is a hypothetical translation of a sequence from the promoter region provided  
 C:Genetics:  
 A:Gene: H2A.X

Query Match 18.28; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AR 2  
 DB 5 AR 6

## RESULT 43

QY 1 AR 2  
 DB 5 AR 6

Query Match 18.28; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AR 2  
 DB 5 AR 6

RESULT 44  
 155411  
 hypothetical histone H2A.X (mistranslated) - human (fragment)  
 C:Species: Homo sapiens (man)  
 A:Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
 C:Accession: 155411  
 R:Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.  
 J. Biol. Chem. 269, 24189-24194, 1994  
 A:Title: Characterization of the human histone H2A.X gene: comparison of its promoter with  
 A:Reference number: 155411; MUID:9501456; PMID:7923675  
 A:Accession: 155411  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <IVA>  
 A:Cross-references: GB:S73863; NID:q76525; PDB:AAA1414.1; PDB:1q451-451  
 A:Note: this is a hypothetical translation of a sequence from the promoter region provided  
 C:Genetics:  
 A:Gene: H2A.X

Query Match 18.28; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AR 2  
 DB 5 AR 6

RESULT 45  
 155411  
 hypothetical histone H2A.X (mistranslated) - human (fragment)  
 C:Species: Homo sapiens (man)  
 A:Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
 C:Accession: 155411  
 R:Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.  
 J. Biol. Chem. 269, 24189-24194, 1994  
 A:Title: Characterization of the human histone H2A.X gene: comparison of its promoter with  
 A:Reference number: 155411; MUID:9501456; PMID:7923675  
 A:Accession: 155411  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <IVA>  
 A:Cross-references: GB:S73863; NID:q76525; PDB:AAA1414.1; PDB:1q451-451  
 A:Note: this is a hypothetical translation of a sequence from the promoter region provided  
 C:Genetics:  
 A:Gene: H2A.X

Query Match 18.28; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AR 2  
 DB 5 AR 6

RESULT 46  
 155411  
 hypothetical histone H2A.X (mistranslated) - human (fragment)  
 C:Species: Homo sapiens (man)  
 A:Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
 C:Accession: 155411  
 R:Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.  
 J. Biol. Chem. 269, 24189-24194, 1994  
 A:Title: Characterization of the human histone H2A.X gene: comparison of its promoter with  
 A:Reference number: 155411; MUID:9501456; PMID:7923675  
 A:Accession: 155411  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <IVA>  
 A:Cross-references: GB:S73863; NID:q76525; PDB:AAA1414.1; PDB:1q451-451  
 A:Note: this is a hypothetical translation of a sequence from the promoter region provided  
 C:Genetics:  
 A:Gene: H2A.X

Query Match 18.28; Score 2; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AR 2  
 DB 5 AR 6

R:Ernstroem, U.; Gafvelin, G.; Rud'ja, J.M.  
 Biosci. Rep. 10: 403-412, 1990  
 A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship of  
 A:Reference number: A60957; MUID:91064427; PMID:2245064  
 A:Accession: A60957  
 A:Molecule type: protein  
 A:Residues: 1-9 <ERN>  
 C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral  
 in a variety of immunoassays  
 C:Comment: this peptide was isolated in two forms. One form contained the pyroglutamate  
 r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a  
 C:Superfamily: thymic factor  
 C:Keywords: blocked amino end; pyroglutamic acid  
 F:/Modified site: pyroglutamate carboxylic acid (Glx) (in FTS) \*status experimental  
 F:/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) \*status experimental

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0

QY 3 KS 4  
 II  
 KS 4

Db

RESULT 47  
 S35538  
 Ribosomal protein S7 - Mycobacterium intracellulare (Strasbourg)  
 C:Species: Mycobacterium intracellulare  
 C:Date: 09-Dec-1993 #sequence\_revision 14 NID:1497 #text\_change 13-Aug-1994  
 C:Accession: S35538  
 R:Nair, J.; Kouse, D.; Morris, S.  
 Nucleic Acids Res. 21: 1039, 1993  
 A:Title: Nucleotide sequence analysis of the ribosomal S7 gene of Mycobacterium intracellulare  
 A:Reference number: S35537; MUID:9197130; PMID:8451174  
 A:Accession: S35538  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-9 <NAI>  
 A:Cross-references: EMBL:08171; NID:q149994; PIDN:AAA5476.1; PID:q551901  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994  
 C:Superfamily: Escherichia coli ribosomal protein S7  
 C:Keywords: protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0

QY 2 RK 3  
 II  
 RK 4

Db

RESULT 48  
 S30494  
 cat gene leader peptide - Streptococcus agalactiae plasmid pIP501  
 C:Species: Streptococcus agalactiae  
 C:Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 24-Sep-1999  
 C:Accession: S30494  
 R:Tricu-Cuot, P.; de Cespedes, G.; Hcraud, T.  
 Plasmid 28, 272-276, 1992  
 A:Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Streptococcus  
 A:Reference number: JQ1950; MUID:93096867; PMID:1461442  
 A:Accession: S30494  
 A:Molecule type: DNA  
 A:Residues: 1-9 <TRI>  
 A:Cross-references: EMBL:X65462; NID:q49071; PIDN:CAA464.1; PID:q51554  
 C:Genetics:  
 A:Genome: plasmid pIP501  
 C:Superfamily: unassigned leader peptides

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0

QY 2 RK 3  
 II  
 RK 4

Db

Matches 2; Conservative 0; Mismatches 0; Indels 0

QY 3 KS 4  
 II  
 KS 4

Db

RESULT 49  
 B24362  
 chloramphenicol acetyl transferase leader peptide - Staphylococcus aureus (Pasteur)  
 C:Species: Staphylococcus aureus  
 C:Date: 07-Apr-1984 #sequence\_revision 10-Apr-1994 #text\_change 11-May-2000  
 C:Accession: B24362  
 R:Bruckner, R.; Walz, J.  
 EMBL J. 4: 2235-2237, 1987  
 A:Title: Regulation of the multicatalytic (multicatalytic acetyl transferase gene) of the  
 A:Reference number: A0401; MUID:9006139; PMID:3455779  
 A:Accession: B24362  
 A:Molecule type: DNA  
 A:Residues: 1-9 <BRU>  
 A:Cross-references: EMBL:046662.1; PID:q551901  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1987  
 C:Superfamily: chloramphenicol acetyl transferase leader peptide  
 C:Keywords: chloramphenicol acetyl transferase; chloramphenicol acetyl transferase leader peptide

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0

QY 3 KS 4  
 II  
 KS 4

Db

RESULT 50  
 S08898  
 Ribosomal protein S7 - Mycobacterium intracellulare (Strasbourg)  
 C:Species: Mycobacterium intracellulare  
 C:Date: 10-Feb-1993 #sequence\_revision 13-Feb-1993 #text\_change 13-Feb-1993  
 C:Accession: S08898  
 R:Nair, J.; Kouse, D.; Morris, S.  
 Nucleic Acids Res. 21: 1039, 1993  
 A:Title: Nucleotide sequence analysis of the ribosomal S7 gene of Mycobacterium intracellulare  
 A:Reference number: S08897; MUID:9197130; PMID:8451174  
 A:Accession: S08898  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: protein  
 A:Residues: 1-9 <NAI>  
 A:Cross-references: EMBL:08171; NID:q149994; PIDN:AAA5476.1; PID:q551901  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994  
 C:Superfamily: Escherichia coli ribosomal protein S7  
 C:Keywords: protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0

QY 3 RK 4  
 II  
 RK 4

Db

Search and Query Match 18.2%; Score 2; DB 2; Length 9;  
 Total Time 12.34 seconds

GenCore version: 5.1.6  
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# OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 6.25 seconds  
(without alignment:s)  
82.767 Million cell updates/sec

Title: US-09-787-443-22

Perfect score: 11

Sequence: 1 AKSRDWTAK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7.7

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	3	27.3	8	1	LPMS_STARP	P21211 staphylococ
2	3	27.3	10	1	ARKH_LOCM1	P81626 locusta miq
3	3	27.3	10	1	GS09_BACSU1	P80243 bacillus su
4	3	27.3	11	1	UYB2_YEAST	P99313 saccharomyc
5	3	27.3	13	1	NEUT_CAVPO3	P12560 cavia porce
6	3	27.3	13	1	RS19_ASHYP	Q44592 ash yellow
7	3	27.3	13	1	YPE2_LACLC	P42021 lactococcus
8	3	27.3	14	1	HCYA_MEGCR	Q10583 megathura c
9	3	27.3	15	1	ACEA_ACICA	P24467 acinetobact
10	3	27.3	15	1	RS20_BACST	P59681 bacillus st
11	3	27.3	15	1	TAL_TREBR	P46070 tremella br
12	2	18.2	8	1	ACT_THUAL	P18691 thannus alb
13	2	18.2	8	1	ACT_CARMA	P60709 carcinus ma
14	2	18.2	8	1	AL12_CARMA	P81915 carcinus ma
15	2	18.2	8	1	AL18_CARMA	P81821 carcinus ma
16	2	18.2	8	1	ALL3_CYDPO	P82154 cydia pomon
17	2	18.2	8	1	ALL4_CYDPO	P82155 cydia pomon
18	2	18.2	8	1	ALL5_CYDPO	P82156 cydia pomon
19	2	18.2	8	1	RS1_ERWCH	P37485 erwinia chi
20	2	18.2	8	1	RS7_MYC11	P34564 mycobacteri
21	2	18.2	8	1	UC26_MAI2E	P83632 zea mays (m
22	2	18.2	9	1	FARA_CALVO	P41865 calliphora
23	2	18.2	9	1	IPYR_RHOVI	P82392 rhodopsin
24	2	18.2	9	1	LPCA_STAA0	P16984 staphylococ
25	2	18.2	9	1	NEF_HV12B	P12481 human immun
26	2	18.2	9	1	NEUX_HUMAN	P84277 homo sapien
27	2	18.2	9	1	PPK1_PERAM	P82691 periplaneta
28	2	18.2	9	1	SAMP_MUSCA	P15095 mustelus ca
29	2	18.2	9	1	THYF_PIG	P31255 sus scrofa
30	2	18.2	9	1	TRCL_CALVO	P41517 calliphora
31	2	18.2	9	1	ULAK_MOUSE	P96031 mus muscu
32	2	18.2	10	1	AL19_CARMA	P81822 carcinus ma
33	2	18.2	10	1	CATB_SHEEP	P83205 ovnis aries

34	2	18.2	10	1	OX2_SHEEP	P80306 ovnis aries
35	2	18.2	10	1	OX2_SHEEP	P80307 ovnis aries
36	2	18.2	10	1	ETBA_PERSI	P14577 ceratopoda
37	2	18.2	10	1	MALE_KLEPN	Q55314 klebsiella
38	2	18.2	10	1	NE40_CUBAC	P55462 neorhabd
39	2	18.2	10	1	PG2_BAVIN	P82423 bos taur
40	2	18.2	10	1	SYR_TAMIP	Q46454 carpylidact
41	2	18.2	10	1	TRMS_PANTL	P56423 rana tempor
42	2	18.2	10	1	TRMS_PANTL	P22489 rana tempor
43	2	18.2	10	1	TRMS_PANTL	P01242 sus scrofa
44	2	18.2	10	1	TRMS_PANTL	P40751 archis an
45	2	18.2	10	1	TRMS_PANTL	P40751 archis an
46	2	18.2	10	1	TRMS_PANTL	P30395 homo sapien
47	2	18.2	10	1	TRMS_PANTL	P30395 homo sapien
48	2	18.2	10	1	TRMS_PANTL	P12797 medusella
49	2	18.2	10	1	TRMS_PANTL	P11496 periplaneta
50	2	18.2	10	1	TRMS_PANTL	P81045 bacillus su
51	2	18.2	10	1	TRMS_PANTL	P56571 rat us moy
52	2	18.2	10	1	TRMS_PANTL	P49820 canis fami
53	2	18.2	10	1	TRMS_PANTL	P59472 pseudocatta
54	2	18.2	10	1	TRMS_PANTL	P55574 pse akmanas
55	2	18.2	10	1	TRMS_PANTL	P46444 comonomas
56	2	18.2	10	1	TRMS_PANTL	P42411 ceratopoda
57	2	18.2	10	1	TRMS_PANTL	P83424 ceratopoda
58	2	18.2	10	1	TRMS_PANTL	P82654 neoplodact
59	2	18.2	10	1	TRMS_PANTL	P43424 penaeus ma
60	2	18.2	10	1	TRMS_PANTL	Q10584 megalothura
61	2	18.2	10	1	TRMS_PANTL	P22426 locusta miq
62	2	18.2	10	1	TRMS_PANTL	P24469 sesobacta
63	2	18.2	10	1	TRMS_PANTL	P86207 quinko brio
64	2	18.2	10	1	TRMS_PANTL	P40864 bacillus su
65	2	18.2	10	1	TRMS_PANTL	P82654 neoplodact
66	2	18.2	10	1	TRMS_PANTL	P82654 neoplodact
67	2	18.2	10	1	TRMS_PANTL	P88611 kassini sou
68	2	18.2	10	1	TRMS_PANTL	P56572 rat us moy
69	2	18.2	10	1	TRMS_PANTL	P81147 calliphora
70	2	18.2	10	1	TRMS_PANTL	P82046 white spe
71	2	18.2	10	1	TRMS_PANTL	P82046 white spe
72	2	18.2	10	1	TRMS_PANTL	P27476 oscherotoma
73	2	18.2	10	1	TRMS_PANTL	P82496 liliobacta
74	2	18.2	10	1	TRMS_PANTL	P82497 liliobacta
75	2	18.2	10	1	TRMS_PANTL	P42717 paraplodyla
76	2	18.2	10	1	TRMS_PANTL	P82351 liliobacta
77	2	18.2	10	1	TRMS_PANTL	P40864 bacillus su
78	2	18.2	10	1	TRMS_PANTL	P01518 ceratopoda
79	2	18.2	10	1	TRMS_PANTL	P28449 bos taur
80	2	18.2	10	1	TRMS_PANTL	P80941 lysanctia g
81	2	18.2	10	1	TRMS_PANTL	P14472 hyalocetes
82	2	18.2	10	1	TRMS_PANTL	P14478 oryctolates
83	2	18.2	10	1	TRMS_PANTL	P82415 rana escul
84	2	18.2	10	1	TRMS_PANTL	P54496 rana escul
85	2	18.2	10	1	TRMS_PANTL	P46574 rat us moy
86	2	18.2	10	1	TRMS_PANTL	P23511 trammeltes
87	2	18.2	10	1	TRMS_PANTL	P43012 trammeltes
88	2	18.2	10	1	TRMS_PANTL	P88496 paraplodyla
89	2	18.2	10	1	TRMS_PANTL	P81796 liliobacta
90	2	18.2	10	1	TRMS_PANTL	P14724 quinko brio
91	2	18.2	10	1	TRMS_PANTL	P41546 rana tempor
92	2	18.2	10	1	TRMS_PANTL	P41347 liliobacta
93	2	18.2	10	1	TRMS_PANTL	P55959 paraplodyla
94	2	18.2	10	1	TRMS_PANTL	P49844 canis fami
95	2	18.2	10	1	TRMS_PANTL	P20314 pig us moy
96	2	18.2	10	1	TRMS_PANTL	P17243 pig us moy
97	2	18.2	10	1	TRMS_PANTL	P81667 penaeus ma
98	2	18.2	10	1	TRMS_PANTL	P41122 phyllobacta
99	2	18.2	10	1	TRMS_PANTL	P80941 lysanctia g
100	2	18.2	10	1	TRMS_PANTL	P54845 canis fami
101	2	18.2	10	1	TRMS_PANTL	P99502 canis fami
102	2	18.2	10	1	TRMS_PANTL	P81155 sus scrofa
103	2	18.2	10	1	TRMS_PANTL	P84404 bacillus su
104	2	18.2	10	1	TRMS_PANTL	P56045 escherichia
105	2	18.2	10	1	TRMS_PANTL	P82046 white spe
106	2	18.2	10	1	TRMS_PANTL	P83054 escherichia





[illegible]

399	1	9.1	11	1	CX5B_CONAL	P48824 Citrus aurantifolius	424	1	1	1	1	K22_KASMA	P46624 Cassia tora
400	1	9.1	11	1	CX11_CONMR	P48807 Citrus maritima	424	1	1	1	1	K22_KASMA	P46624 Cassia tora
401	1	9.1	11	1	REF_CIOFPA	P4350 Citrus glaberrima	424	1	1	1	1	K22_KASMA	P46624 Cassia tora
402	1	9.1	11	1	FAR6_PENMU	P43321 Pandanus peltatus	425	1	1	1	1	K22_KASMA	P46624 Cassia tora
403	1	9.1	11	1	FAR9_CALVPO	P43864 Calliphora vicina	426	1	1	1	1	K22_KASMA	P46624 Cassia tora
404	1	9.1	11	1	H570_PINPS	P86624 Pinus pinaster	427	1	1	1	1	K22_KASMA	P46624 Cassia tora
405	1	9.1	11	1	LADD_ONCMY	P86018 Eucalyptus globulus	428	1	1	1	1	K22_KASMA	P46624 Cassia tora
406	1	9.1	11	1	LPW_THETH	P45624 Therapsid thomasi	429	1	1	1	1	K22_KASMA	P46624 Cassia tora
407	1	9.1	11	1	LSK1_LEDMA	P44228 Leptodermis	430	1	1	1	1	K22_KASMA	P46624 Cassia tora
408	1	9.1	11	1	LSKP_PERAM	P46845 Periphanthera	431	1	1	1	1	K22_KASMA	P46624 Cassia tora
409	1	9.1	11	1	MHL1_KLEPN	P40582 Kleptocarpus	432	1	1	1	1	K22_KASMA	P46624 Cassia tora
410	1	9.1	11	1	MHL1_THETS	P43989 Therapsid thomasi	433	1	1	1	1	K22_KASMA	P46624 Cassia tora
411	1	9.1	11	1	MORN_HUMAN	P41163 Homo sapiens	434	1	1	1	1	K22_KASMA	P46624 Cassia tora
412	1	9.1	11	1	MORN_HUMAN	P42684 Carassius auratus	435	1	1	1	1	K22_KASMA	P46624 Cassia tora
413	1	9.1	11	1	PVK1_PERAM	P41847 Periphanthera	436	1	1	1	1	K22_KASMA	P46624 Cassia tora
414	1	9.1	11	1	RANC_RANPI	P40951 Rana pipiens	437	1	1	1	1	K22_KASMA	P46624 Cassia tora
415	1	9.1	11	1	R441_LITRO	P42374 Litorea rubra	438	1	1	1	1	K22_KASMA	P46624 Cassia tora
416	1	9.1	11	1	RRLP_CHAV	P43179 Chondrichthys	439	1	1	1	1	K22_KASMA	P46624 Cassia tora
417	1	9.1	11	1	T2P2_PROVU	P41244 Proteus vulgaris	440	1	1	1	1	K22_KASMA	P46624 Cassia tora
418	1	9.1	11	1	TIN1_HOPT1	P42655 Hoplostethus	441	1	1	1	1	K22_KASMA	P46624 Cassia tora
419	1	9.1	11	1	TKC2_CALWI	P41558 Calliphora vicina	442	1	1	1	1	K22_KASMA	P46624 Cassia tora
420	1	9.1	11	1	TKN1_PSECU	P42906 Pseudocypripedium	443	1	1	1	1	K22_KASMA	P46624 Cassia tora
421	1	9.1	11	1	TKN1_PSECU	P42906 Pseudocypripedium	444	1	1	1	1	K22_KASMA	P46624 Cassia tora
422	1	9.1	11	1	TKN1_PSECU	P42906 Pseudocypripedium	445	1	1	1	1	K22_KASMA	P46624 Cassia tora
423	1	9.1	11	1	TKN1_PSECU	P42906 Pseudocypripedium	446	1	1	1	1	K22_KASMA	P46624 Cassia tora
424	1	9.1	11	1	TKN2_PSECU	P42906 Pseudocypripedium	447	1	1	1	1	K22_KASMA	P46624 Cassia tora
425	1	9.1	11	1	TKN3_PSECU	P42906 Pseudocypripedium	448	1	1	1	1	K22_KASMA	P46624 Cassia tora
426	1	9.1	11	1	TKN4_PSECU	P42906 Pseudocypripedium	449	1	1	1	1	K22_KASMA	P46624 Cassia tora
427	1	9.1	11	1	TKN5_PSECU	P42906 Pseudocypripedium	450	1	1	1	1	K22_KASMA	P46624 Cassia tora
428	1	9.1	11	1	TKN6_PSECU	P42906 Pseudocypripedium	451	1	1	1	1	K22_KASMA	P46624 Cassia tora
429	1	9.1	11	1	TKNA_CHICK	P42906 Pseudocypripedium	452	1	1	1	1	K22_KASMA	P46624 Cassia tora
430	1	9.1	11	1	TKNA_GAMMO	P42906 Pseudocypripedium	453	1	1	1	1	K22_KASMA	P46624 Cassia tora
431	1	9.1	11	1	TKNA_HORSE	P42906 Pseudocypripedium	454	1	1	1	1	K22_KASMA	P46624 Cassia tora
432	1	9.1	11	1	TKNA_GNMY	P42906 Pseudocypripedium	455	1	1	1	1	K22_KASMA	P46624 Cassia tora
433	1	9.1	11	1	TKNA_RANCA	P42906 Pseudocypripedium	456	1	1	1	1	K22_KASMA	P46624 Cassia tora
434	1	9.1	11	1	TKNA_RANCA	P42906 Pseudocypripedium	457	1	1	1	1	K22_KASMA	P46624 Cassia tora
435	1	9.1	11	1	TKNA_SCYCA	P42906 Pseudocypripedium	458	1	1	1	1	K22_KASMA	P46624 Cassia tora
436	1	9.1	11	1	TKND_RANCA	P42906 Pseudocypripedium	459	1	1	1	1	K22_KASMA	P46624 Cassia tora
437	1	9.1	11	1	TKN_ELEMO	P42906 Pseudocypripedium	460	1	1	1	1	K22_KASMA	P46624 Cassia tora
438	1	9.1	11	1	TKN_PHYPU	P42906 Pseudocypripedium	461	1	1	1	1	K22_KASMA	P46624 Cassia tora
439	1	9.1	11	1	UF05_MOUSE	P46615 Physalis physalis	462	1	1	1	1	K22_KASMA	P46624 Cassia tora
440	1	9.1	11	1	ULAG_HUMAN	P46615 Physalis physalis	463	1	1	1	1	K22_KASMA	P46624 Cassia tora
441	1	9.1	11	1	CALM_TETTH	P46615 Physalis physalis	464	1	1	1	1	K22_KASMA	P46624 Cassia tora
442	1	9.1	11	1	COL1_LITXA	P46615 Physalis physalis	465	1	1	1	1	K22_KASMA	P46624 Cassia tora
443	1	9.1	11	1	COL1_LITXA	P46615 Physalis physalis	466	1	1	1	1	K22_KASMA	P46624 Cassia tora
444	1	9.1	11	1	CX13_CONMR	P46615 Physalis physalis	467	1	1	1	1	K22_KASMA	P46624 Cassia tora
445	1	9.1	11	1	CX13_CONMR	P46615 Physalis physalis	468	1	1	1	1	K22_KASMA	P46624 Cassia tora
446	1	9.1	11	1	CX13_CONMR	P46615 Physalis physalis	469	1	1	1	1	K22_KASMA	P46624 Cassia tora
447	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	470	1	1	1	1	K22_KASMA	P46624 Cassia tora
448	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	471	1	1	1	1	K22_KASMA	P46624 Cassia tora
449	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	472	1	1	1	1	K22_KASMA	P46624 Cassia tora
450	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	473	1	1	1	1	K22_KASMA	P46624 Cassia tora
451	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	474	1	1	1	1	K22_KASMA	P46624 Cassia tora
452	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	475	1	1	1	1	K22_KASMA	P46624 Cassia tora
453	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	476	1	1	1	1	K22_KASMA	P46624 Cassia tora
454	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	477	1	1	1	1	K22_KASMA	P46624 Cassia tora
455	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	478	1	1	1	1	K22_KASMA	P46624 Cassia tora
456	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	479	1	1	1	1	K22_KASMA	P46624 Cassia tora
457	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	480	1	1	1	1	K22_KASMA	P46624 Cassia tora
458	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	481	1	1	1	1	K22_KASMA	P46624 Cassia tora
459	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	482	1	1	1	1	K22_KASMA	P46624 Cassia tora
460	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	483	1	1	1	1	K22_KASMA	P46624 Cassia tora
461	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	484	1	1	1	1	K22_KASMA	P46624 Cassia tora
462	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	485	1	1	1	1	K22_KASMA	P46624 Cassia tora
463	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	486	1	1	1	1	K22_KASMA	P46624 Cassia tora
464	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	487	1	1	1	1	K22_KASMA	P46624 Cassia tora
465	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	488	1	1	1	1	K22_KASMA	P46624 Cassia tora
466	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	489	1	1	1	1	K22_KASMA	P46624 Cassia tora
467	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	490	1	1	1	1	K22_KASMA	P46624 Cassia tora
468	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	491	1	1	1	1	K22_KASMA	P46624 Cassia tora
469	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	492	1	1	1	1	K22_KASMA	P46624 Cassia tora
470	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	493	1	1	1	1	K22_KASMA	P46624 Cassia tora
471	1	9.1	11	1	FAR1_CALVO	P46615 Physalis physalis	494	1	1	1	1	K22_KASMA	P46624 Cassia tora

Query Match: 100% Score: 100 Length: 81  
 Best Local Similarity: 100% (100% of 100%)

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MTA 9  
III  
DB 1 MTA 3

## RESULT 2

AKHX\_LOCM1 STANDARD: PRT; 10 AA.  
AC P81626;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Peptide hormone.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC Tissue-Corpora cardiaca;  
RA Siegfert K.J.;  
RL Submitted (DRC-1998) to the SWISS-PRGT data bank.  
CC -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF INSTAR  
INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.  
CC -!- SIMILARITY: BELONGS TO THE AKH / RHCH / RHCH FAMILY.  
DR InterPro: IPR002047; AKH.  
KW PROSITE: PS00256; AKH; 1.  
DR Neuropeptide; Amidation: Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION  
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 27.38; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6  
III  
DB 5 SRD 7

## RESULT 3

GS09\_BACSU STANDARD: PRT; 10 AA.  
AC P80243;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE General stress protein 9 (GSP9) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=168 / 1S58;  
RX MEDLINE=94282319; PubMed=8012595;  
RA Voelker U., Engelmann S., Maul B., Riechdorf S., Voelker A.,  
RA Schmid R., Mech H., Hecker M.;  
RT 'Analysis of the induction of general stress proteins of Bacillus subtilis.';  
RL Microbiology 140:741-752(1994).  
CC -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE  
LIMITATION AND OXYGEN LIMITATION.  
CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.  
KW Heat shock.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1168 MW; 99766442D5A2C05A CRC64;

Query Match 27.38; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 4  
III  
DB 1 SRD 4

## RESULT 4

UAP2\_YEAST STANDARD: PRT; 11 AA.  
AC P99013;  
DT 01-NOV-1996 (Rel. 32, Created)  
DT 01-NOV-1996 (Rel. 32, Last sequence update)  
DT 01-NOV-1996 (Rel. 32, Last annotation update)  
DE Unknown protein (p14.2) from yeast (Spod. 20.60K2F) (Fragment)  
OS Saccharomyces cerevisiae (baker's yeast).  
OC Eukaryota; Eukaryota; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycotina; Saccharomycetes; Saccharomycotina; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=X218-1A;  
RA Siegfert K.J.;  
RL Submitted (DRC-1996) to the SWISS-PRGT data bank.  
CC -!- MISCANALYSIS: ON 01-NOV-96 THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN WAS 6.4. THIS MW IS 1.2 KDa  
DR SWISS-PROT: P99013; YEAST.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1428 MW; 10406210D7421A CRC64;

Query Match 27.38; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APR 4  
III  
DB 7 APR 4

## RESULT 5

NECI\_CAVIP STANDARD: PRT; 15 AA.  
AC P42566;  
DT 01-DEC-1994 (Rel. 23, Created)  
DT 01-DEC-1994 (Rel. 23, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neurotensin (NT).  
GN NTS.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricomorpha; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Small intestine;  
RX MEDLINE=86244785; PubMed=387996;  
RA Shaw C., Thom C., Campbell M.;  
RI 'Islet-1 neurotensin receptor isolation from Guinea pig intestine.';  
RL FEBS Lett. 252:187-192(1989).  
CC -!- FUNCTION: Specific mouse neurotensin binding peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: RESEMBLES TO THE NEUROTENSIN FAMILY.  
DR PIR: A53669; A44068  
KW Vasodilator; Peptide; Brain; Neurotensin; Antagonist.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 15 AA; 1740 MW; 47834344C4115B5 CRC64;

Query Match 27.38; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 5



P28467:  
 01-DEC-1992 (Rel. 24, Created)  
 01-DEC-1992 (Rel. 24, Last sequence update)  
 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Isocitrate lyase (EC 4.1.3.1) (isocitrase) (isocitratase) (IDL)  
 DE (Fragment).  
 GN ACBA.  
 OS Acinetobacter calcoaceticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=471;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92041568; PubMed=1938889;  
 RA Hoyt J.C., Johnson K.E., Reeves H.C.;  
 RT "Purification and characterization of Acinetobacter calcoaceticus  
 isocitrate lyase.";  
 RL J. Bacteriol. 173:6844-6848(1991).  
 CC -I- CATALYTIC ACTIVITY: isocitrate -> succinate + glyoxylate.  
 CC -I- PATHWAY: FIRST STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE  
 CC TRICARBOXYLIC ACID CYCLE (IN BACTERIA, PLANTS, AND FUNGI).  
 CC -I- SUBUNIT: Homotetramer (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -I- SIMILARITY: BELONGS TO THE ISOCITRATE LYASE FAMILY.  
 DR PIR: A41338; A41338.  
 DR InterPro: IPR000918; Isocit\_lyase.ph.  
 DR PROSITE: PS00161; ISOCITRATE\_LYASE; PARTIAL.  
 KW Glyoxylate bypass; Tricarboxylic acid cycle; Lyase.  
 FT NON\_TER 15  
 FT SEQUENCE 15 AA; 1710 MW; 81AE726B1F2F9EE5 CRC64;  
 Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No.1.le-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 TAI 10  
 Db III  
 5 TAI 7

RESULT 10  
 RS20\_BACST  
 ID RS20\_BACST STANDARD; PRT: 15 AA.  
 AC P59681.  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE 30S ribosomal protein S20 (RS20) (Fragment).  
 GN RPS2.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
 OX NCBI\_TaxID=1422;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=10;  
 RX PubMed=4607606;  
 RA Yaguchi M., Matheson A.T., Visentin L.P.;  
 RT "Procarboxylic ribosomal proteins: N-terminal sequences, hemolysates and  
 RT structural correspondence of 30 S ribosomal proteins from Escherichia  
 coli and Bacillus stearothermophilus.";  
 RL FEBS Lett. 46:296-300(1974).  
 CC -I- FUNCTION: Binds directly to 16S ribosomal RNA (By similarity).  
 CC -I- SIMILARITY: BELONGS TO THE S20P FAMILY OF RIBOSOMAL PROTEINS.  
 DR HAMAP: MF\_00500; -- 1  
 KW Ribosomal\_protein; rRNA-binding.  
 FT INIT\_MET 0  
 FT NON\_TER 15  
 FT SEQUENCE 15 AA; 1645 MW; 4E4646265E4C6286 CRC64;  
 Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No.1.le-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AIX 11  
 Db III  
 6 AIX 8

RESULT 11  
 TAL\_TREPR  
 ID TAL\_TREPR STANDARD; PRT: 15 AA  
 AC P44070;  
 DT 01-FEB-1994 (Rel. 24, Created)  
 DT 01-FEB-1994 (Rel. 24, Last sequence update)  
 DE Tremella fuciformis (Rel. 24, Last annotation update)  
 DE Tremella fuciformis A1.  
 OS Tremella fuciformis (Rel. 24, Created)  
 OC Eukaryota; Fungi; Basidiomycota; Agaricomycetes; Retortomycetes  
 OC Tremellales; Tremella.  
 OX NCBI\_TaxID=29767;  
 RN [1]  
 RP SEQUENCE.  
 RA DUBREUIL Y., STREUMER Y., LESTER A., S. ZUK A.;  
 RC "Structures of Tremella fuciformis A1 and A9241 with peptide  
 RC fragments of Tremella fuciformis A1."  
 RC Biochemistry 23:1444-1449(1984).  
 CC -I- FUNCTION: TREMELLA A1 IS A PROTEIN OF THE A MAINTAIN THE CELL  
 CC AND TREMELLA FUCIFORMIS A9241 MAINTAIN THE A MAINTAIN THE CELL  
 CC PROTEOMES. Primary structure of Tremella fuciformis A1 and A9241  
 CC DUBREUIL Y., STREUMER Y., LESTER A., S. ZUK A.;  
 CC SEQUENCE 15 AA; 150 MW; 6AA6A4E2D05A5129E944;  
 Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No.1.le-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 SEP 4  
 Db III  
 5 SEP 7

RESULT 12  
 TAL\_TREPR  
 ID TAL\_TREPR STANDARD; PRT: 15 AA.  
 AC P44070;  
 DT 01-NOV-1994 (Rel. 16, Created)  
 DT 01-NOV-1994 (Rel. 16, Last sequence update)  
 DT 01-NOV-1994 (Rel. 16, Last annotation update)  
 DE Actinensin, an actin-specific enzyme inhibitor.  
 DE Actinensin, an actin-specific enzyme inhibitor.  
 OS Thapsius albaricus (Yellowish fungi) (Noctuidae; Macrolepidoptera).  
 OC Eukaryota; Metazoa; Chordata; Insecta; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostomi; Neoteleostei;  
 OC Acantomorpha; Acantopterygii; Teleostei; Euteleostomi; Neoteleostei;  
 OC Scombridae; Thunnus.  
 OX NCBI\_TaxID=8246;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE Muscle;  
 RX MEDLINE=8802622; PubMed=417088;  
 RA Kohama Y., Watanabe S., Kikuchi H.;  
 RT "Isolation of actinensin, an actin-specific enzyme inhibitor from Thapsia  
 RT albaricus.";  
 RL Biochem. Biophys. Res. Commun. 135:450-453(1988).  
 DR PIR: A14570; A14570.  
 CC SEQUENCE 15 AA; 150 MW; 6AA6A4E2D05A5129E944;  
 Query Match 27.3%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred.No.1.le-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 IK 11  
 Db III  
 4 IK 5

RESULT 14

```

ACT_CARMA          STANDARD:          PRT:          8 AA.
AC  P80709;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Actin (Fragment).
OS  Carcinus maenas (Common shore crab) (Green crab).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC  Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX  NCBI_TaxID:6759;
RN  [1]
RP  SEQUENCE.
RA  Lachaise F., Somme G., Carpentier G., Granjeon P., Wolsten S.,
RA  Baghdassarian D.:
RT  "A transaldolase. An enzyme implicated in crab stored leucostatin",
RL  Endocrine 5:23-32(1996).
CC  -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC  IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNIQUELY EASILY EXPRESSED
CC  IN ALL EUKARYOTIC CELLS.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DIFFERENTIAL P4 4 1615 PROTEIN IS
CC  6.8, ITS MW IS: 46 kDa.
CC  -1- SIMILARITY: Belongs to the actin family.
DR  InterPro: IPR004001; Actin.
DR  ProSite: PS00406; ACTINS_1; Actin-like.
DR  ProSite: PS00406; ACTINS_2; PARTIAL.
DR  ProSite: PS01192; ACTINS_ACT-LIKE; PARTIAL.
KW  Structural protein.
FT  NON_TER 1
FT  NON_TER 8
FT  NON_TER 8
SQ  SEQUENCE: 8 AA: 976 MW: 1424005A3ZCAAEAA CKE64.

Query Match          18.2%  Score 2: 18.2%  Length 8:
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2 RK 3
    1
Db  7 RK 8

RESULT 14
AL12_CARMA          STANDARD:          PRT:          8 AA.
AC  P81815;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  Carcinastatin 12.
OS  Carcinus maenas (Common shore crab) (Green crab).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC  Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX  NCBI_TaxID:6759;
RN  [1]
RP  SEQUENCE.
RA  Tissue-cerebral ganglion, and thoracic ganglion;
RX  MEDLINE:9461295;
RA  Devo H., Johnsen A.H., Maestro J. L., Scott A.J., Jansen R.P.,
RA  Thorpe A.:
RT  "Isolation and identification of multiple neuropeptides of the
RT  allatostatin superfamily in the shore crab Carcinus maenas",
RL  Eur. J. Biochem. 250:727-734(1997).
CC  -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC  -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW  Neuropeptide; Multigene family.
SQ  SEQUENCE: 8 AA: 913 MW: 672879QDCR569AH7 CPE64.

Query Match          18.2%  Score 2: 18.2%  Length 8:
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACT_CARMA          STANDARD:          PRT:          8 AA.
AC  P82154;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  Cydian pumilio 3.
OS  Cydia pomonella (Hummel bug).
OC  Eukaryota; Metazoa; Arthropoda; Decapoda; Pleocyemata; Brachyura;
OC  Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC  Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX  NCBI_TaxID:6759;
RN  [1]
RP  SEQUENCE.
RA  Tissue-cerebral ganglion, and thoracic ganglion;
RX  MEDLINE:9461295;
RA  Devo H., Johnsen A.H., Maestro J. L., Scott A.J., Jansen R.P.,
RA  Thorpe A.:
RT  "Isolation and identification of multiple neuropeptides of the
RT  allatostatin superfamily in the shore crab Carcinus maenas",
RL  Eur. J. Biochem. 250:727-734(1997).
CC  -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC  -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW  Neuropeptide; Multigene family.
SQ  SEQUENCE: 8 AA: 913 MW: 672879QDCR569AH7 CPE64.

Query Match          18.2%  Score 2: 18.2%  Length 8:
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```











KW Pyroglutamate carboxylic acid. PYRGLUT-NE CAPWXYVLT\* AA:10  
 FT MOD\_RES 1  
 SQ SEQUENCE 9 AA: 876 MW: 650088786656 (6.0 kDa)

Query Match 18.2% Score 2: DB 1: Length 42  
 Best Local Similarity 100.0% Pred. No. 1 to 45  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KS 4  
 II  
 Db 3 KS 4

## RESULT 30

TKCI\_CALVO  
 ID TKCI\_CALVO STANDARD: PRT: 9 AA  
 AC P41517  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin I.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Proctophila.  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Musciformia; Musciformia; Musciformia  
 CC Calliphoridae; Calliphora  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols K., Nardone, R.,  
 RA Naessle D.R.  
 RT "Callitachykinin I and II, two novel, myotropic peptides isolated from  
 RT the blowfly, Calliphora vomitoria, that have resemblances to  
 RT tachykinins."  
 RL Peptides 15:761-768(1994).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA: 981 MW: 241708685900 (24.1 kDa)

Query Match 18.2% Score 2: DB 1: Length 9;  
 Best Local Similarity 100.0% Pred. No. 1 to 45;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 TA 9  
 II  
 Db 3 TA 4

## RESULT 31

ULAK\_MOUSE  
 ID ULAK\_MOUSE STANDARD: PRT: 9 AA  
 AC P99031;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 20-page of liver tissue (Spot 21, 0.1418)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RP TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Van D.X.,  
 RA Hoogland C., Appel R.D., Binz P.A., Hochstrasser G.F.,  
 RA Cothorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.

KW Pyroglutamate carboxylic acid. PYRGLUT-NE CAPWXYVLT\* AA:10  
 FT MOD\_RES 1  
 SQ SEQUENCE 9 AA: 876 MW: 650088786656 (6.0 kDa)

Query Match 18.2% Score 2: DB 1: Length 42  
 Best Local Similarity 100.0% Pred. No. 1 to 45  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KS 4  
 II  
 Db 3 KS 4

## RESULT 32

ULAK\_MOUSE  
 ID ULAK\_MOUSE STANDARD: PRT: 9 AA  
 AC P99031;  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Calpains in B (15-5422) (15-5422) (Fragment)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RP TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Van D.X.,  
 RA Hoogland C., Appel R.D., Binz P.A., Hochstrasser G.F.,  
 RA Cothorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.

Query Match 18.2% Score 2: DB 1: Length 19;  
 Best Local Similarity 100.0% Pred. No. 1 to 45;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 TA 9  
 II  
 Db 3 TA 4

## RESULT 33

ULAK\_MOUSE  
 ID ULAK\_MOUSE STANDARD: PRT: 9 AA  
 AC P99031;  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Calpains in B (15-5422) (15-5422) (Fragment)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RP TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Van D.X.,  
 RA Hoogland C., Appel R.D., Binz P.A., Hochstrasser G.F.,  
 RA Cothorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.

CC -1- FUNCTION: Thiol protease which is believed to participate in  
 CC intracellular degradation and turnover of proteins. Has also been  
 CC implicated in tumor invasion and metastasis.  
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity  
 CC for peptide bonds. Preferentially cleaves -Ar-Arg-Xaa bonds in  
 CC small molecule substrates (thus differing from cathepsin B). In  
 CC addition to being an endopeptidase, shows peptidyl dipeptidase  
 CC activity, liberating C-terminal dipeptides.  
 CC -1- SUBUNIT: Dimer of a heavy chain and a light chain cross linked  
 CC by a disulfide bond (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 DR InterPro: IPR000169; SHprot\_arcite.  
 DR PROSITE: PS00640; THIOI\_PROTEASE\_ASN; PARTIAL.  
 DR PROSITE: PS00139; THIOI\_PROTEASE\_CYS; PARTIAL.  
 DR PROSITE: PS00639; THIOI\_PROTEASE\_HIS; PARTIAL.  
 KW Hydrolase; Thiol protease; Lysosome.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1177 MW; 87957800GAA05HA (36964)

Query Match 18.2% Score 21 18 12 Length 10  
 Best Local Similarity 100.0% Pred. No. 9.76e+00  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2  
 II  
 Db 7 AR 8

## RESULT 34

COXQ\_RABIT  
 ID COXQ\_RABIT STANDARD; PRT; 13 AA.  
 AC P80316;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide V11-Liver/Heart (E01945.1)  
 DE (Fragment).  
 GN COX8H.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadenbach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED CYTOCHROME  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) + 4 ferrocyclochrome  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE V111 FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1027 MW; 20325C34018754386 (36964)

Query Match 18.2% Score 21 18 12 Length 10  
 Best Local Similarity 100.0% Pred. No. 9.76e+00  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2  
 II  
 Db 6 AR 7

## RESULT 35

COXQ\_SHEEP  
 ID COXQ\_SHEEP STANDARD; PRT; 13 AA.  
 AC P80317;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

II 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide V111-Liver/Heart (E01945.1)  
 DE (Fragment).  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) + 4 ferrocyclochrome  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE V111 FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1027 MW; 20325C34018754386 (36964)

QY 1 AR 2  
 II  
 Db 7 AR 8

## RESULT 36

COXQ\_RABIT  
 ID COXQ\_RABIT STANDARD; PRT; 13 AA.  
 AC P80316;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide V11-Liver/Heart (E01945.1)  
 DE (Fragment).  
 GN COX8H.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxId=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart, and Liver;  
 RA Freund R., Kadenbach B.;  
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED CYTOCHROME  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) + 4 ferrocyclochrome  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE V111 FAMILY.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1027 MW; 20325C34018754386 (36964)

Query Match 18.2% Score 21 18 12 Length 10  
 Best Local Similarity 100.0% Pred. No. 9.76e+00  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2  
 II  
 Db 6 AR 7



## RESULT 40

SYK\_CAMUP STANDARD; PRT: 10 AA.  
 AC 046464;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lysyl-tRNA synthetase (EC 6.1.1.6) (lysine--tRNA ligase) (lyskrs)  
 DE (Fragment).  
 GN LYSS.  
 OS Campylobacter upsallensis.  
 OC Bacteria: Proteobacteria; Epsilonproteobacteria, Campylobacteriales.  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=28080;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 43954;  
 RX MEDLINE=97149302; PubMed=8996110;  
 RA Bourke B., Rashid S.T., Bingham H.L., Chan V.H.  
 RT \*Characterization of Campylobacter upsallensis for and its  
 RT localization in a highly conserved region of the Campylobacter  
 RT genome.\*;  
 RI Gene 183:219-224(1996).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) AMP + diphosphate  
 CC + L-lysyl-tRNA(Lys).  
 CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@sib.ch](mailto:license@sib.ch).  
 CC  
 CC FEML: 177076; AAB41342.1;  
 DR HMAP: MF\_00252;  
 DR InterPro: IPR006195; tRNA\_Ligase-II.  
 DR PROSITE: PS00862; AA\_TRNA\_LIGASE\_II; PARTIAL.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Metal-binding; Magnesium.  
 FT NON\_TER 1  
 FT SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372R05 CRG64;

Query Match 18.2% Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+33;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4  
 II  
 Db 2 KS 3

## RESULT 41

TEMK\_RANTE STANDARD; PRT: 10 AA.  
 AC P56923;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Temporin K.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,

BA Pantoic acid and imidazole peptides from the European red frog Rana  
 RI temporaria.  
 RI Eur J Biochem 242:269-274(1996).  
 CC -!- FUNCTION: Has an imidazole peptide activity against Gram positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the temporin family.  
 KW Amphibian defense peptide; Antimicrobial; Antifungal; Antitumor.  
 FT MOD\_RES 1; 10; AMALAN.  
 FT SEQUENCE 10 AA; 1123 MW; 31040B-0722457 CRG64;

Query Match 18.2% Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+33;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4  
 II  
 Db 2 KS 3

## RESULT 42

TEMK\_RANTE STANDARD; PRT: 10 AA.  
 AC P22489;  
 DT 01-AUG-1999 (Rel. 37, Last sequence update)  
 DT 01-AUG-1999 (Rel. 37, Last sequence update)  
 DE Rana caesiobaud (Syn. 1794)  
 OS Rana caesiobaud (Syn. 1794)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=6400;  
 RN [1]  
 RP SEQUENCE; AMB SYNOPSIS;  
 RI TISSUE=Brain;  
 RI MEDLINE=91254127; PubMed=2580443;  
 RA Kozawa H., Hino J., Mieda T., Kikawa K., Matsuo H.  
 RT \*Isolation of four novel tachykinins from frog (Rana caesiobaud)  
 RT brain and intestine.\*;  
 RI Procter J. Physiol 455:585-593(1996) 505(1991).  
 RN [2]  
 RP SEQUENCE;  
 RI TISSUE=Intestine;  
 RI MEDLINE=94022216; PubMed=247666;  
 RA Kozawa K., Kozawa H., Hino J., Mamiya N., Matsuo H.  
 RT \*Four novel tachykinins in frog (Rana caesiobaud) brain and  
 RT intestine.\*;  
 RI Results (rel. 40) 89(1995)  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WITH EXCITORY NEURONS,  
 CC EVOKED BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SUPPLEMENTS, AND IN ANURA (DIRECTLY OR INDIRECTLY) MANY OTHER  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR ERL 061846; BLOC;  
 DR PROSITE: PS00277; TACHYKININ;  
 DR Tachykinin; Neuropeptide; Antifungal;  
 KW MOD\_RES 1; 10; AMALAN.  
 FT SEQUENCE 10 AA; 1210 MW; 9125563056AB5 CRG64;

Query Match 18.2% Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+33;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4  
 II  
 Db 2 KS 3

## RESULT 43

TKNK\_PIG  
ID TKNK\_PIG STANDARD: PRT: 10 AA.  
AC P01292;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Neurokinin B (NKB) (Neuromedin K)  
GN TAC3 OR NKNB.  
OS Sus scrofa (Pig), and  
OS Rana ridibunda (Laughing frog) (Marsh frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823, 8406;  
RN [1]  
RP SEQUENCE.  
RC SPECIES-Pig; TISSUE-Spinal cord;  
RX MEDLINE-83282812; PubMed-6576785;  
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;  
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine  
spinal cord.";  
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).  
RN [2]  
RP SEQUENCE.  
RC SPECIES-R. ridibunda; TISSUE-Brain;  
RX MEDLINE-92044543; PubMed-1658233;  
RA O'Harte F., Purcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;  
RT "Ranakinin: a novel NKT tachykinin receptor agonist isolated with  
neurokinin B from the brain of the frog Rana ridibunda.";  
RL J. Neurochem. 57:2086-2091(1991).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS.  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR: A01560; SPPOGN.  
DR InterPro: IPR002040; Tachykinin.  
DR PROSITE: PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA: 1211 MW: 4167.629 C9CAA1 CR064;

Query Match 18.2% Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e-03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 DM 7  
DB 1 DM 2

RESULT 44  
TKUL\_UREUN  
ID TKUL\_UREUN STANDARD: PRT: 10 AA.  
AC P40751;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Urechis tachykinin 1.  
OS Urechis unicinctus.  
OC Eukaryota; Metazoa; Echiura; Xenopneusta; Erechtidae; Erechtis.  
OX NCBI\_TaxID=6432;  
RN [1]  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE-Ventral nerve cord;  
RX MEDLINE-93236558; PubMed-8476410;  
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
RT "Two novel tachykinin-related neuropeptides in the echiroid worm,  
Urechis unicinctus.";  
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY WALL  
CC MUSCLE OF THE ANIMAL.  
CC -!- SUBCELLULAR LOCATION: Secreted.

QY 1 SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA: 1173 MW: 4167.629 C9CAA1 CR064;  
Query Match 18.2% Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e-03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 SP 5  
DB 9 SP 10  
RESULT 45  
TKU2\_UREUN  
ID TKU2\_UREUN STANDARD: PRT: 10 AA.  
AC P40752;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Urechis tachykinin 1.  
OS Urechis unicinctus.  
OC Eukaryota; Metazoa; Echiura; Xenopneusta; Erechtidae; Erechtis.  
OX NCBI\_TaxID=6432;  
RN [1]  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE-Ventral nerve cord;  
RX MEDLINE-93236558; PubMed-8476410;  
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
RT "Two novel tachykinin-related neuropeptides in the echiroid worm,  
Urechis unicinctus.";  
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY WALL  
CC MUSCLE OF THE ANIMAL.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
SQ SEQUENCE 10 AA: 1174 MW: 4167.629 C9CAA1 CR064;  
Query Match 18.2% Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 9.7e-03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AP 2  
DB 9 AP 10  
RESULT 46  
UEFA\_HUMAN  
ID UEFA\_HUMAN STANDARD: PRT: 10 AA.  
AC P40945;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from a cDNA library of placenta (Spec. 45) (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Hominidae; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-Plasma;  
RX MEDLINE-93092347; PubMed-140097;  
RA Hughes G., Fritschy S., Rayner F., Pasquini C.,  
RA Sanchez J., James R., Tisset J. L., Bellqvist B.,  
RA Hochstrasser D.;  
RL Electrophoresis 13:767-714(1992).  
CC -!- MISCELLANEOUS: ON THE 20 GEN. THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 7.2, IIS MW IS: 15 kDa.



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DR SWISS-2DPAGE: P30095; HUMAN.
FT NON_TER 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1233 MW: 37AD72B409658167 CR664:

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RD 6
DB 7 RD 8

RESULT 47
UXA6_CHLTR
ID UXA6_CHLTR STANDARD; PRT; 10 AA.
AC P38007;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiales; Chlamydia
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi R., Sanchez Campillo M.,
RA Comanducci M., Christensen G., Birkeland S., Viretoul E., Ratti G.,
RA Pallini V.;
RA Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PT OF THIS UNKNOWN
CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
DR Siena-2DPAGE: P38007;
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1243 MW: DAD39A3330435349 CR664:

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IK 11
DB 6 IK 7

RESULT 48
BRK_MEGFL
ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascollakinin ([Thr6]bradykinin-lys-Ala) (Contains bradykinin like
DE peptide ([Thr6]bradykinin)).
OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Hymenoptera;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OC Scoliidae; Megascollia.
OX NCBI_TaxID=7437;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascollia flavifrons.";
RL Toxicon 25:527-535(1987).
RN [2]
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yasuhara T., Mantel P.;

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PI Two kinins isolated from the venom of Megascollia flavifrons.
PI Toxicon 25:527-535(1987).
QC 1. FUNCTION: potent kinin-like activity (like although wasp
QC 2. FUNCTION: potent kinin-like activity (like although wasp
QC 3. FUNCTION: potent kinin-like activity (like although wasp
QC 4. FUNCTION: potent kinin-like activity (like although wasp
QC 5. FUNCTION: potent kinin-like activity (like although wasp
QC 6. FUNCTION: potent kinin-like activity (like although wasp
QC 7. FUNCTION: potent kinin-like activity (like although wasp
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QC 98. FUNCTION: potent kinin-like activity (like although wasp
QC 99. FUNCTION: potent kinin-like activity (like although wasp
QC 100. FUNCTION: potent kinin-like activity (like although wasp

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RA Graumann P.L., Schmid R., Marahiel M.A.:  
 RL Submitted (Oct-1997) to the SWISS-PROT data bank.  
 RN [2]  
 RP CHARACTERIZATION.  
 RC STRAIN-168 / JH642;  
 RX MEDLINE-96345629; PubMed-8755892;  
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.:  
 RT "Cold shock stress-induced proteins in *Bacillus subtilis*."  
 RL J. Bacteriol. 178:4611-4619(1996).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- INDUCTION: In response to low temperature.  
 CC -!- CAUTION: Could not be found in the genome of *B. subtilis* 168.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1360 MW; 15F6GCEE61227330 CR64;

Query Match: 18.2%; Score 2; DB 1; Length 11;  
 Best local Similarity 100.0%; Pred. No. 10.04;  
 Matches 2; Conservative 0; Mismatches 0; Gaps 0

QY 10 IK 11  
 Db 4 IK 5

Search completed: September 30, 2003, 10:26:11  
 Job time : 7.25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Computer Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 41.6667 seconds  
(without alignments)  
89.639 Million cell updates/sec

Title: US-09-787-443-22  
Perfect score: 11  
Sequence: 1 ARKSRDMTAK 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1459

Minimum DB seq length: 8  
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

- Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_ordanelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacterioph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	12	8	P82164
2	3	27.3	9	2	Q31363
3	3	27.3	9	4	Q9UKJ6
4	3	27.3	9	8	Q9T211
5	3	27.3	9	13	Q9IA14
6	3	27.3	10	10	P82434
7	3	27.3	10	15	Q8UT83
8	3	27.3	11	2	Q47602
9	3	27.3	12	2	Q46039
10	3	27.3	12	2	Q93208
11	3	27.3	12	2	Q52112
12	3	27.3	12	2	Q8GMV1
13	3	27.3	12	2	Q8GMV8
14	3	27.3	12	2	Q8GMV2
15	3	27.3	12	5	Q8T0Y6
16	3	27.3	12	5	Q26429

17	3	27.3	12	1	P82235
18	3	27.3	12	1	P82237
19	3	27.3	12	1	Q9UKJ6
20	3	27.3	12	1	P82238
21	3	27.3	12	1	P82239
22	3	27.3	12	1	P82240
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24	3	27.3	12	1	P82242
25	3	27.3	12	1	P82243
26	3	27.3	12	1	P82244
27	3	27.3	12	1	P82245
28	3	27.3	12	1	P82246
29	3	27.3	12	1	P82247
30	3	27.3	12	1	P82248
31	3	27.3	12	1	P82249
32	3	27.3	12	1	P82250
33	3	27.3	12	1	P82251
34	3	27.3	12	1	P82252
35	3	27.3	12	1	P82253
36	3	27.3	12	1	P82254
37	3	27.3	12	1	P82255
38	3	27.3	12	1	P82256
39	3	27.3	12	1	P82257
40	3	27.3	12	1	P82258
41	3	27.3	12	1	P82259
42	3	27.3	12	1	P82260
43	3	27.3	12	1	P82261
44	3	27.3	12	1	P82262
45	3	27.3	12	1	P82263
46	3	27.3	12	1	P82264
47	3	27.3	12	1	P82265
48	3	27.3	12	1	P82266
49	3	27.3	12	1	P82267
50	3	27.3	12	1	P82268
51	3	27.3	12	1	P82269
52	3	27.3	12	1	P82270
53	3	27.3	12	1	P82271
54	3	27.3	12	1	P82272
55	3	27.3	12	1	P82273
56	3	27.3	12	1	P82274
57	3	27.3	12	1	P82275
58	3	27.3	12	1	P82276
59	3	27.3	12	1	P82277
60	3	27.3	12	1	P82278
61	3	27.3	12	1	P82279
62	3	27.3	12	1	P82280
63	3	27.3	12	1	P82281
64	3	27.3	12	1	P82282
65	3	27.3	12	1	P82283
66	3	27.3	12	1	P82284
67	3	27.3	12	1	P82285
68	3	27.3	12	1	P82286
69	3	27.3	12	1	P82287
70	3	27.3	12	1	P82288
71	3	27.3	12	1	P82289
72	3	27.3	12	1	P82290
73	3	27.3	12	1	P82291
74	3	27.3	12	1	P82292
75	3	27.3	12	1	P82293
76	3	27.3	12	1	P82294
77	3	27.3	12	1	P82295
78	3	27.3	12	1	P82296
79	3	27.3	12	1	P82297
80	3	27.3	12	1	P82298
81	3	27.3	12	1	P82299
82	3	27.3	12	1	P82300
83	3	27.3	12	1	P82301
84	3	27.3	12	1	P82302
85	3	27.3	12	1	P82303
86	3	27.3	12	1	P82304
87	3	27.3	12	1	P82305
88	3	27.3	12	1	P82306
89	3	27.3	12	1	P82307

90	2	18.2	8	8	P92211	P92211: anagapron c	165	2	18.2	1	8	18.2	Q8437 callosossa
91	2	18.2	8	8	P92428	P92428: periditylon	164	2	18.2	1	8	18.2	Q84211 spinoschia
92	2	18.2	8	8	P92386	P92386: hordeum mar	165	2	18.2	1	8	18.2	Q84367 bostrychia
93	2	18.2	8	8	P93959	P93959: hordeum ere	166	2	18.2	1	8	18.2	Q84365 varanus dca
94	2	18.2	8	8	P93985	P93985: aegilops co	167	2	18.2	1	8	18.2	Q84280 spinoschia
95	2	18.2	8	8	Q84V91	Q84V91: varanus tim	168	2	18.2	1	8	18.2	Q84368 callosossa
96	2	18.2	8	8	Q84V99	Q84V99: locusta fca	169	2	18.2	1	8	18.2	Q84V98 varanus ncl
97	2	18.2	8	8	Q84D47	Q84D47: hydrastrole	170	2	18.2	1	8	18.2	Q84335 bostrychia
98	2	18.2	8	8	Q84VE4	Q84VE4: varanus mel	171	2	18.2	1	8	18.2	Q84332 astriongia
99	2	18.2	8	8	Q84V43	Q84V43: taeniatheca	172	2	18.2	1	8	18.2	Q84V18 varanus cve
100	2	18.2	8	8	Q84VB2	Q84VB2: varanus sal	173	2	18.2	1	8	18.2	Q84D12 lissoschia
101	2	18.2	8	8	Q84V31	Q84V31: heterantrel	174	2	18.2	1	8	18.2	Q84V19 varanus dca
102	2	18.2	8	8	P93981	P93981: erithiodur	175	2	18.2	1	8	18.2	Q84V35 bostrychia
103	2	18.2	8	8	Q84VF9	Q84VF9: varanus ind	176	2	18.2	1	8	18.2	Q84V66 bostrychia
104	2	18.2	8	8	P93992	P93992: australopyr	177	2	18.2	1	8	18.2	Q84V11 varanus dca
105	2	18.2	8	8	P92426	P92426: pseudoroegn	178	2	18.2	1	8	18.2	Q84V13 bostrychia
106	2	18.2	8	8	P92431	P92431: aegilops fa	179	2	18.2	1	8	18.2	Q84V36 callosossa
107	2	18.2	8	8	Q84VF3	Q84VF3: varanus kel	180	2	18.2	1	8	18.2	Q84V76 pseudosperm
108	2	18.2	8	8	Q84VA7	Q84VA7: varanus sal	181	2	18.2	1	8	18.2	Q84V42 varanus dca
109	2	18.2	8	8	Q84VB5	Q84VB5: varanus sal	182	2	18.2	1	8	18.2	Q84V63 callosossa
110	2	18.2	8	8	P92422	P92422: psathyrosta	183	2	18.2	1	8	18.2	Q84V64 coel bostr
111	2	18.2	8	9	Q8H9K4	Q8H9K4: bacterioepha	184	2	18.2	1	8	18.2	Q84V62 callosossa
112	2	18.2	8	9	Q8H9J9	Q8H9J9: bacterioepha	185	2	18.2	1	8	18.2	Q84V22 hypones sp
113	2	18.2	8	9	Q8H9J7	Q8H9J7: bacterioepha	186	2	18.2	1	8	18.2	Q84V61 callosossa
114	2	18.2	8	9	Q8H9J5	Q8H9J5: bacterioepha	187	2	18.2	1	8	18.2	Q84V60 porphyra ml
115	2	18.2	8	9	Q8H9J3	Q8H9J3: bacterioepha	188	2	18.2	1	8	18.2	Q84V61 varanus dca
116	2	18.2	8	9	Q8H9J1	Q8H9J1: bacterioepha	189	2	18.2	1	8	18.2	Q8H9J5 spinoschia
117	2	18.2	8	9	Q8H9I9	Q8H9I9: bacterioepha	190	2	18.2	1	8	18.2	Q8H9J7 spinoschia
118	2	18.2	8	9	Q8H9I8	Q8H9I8: bacterioepha	191	2	18.2	1	8	18.2	Q8H9K6 strachella
119	2	18.2	8	9	Q8H9I6	Q8H9I6: bacterioepha	192	2	18.2	1	8	18.2	Q8H9J8 ptychopora
120	2	18.2	8	9	Q8H9I4	Q8H9I4: bacterioepha	193	2	18.2	1	8	18.2	Q8H9A5 strachella
121	2	18.2	8	9	Q8H9I3	Q8H9I3: bacterioepha	194	2	18.2	1	8	18.2	Q8H9A4 strachella
122	2	18.2	8	9	Q8H9I2	Q8H9I2: bacterioepha	195	2	18.2	1	8	18.2	Q8H9A3 strachella
123	2	18.2	8	9	Q8H9H6	Q8H9H6: bacterioepha	196	2	18.2	1	8	18.2	Q8H9A6 callosossa
124	2	18.2	8	9	Q8H9H5	Q8H9H5: bacterioepha	197	2	18.2	1	8	18.2	Q8H9A5 callosossa
125	2	18.2	8	9	Q8H9H3	Q8H9H3: bacterioepha	198	2	18.2	1	8	18.2	Q8H9A4 callosossa
126	2	18.2	8	10	Q8GT55	Q8GT55: ayegegetiro	199	2	18.2	1	8	18.2	Q8H9A4 callosossa
127	2	18.2	8	11	Q89M80	Q89M80: mus muscu	200	2	18.2	1	8	18.2	Q8H9A4 callosossa
128	2	18.2	8	11	Q89V58	Q89V58: mus sp. mep	201	2	18.2	1	8	18.2	Q8H9A5 callosossa
129	2	18.2	8	11	Q8H9M5	Q8H9M5: mus muscu	202	2	18.2	1	8	18.2	Q8H9A4 callosossa
130	2	18.2	8	11	Q82933	Q82933: rattus norv	203	2	18.2	1	8	18.2	Q8H9A4 callosossa
131	2	18.2	8	12	Q89965	Q89965: polymyrmico	204	2	18.2	1	8	18.2	Q8H9A4 callosossa
132	2	18.2	8	12	Q84271	Q84271: human papil	205	2	18.2	1	8	18.2	Q8H9A4 callosossa
133	2	18.2	8	12	Q84273	Q84273: human papil	206	2	18.2	1	8	18.2	Q8H9A4 callosossa
134	2	18.2	8	13	P87488	P87488: oncorhynch	207	2	18.2	1	8	18.2	Q8H9A4 callosossa
135	2	18.2	9	1	Q50832	Q50832: metarozoc	208	2	18.2	1	8	18.2	Q8H9A4 callosossa
136	2	18.2	9	2	Q8E3T0	Q8E3T0: borrelia af	209	2	18.2	1	8	18.2	Q8H9A4 callosossa
137	2	18.2	9	2	Q8F556	Q8F556: escherichia	210	2	18.2	1	8	18.2	Q8H9A4 callosossa
138	2	18.2	9	2	P72345	P72345: pseudomonas	211	2	18.2	1	8	18.2	Q8H9A4 callosossa
139	2	18.2	9	2	Q45852	Q45852: clostridium	212	2	18.2	1	8	18.2	Q8H9A4 callosossa
140	2	18.2	9	2	Q48687	Q48687: lactococcus	213	2	18.2	1	8	18.2	Q8H9A4 callosossa
141	2	18.2	9	2	Q47063	Q47063: escherichia	214	2	18.2	1	8	18.2	Q8H9A4 callosossa
142	2	18.2	9	2	Q8H792	Q8H792: borrelia tu	215	2	18.2	1	8	18.2	Q8H9A4 callosossa
143	2	18.2	9	2	Q51765	Q51765: pseudomonas	216	2	18.2	1	8	18.2	Q8H9A4 callosossa
144	2	18.2	9	2	Q8H9C4	Q8H9C4: borrelia tu	217	2	18.2	1	8	18.2	Q8H9A4 callosossa
145	2	18.2	9	2	Q8GL26	Q8GL26: borrelia tu	218	2	18.2	1	8	18.2	Q8H9A4 callosossa
146	2	18.2	9	4	Q8H9F9	Q8H9F9: homo sapien	219	2	18.2	1	8	18.2	Q8H9A4 callosossa
147	2	18.2	9	4	Q89E26	Q89E26: homo sapien	220	2	18.2	1	8	18.2	Q8H9A4 callosossa
148	2	18.2	9	4	Q16276	Q16276: homo sapien	221	2	18.2	1	8	18.2	Q8H9A4 callosossa
149	2	18.2	9	4	Q8H522	Q8H522: homo sapien	222	2	18.2	1	8	18.2	Q8H9A4 callosossa
150	2	18.2	9	4	Q16386	Q16386: homo sapien	223	2	18.2	1	8	18.2	Q8H9A4 callosossa
151	2	18.2	9	4	Q8H4M8	Q8H4M8: homo sapien	224	2	18.2	1	8	18.2	Q8H9A4 callosossa
152	2	18.2	9	4	Q89QW0	Q89QW0: homo sapien	225	2	18.2	1	8	18.2	Q8H9A4 callosossa
153	2	18.2	9	4	Q89QJ4	Q89QJ4: homo sapien	226	2	18.2	1	8	18.2	Q8H9A4 callosossa
154	2	18.2	9	5	Q89C36	Q89C36: homo sapien	227	2	18.2	1	8	18.2	Q8H9A4 callosossa
155	2	18.2	9	5	Q89WD6	Q89WD6: leptotritons	228	2	18.2	1	8	18.2	Q8H9A4 callosossa
156	2	18.2	9	6	Q828093	Q828093: bos taurus	229	2	18.2	1	8	18.2	Q8H9A4 callosossa
157	2	18.2	9	8	Q8H9M3	Q8H9M3: hawitria ti	230	2	18.2	1	8	18.2	Q8H9A4 callosossa
158	2	18.2	9	8	Q8H9J5	Q8H9J5: bostrychia	231	2	18.2	1	8	18.2	Q8H9A4 callosossa
159	2	18.2	9	8	Q8H9J7	Q8H9J7: callosossa	232	2	18.2	1	8	18.2	Q8H9A4 callosossa
160	2	18.2	9	8	Q8H9T9	Q8H9T9: bostrychia	233	2	18.2	1	8	18.2	Q8H9A4 callosossa
161	2	18.2	9	8	Q85GN1	Q85GN1: petargonium	234	2	18.2	1	8	18.2	Q8H9A4 callosossa
162	2	18.2	9	8	Q87389	Q87389: callosossa	235	2	18.2	1	8	18.2	Q8H9A4 callosossa

236	2	18.2	10	2	Q9X531	Q9X531	escherichia	374	2	18.2	10	2	Q9X531	Q9X531	escherichia	374
237	2	18.2	10	2	Q9R739	Q9R739	helicobacte	310	2	18.2	10	2	Q9R739	Q9R739	helicobacte	310
238	2	18.2	10	2	P83067	P83067	baclillus ce	311	2	18.2	10	2	P83067	P83067	baclillus ce	311
239	2	18.2	10	2	P83064	P83064	baclillus ce	312	2	18.2	10	2	P83064	P83064	baclillus ce	312
240	2	18.2	10	2	P82588	P82588	streptococ	313	2	18.2	10	2	P82588	P82588	streptococ	313
241	2	18.2	10	2	Q8Q895	Q8Q895	horrelia bu	314	2	18.2	10	2	Q8Q895	Q8Q895	horrelia bu	314
242	2	18.2	10	4	Q8NER0	Q8NER0	homo sapien	315	2	18.2	10	4	Q8NER0	Q8NER0	homo sapien	315
243	2	18.2	10	4	Q8NEY9	Q8NEY9	homo sapien	316	2	18.2	10	4	Q8NEY9	Q8NEY9	homo sapien	316
244	2	18.2	10	4	Q9UCU6	Q9UCU6	homo sapien	317	2	18.2	10	4	Q9UCU6	Q9UCU6	homo sapien	317
245	2	18.2	10	4	Q9NFC6	Q9NFC6	homo sapien	318	2	18.2	10	4	Q9NFC6	Q9NFC6	homo sapien	318
246	2	18.2	10	4	Q9NFC7	Q9NFC7	homo sapien	319	2	18.2	10	4	Q9NFC7	Q9NFC7	homo sapien	319
247	2	18.2	10	4	Q8N6S1	Q8N6S1	homo sapien	320	2	18.2	10	4	Q8N6S1	Q8N6S1	homo sapien	320
248	2	18.2	10	5	Q8WPL6	Q8WPL6	oik-plasma	321	2	18.2	10	5	Q8WPL6	Q8WPL6	oik-plasma	321
249	2	18.2	10	5	P82384	P82384	drosophila	322	2	18.2	10	5	P82384	P82384	drosophila	322
250	2	18.2	10	5	P82217	P82217	beetle mori	323	2	18.2	10	5	P82217	P82217	beetle mori	323
251	2	18.2	10	6	Q9TR47	Q9TR47	bos taurus	324	2	18.2	10	6	Q9TR47	Q9TR47	bos taurus	324
252	2	18.2	10	6	Q9TR48	Q9TR48	bos taurus	325	2	18.2	10	6	Q9TR48	Q9TR48	bos taurus	325
253	2	18.2	10	6	Q9N1X1	Q9N1X1	equus catal	326	2	18.2	10	6	Q9N1X1	Q9N1X1	equus catal	326
254	2	18.2	10	6	Q95W70	Q95W70	trichosurus	327	2	18.2	10	6	Q95W70	Q95W70	trichosurus	327
255	2	18.2	10	6	P83205	P83205	oris aries	328	2	18.2	10	6	P83205	P83205	oris aries	328
256	2	18.2	10	7	Q95H88	Q95H88	papio anubi	329	2	18.2	10	7	Q95H88	Q95H88	papio anubi	329
257	2	18.2	10	7	Q95H99	Q95H99	papio anubi	330	2	18.2	10	7	Q95H99	Q95H99	papio anubi	330
258	2	18.2	10	8	Q9TRF7	Q9TRF7	aqaria aqari	331	2	18.2	10	8	Q9TRF7	Q9TRF7	aqaria aqari	331
259	2	18.2	10	8	Q9TRF9	Q9TRF9	aqaria aqari	332	2	18.2	10	8	Q9TRF9	Q9TRF9	aqaria aqari	332
260	2	18.2	10	8	P92594	P92594	aqaria aqari	333	2	18.2	10	8	P92594	P92594	aqaria aqari	333
261	2	18.2	10	8	P92616	P92616	aqaria aqari	334	2	18.2	10	8	P92616	P92616	aqaria aqari	334
262	2	18.2	10	8	Q9TF09	Q9TF09	teratosaur	335	2	18.2	10	8	Q9TF09	Q9TF09	teratosaur	335
263	2	18.2	10	8	Q9B4W4	Q9B4W4	pachyrhino	336	2	18.2	10	8	Q9B4W4	Q9B4W4	pachyrhino	336
264	2	18.2	10	8	Q9TG81	Q9TG81	diplogloss	337	2	18.2	10	8	Q9TG81	Q9TG81	diplogloss	337
265	2	18.2	10	8	P92654	P92654	euprepis au	338	2	18.2	10	8	P92654	P92654	euprepis au	338
266	2	18.2	10	8	Q9TKG2	Q9TKG2	callisperm	339	2	18.2	10	8	Q9TKG2	Q9TKG2	callisperm	339
267	2	18.2	10	8	Q8S104	Q8S104	xantusia be	340	2	18.2	10	8	Q8S104	Q8S104	xantusia be	340
268	2	18.2	10	8	Q9TG86	Q9TG86	diploglossu	341	2	18.2	10	8	Q9TG86	Q9TG86	diploglossu	341
269	2	18.2	10	8	P92758	P92758	teratosaur	342	2	18.2	10	8	P92758	P92758	teratosaur	342
270	2	18.2	10	8	Q9TRF5	Q9TRF5	acoalis spu	343	2	18.2	10	8	Q9TRF5	Q9TRF5	acoalis spu	343
271	2	18.2	10	8	Q8ME52	Q8ME52	porphyra pu	344	2	18.2	10	8	Q8ME52	Q8ME52	porphyra pu	344
272	2	18.2	10	8	Q94V05	Q94V05	varanus ari	345	2	18.2	10	8	Q94V05	Q94V05	varanus ari	345
273	2	18.2	10	8	Q9TLC8	Q9TLC8	bostrychia	346	2	18.2	10	8	Q9TLC8	Q9TLC8	bostrychia	346
274	2	18.2	10	8	Q9TRF1	Q9TRF1	homalosperm	347	2	18.2	10	8	Q9TRF1	Q9TRF1	homalosperm	347
275	2	18.2	10	8	Q9TG65	Q9TG65	abronia oax	348	2	18.2	10	8	Q9TG65	Q9TG65	abronia oax	348
276	2	18.2	10	8	Q94V07	Q94V07	varanus spe	349	2	18.2	10	8	Q94V07	Q94V07	varanus spe	349
277	2	18.2	10	8	Q9TRF8	Q9TRF8	tristatops	350	2	18.2	10	8	Q9TRF8	Q9TRF8	tristatops	350
278	2	18.2	10	8	Q9TG50	Q9TG50	elqaria mu	351	2	18.2	10	8	Q9TG50	Q9TG50	elqaria mu	351
279	2	18.2	10	8	Q9TRF4	Q9TRF4	aqasomyrta	352	2	18.2	10	8	Q9TRF4	Q9TRF4	aqasomyrta	352
280	2	18.2	10	8	Q9TRF3	Q9TRF3	asteromyrta	353	2	18.2	10	8	Q9TRF3	Q9TRF3	asteromyrta	353
281	2	18.2	10	8	Q9TRK0	Q9TRK0	geotrabella	354	2	18.2	10	8	Q9TRK0	Q9TRK0	geotrabella	354
282	2	18.2	10	8	Q9TG98	Q9TG98	shinisaurus	355	2	18.2	10	8	Q9TG98	Q9TG98	shinisaurus	355
283	2	18.2	10	8	P92766	P92766	varanus ari	356	2	18.2	10	8	P92766	P92766	varanus ari	356
284	2	18.2	10	8	Q9TRK0	Q9TRK0	kanzea arti	357	2	18.2	10	8	Q9TRK0	Q9TRK0	kanzea arti	357
285	2	18.2	10	8	Q9T2F3	Q9T2F3	ratios sp	358	2	18.2	10	8	Q9T2F3	Q9T2F3	ratios sp	358
286	2	18.2	10	8	Q94V05	Q94V05	varanus ari	359	2	18.2	10	8	Q94V05	Q94V05	varanus ari	359
287	2	18.2	10	8	Q9TG80	Q9TG80	ophiodos st	360	2	18.2	10	8	Q9TG80	Q9TG80	ophiodos st	360
288	2	18.2	10	8	Q9T2P4	Q9T2P4	ratifus sp	361	2	18.2	10	8	Q9T2P4	Q9T2P4	ratifus sp	361
289	2	18.2	10	8	Q9TG56	Q9TG56	elqaria kin	362	2	18.2	10	8	Q9TG56	Q9TG56	elqaria kin	362
290	2	18.2	10	8	Q94VC9	Q94VC9	varanus pan	363	2	18.2	10	8	Q94VC9	Q94VC9	varanus pan	363
291	2	18.2	10	8	Q9TG71	Q9TG71	karisia im5	364	2	18.2	10	8	Q9TG71	Q9TG71	karisia im5	364
292	2	18.2	10	8	P92707	P92707	frutysaurus	365	2	18.2	10	8	P92707	P92707	frutysaurus	365
293	2	18.2	10	8	Q9TRF6	Q9TRF6	acoalis s	366	2	18.2	10	8	Q9TRF6	Q9TRF6	acoalis s	366
294	2	18.2	10	8	Q9TRH7	Q9TRH7	leptospermu	367	2	18.2	10	8	Q9TRH7	Q9TRH7	leptospermu	367
295	2	18.2	10	8	Q94VF0	Q94VF0	varanus kin	368	2	18.2	10	8	Q94VF0	Q94VF0	varanus kin	368
296	2	18.2	10	8	P92733	P92733	fejervarya	369	2	18.2	10	8	P92733	P92733	fejervarya	369
297	2	18.2	10	8	Q9TGAI	Q9TGAI	beloderma s	370	2	18.2	10	8	Q9TGAI	Q9TGAI	beloderma s	370
298	2	18.2	10	8	Q9TF06	Q9TF06	teratospinn	371	2	18.2	10	8	Q9TF06	Q9TF06	teratospinn	371
299	2	18.2	10	8	Q9TRK2	Q9TRK2	leptospermu	372	2	18.2	10	8	Q9TRK2	Q9TRK2	leptospermu	372
300	2	18.2	10	8	Q9TRG7	Q9TRG7	ephisauris	373	2	18.2	10	8	Q9TRG7	Q9TRG7	ephisauris	373
301	2	18.2	10	8	P92771	P92771	xenosaurus	374	2	18.2	10	8	P92771	P92771	xenosaurus	374
302	2	18.2	10	8	Q94V85	Q94V85	varanus var	375	2	18.2	10	8	Q94V85	Q94V85	varanus var	375
303	2	18.2	10	8	P92648	P92648	liialis jica	376	2	18.2	10	8	P92648	P92648	liialis jica	376
304	2	18.2	10	8	Q9TG59	Q9TG59	elqaria coe	377	2	18.2	10	8	Q9TG59	Q9TG59	elqaria coe	377
305	2	18.2	10	8	Q8S178	Q8S178	xantusia ar	378	2	18.2	10	8	Q8S178	Q8S178	xantusia ar	378
306	2	18.2	10	8	Q9TRQ2	Q9TRQ2	ophisacrus	379	2	18.2	10	8	Q9TRQ2	Q9TRQ2	ophisacrus	379
307	2	18.2	10	8	Q9TRK3	Q9TRK3	leptospermu	380	2	18.2	10	8	Q9TRK3	Q9TRK3	leptospermu	380
308	2	18.2	10	8	Q9TRK7	Q9TRK7	kanzea pulc	381	2	18.2	10	8	Q9TRK7	Q9TRK7	kanzea pulc	381









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Query Match      27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.2e+63;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TAI 10
DB      5 TAI 7

RESULT 10
ID Q93208      PRELIMINARY;      PRT;      12 AA.
AC Q93208;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter sp.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=472;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:ED45-25; PLASMID-pKLH205, and pKLH204;
RX MEDLINE=21272500; PubMed=11376944;
RA Kholodii G.;
RT "the shuffling function of resolvases.";
RL Gene 269:121-130(2001).
DR EMBL; AJ251707; CAC39413.1; .
DR EMBL; AJ250851; CAC39402.1; .
KW Plasmid.
SQ SEQUENCE 12 AA, 1219 MW, D4B99D3E821D6776 CRG64;

Query Match      27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.2e+63;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 MTA 9
DB      1 MTA 3

RESULT 11
ID Q52112      PRELIMINARY;      PRT;      12 AA.
AC Q52112; Q08093; Q08097; Q08128; Q08132; Q56909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE URF2X protein (Fragment).
DR URF2X OR URF2X.
GN URF-2X OR URF2X.
OS Acinetobacter calcoaceticus,
OS Pantoea agglomerans,
OS Alcaligenes sp.,
OS Enterobacter cloacae,
OS Escherichia coli,
OS Yersinia enterocolitica, and
OS mercury resistant bacterium '96 SE13.
OG Plasmid pKLH2, plasmid pKLH256, plasmid pKLH210, plasmid pKLH17, and
OG plasmid pKLH201.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471, 549, 512, 550, 562, 630, 93601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-A.calcoaceticus; PLASMID=pKLH2;
RX MEDLINE=94134837; PubMed=8302940;
RA Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Molecular characterization of an aberrant mercury resistance
transposable element from an environmental Acinetobacter strain.";

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PL Plasmid 443-607 (88,000);
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Pantoea agglomerans; Strain: E.colocae, and F. coli;
RX MEDLINE=97403024; PubMed=94134837;
RA Nikiforov V., Kholodii G., Mindlin S., Gorlenko Z., Kalyanova P.,
RA Mindlin S., Nikiforov V.;
RT "Intercontaminant plasmids from promiscuous mercury resistance transposons
in environmental bacterium";
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Yersinia enterocolitica; Strain: Various strains;
RX MEDLINE=94274477; PubMed=786944;
RA Osborn S.E.V., Turner A.K., Grinsted L.;
RT "Nucleotide sequence within 15,926 nucleotides this as a 1021 kbp
transposable element and provides evidence for the origin of the mer
operon carried by Pseudomonas";
RN [4]
PL Plasmid 443-607 (88,000);
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-A.calcoaceticus; Strain: EMBL4, PLASMID pKLH21;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.;
RA Nikiforov V.G.;
RT "pKLH2-like abort transposons and possible mechanisms of their
dissemination";
RC Submitted (MAR 2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213017; AAA1066.1;
DR EMBL; Y08992; CAA70130.1;
DR EMBL; Y08993; CAA70131.1;
DR EMBL; Y09025; CAA70244.1;
DR EMBL; Y10192; CAA71196.1;
DR EMBL; X78059; CAA54479.1;
DR EMBL; AF144211; AAA344400.1;
DR EMBL; AF251397; CAC39413.1;
KW Plasmid.
FT N. N. 19. 12 AA, 1219 MW, D4B99D3E821D6776 CRG64;
SQ SEQUENCE 12 AA, 1219 MW, D4B99D3E821D6776 CRG64;

Query Match      27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.2e+63;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 MTA 9
DB      1 MTA 3

RESULT 12
ID Q93MV1      PRELIMINARY;      PRT;      12 AA.
AC Q93MV1;
DT 01-MAR-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter sp.
OG Plasmid pKLH204;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=472;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:TC1047;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;

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RT *pKLH2-like aberrant transposons and possible mechanisms of their
RL dissemination.*;1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250245; CAC80792.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3
  III
  RESULT 13
Q8GML2
ID Q8GML2 PRELIMINARY; PRT; 12 AA.
AC Q8GML2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OG Plasmid pKLH203.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3
  III
  RESULT 14
Q8GML2
ID Q8GML2 PRELIMINARY; PRT; 12 AA.
AC Q8GML2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter sp. FD23-35.
OG Plasmid pKLH208.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=109250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ED23-35;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3
  III
  RESULT 15
Q8GML2
ID Q8GML2 PRELIMINARY; PRT; 12 AA.
AC Q8GML2;
DT 01-JUN-2003 (TREMBLrel. 23, Created)
DT 01-JUN-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OG Plasmid pKLH203.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250494; CAC80763.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;
  Query Match 27.3%; Score 3; DB 2; Length 12;
  Best Local Similarity 100.0%; Pred. No. 8.2e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 MTA 9
DB 1 MTA 3
  III
  RESULT 16
Q8GML2
ID Q8GML2 PRELIMINARY; PRT; 12 AA.
AC Q8GML2;
DT 01-JUN-2003 (TREMBLrel. 23, Created)
DT 01-JUN-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 23, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter junii.
OG Plasmid pKLH203.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC13-1;
RA Kholodii G.V., Yurieva O.V., Mindlin S.Z., Gorienko Z.M.,
RA Nikiforov V.G.;
RT *pKLH2-like aberrant transposons and possible mechanisms of their
RT dissemination.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

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RA Raddazzo F.M., Gribbs D.B., Kaufman T.C.
RT *Rescue and regulation of proboscipodid: a homocysteine-dependent
RL Antennapedia Complex.
RL Development 133:257-271(1991).
DR EMBL: S77929; AAB20845.1;
DR FlyBase; FBgn0012734; DpseXp.
FT NON_TER
SQ SEQUENCE 12 AA; 1377 MW; 4608DB8E455A5B4 C62664

Query Match 27.38; Score 3; DB 10; Length 123
Best Local Similarity 100.0%; Pred. No. 8,200,000
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 2 RKS 4
DB 4 RKS 6
111
111
111

RESULT 17
P82246 PRELIMINARY; PRT; 12 AA.
ID P82246
AC P82246
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 50S ribosomal protein L31 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID:3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=leaf;
RX MEDLINE-20435798; PubMed-10874046;
RA Yanauchi K., Subramanian A.R.;
RT *The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).
RL J. Biol. Chem. 275:28456-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
CC DIFFER IN CHARGE.
CC -1- SIMILARITY: BELONGS TO THE L31P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; PARTIAL.
DR PRINTS; PR01249; RIBOSOMALL31; PARTIAL.
DR PROSITE; PS01143; RIBOSOMALL31; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA binding.
FT NON_TER
SQ SEQUENCE 12 AA; 1529 MW; 13B983E951D761F0 C62664

Query Match 27.38; Score 3; DB 10; Length 123
Best Local Similarity 100.0%; Pred. No. 8,200,000
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 2 RKS 4
DB 1 RKS 3
111
111
111

RESULT 18
P82247 PRELIMINARY; PRT; 12 AA.
ID P82247
AC P82247
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 50S ribosomal protein L31 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;

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CC *The plastid ribosomal proteins. Identification of all the proteins in
CC the 50 S subunit of an organelle ribosome (chloroplast).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
CC DIFFER IN CHARGE.
CC -1- SIMILARITY: BELONGS TO THE L31P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002150; Ribosomal_L31.
DR Pfam; PF01197; Ribosomal_L31; PARTIAL.
DR PRINTS; PR01249; RIBOSOMALL31; PARTIAL.
DR PROSITE; PS01143; RIBOSOMALL31; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA binding.
FT NON_TER
SQ SEQUENCE 12 AA; 1529 MW; 13B983E951D761F0 C62664

Query Match 27.38; Score 3; DB 10; Length 123
Best Local Similarity 100.0%; Pred. No. 8,200,000
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 2 RKS 4
DB 1 RKS 3
111
111
111

RESULT 19
P82248 PRELIMINARY; PRT; 12 AA.
ID P82248
AC P82248
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 50S ribosomal protein L31 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;

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DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Histone H6-like protein (Fragment)
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Skin mucus;
RA Fernandes J.M.O., Smith V.J.;
RT "Antimicrobial properties of a histone H6-like peptide from skin
RL secretions of rainbow trout, Oncorhynchus mykiss.";
RL Submitted (APR-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GPAM-POSITIVE AND
CC -!- GRAM-NEGATIVE BACTERIA AT SUBMICROMOLAR CONCENTRATIONS.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
CC -!- MASS SPECTROMETRY: MW=6671; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY.
DR InterPro: IPR000079; HMG14.17; PARTIAL.
KW Nuclear protein; DNA-binding; Antibiotic.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1385 MW; DE4080804A6321AD 76%4;

Query Match 27.3%; Score 3; Len 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 8, 6, 0, 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4
DB 1 1
3 RKS 5

RESULT 2;
Q53501 PRELIMINARY; PRT; 14 AA.
ID Q53501
AC Q53501
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Orf (promoter-like sequence P80) (Fragment).
OS Lactobacillus paracasei
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1597;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Barina A., Topisirovic B.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei
RT subsp. paracasei CgII and their expression in Escherichia coli.
RT Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994)
DR EMBL: S76787; AAR33946.2;
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1475 MW; CHD7E795AFF31414 67%4;

Query Match 27.3%; Score 3; Len 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 9, 1, 0, 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARK 3
DB 1 1
4 ARK 6

RESULT 22
Q52840 PRELIMINARY; PRT; 14 AA.
ID Q52840
AC Q52840
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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ID Q52840
AC Q52840
DT 01-MAY-2001 (EMBLrel. 19, Last sequence update)
DT 01-MAY-2001 (EMBLrel. 19, Last sequence update)
DE Xanthopus exilis (Fragm.)
OS Bacteria; Firmicutes; Bacillales; Bacillaceae;
OC Firmicutes; Bacillales; Bacillaceae;
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Barina A., Topisirovic B.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei
RT subsp. paracasei CgII and their expression in Escherichia coli.
RT Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994)
DR EMBL: S76787; AAR33946.2;
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1475 MW; CHD7E795AFF31414 67%4;

Query Match 27.3%; Score 3; Len 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 9, 1, 0, 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARK 3
DB 1 1
4 ARK 6

RESULT 24
Q53091 PRELIMINARY; PRT; 14 AA.
ID Q53091
AC Q53091
DT 01-MAY-2001 (EMBLrel. 19, Last sequence update)
DT 01-MAY-2001 (EMBLrel. 19, Last sequence update)
DE Xanthopus exilis (Fragm.)
OS Bacteria; Firmicutes; Bacillales; Bacillaceae;
OC Firmicutes; Bacillales; Bacillaceae;
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Barina A., Topisirovic B.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei
RT subsp. paracasei CgII and their expression in Escherichia coli.
RT Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994)
DR EMBL: S76787; AAR33946.2;
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1475 MW; CHD7E795AFF31414 67%4;

Query Match 27.3%; Score 3; Len 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 9, 1, 0, 0;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARK 3
DB 1 1
4 ARK 6

RESULT 24
Q53091 PRELIMINARY; PRT; 14 AA.
ID Q53091
AC Q53091
DT 01-MAY-2001 (EMBLrel. 19, Last sequence update)
DT 01-MAY-2001 (EMBLrel. 19, Last sequence update)
DE Xanthopus exilis (Fragm.)
OS Bacteria; Firmicutes; Bacillales; Bacillaceae;
OC Firmicutes; Bacillales; Bacillaceae;
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95219758; PubMed=7704831;
RA Djordjevic G., Bojovic B., Barina A., Topisirovic B.;
RT "Cloning of promoter-like sequences from Lactobacillus paracasei
RT subsp. paracasei CgII and their expression in Escherichia coli.
RT Lactococcus lactis, and Lactobacillus reuteri.";
RL Can. J. Microbiol. 40:1043-1050(1994)
DR EMBL: S76787; AAR33946.2;
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1475 MW; CHD7E795AFF31414 67%4;

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RT \*Nuclear factor Y activates the human xanthine oxidoreductase gene promoter.\*

RL FEBS Lett. 480:84-88(2000).

DR EMBL: AF203979; AAF15890.1;

FT NON\_TER 14 14

SQ SEQUENCE 14 AA: 1626 MW: D300FB701792F022 CRC64;

Query Match 27.3% Score 3; DR 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MTA 9

DB 1 MTA 3

#### RESULT 25

Q9SMV4

ID Q9SMV4 PRELIMINARY; PRT: 14 AA.

AC Q9SMV4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-MAY 2000 (TrEMBLrel. 13, Last annotation update);

DE Monosaccharide transporter (Fragment).

GN ATSTP1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI\_taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RA Truernit E.;

RL Thesis (1997), Universitaet Erlangen, Lehrstuhl Botanik II.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RX MEDLINE=99406514; PubMed=10476074;

RA Stadler R., Truernit E., Gahrz M., Sauer N.;

RT \*The AtSUC1 sucrose carrier may represent the osmotic driving force

RT for anther dehiscence and pollen tube growth in Arabidopsis.\*;

RL Plant J. 19:269-278(1999).

DR EMBL: AJ001363; CAB59189.1;

FT NON\_TER 14 14

SQ SEQUENCE 14 AA: 1551 MW: 7FE47997UA0A2A24 CRC64;

Query Match

Best Local Similarity 27.3% Score 3; DR 10; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3

DB 6 ARK 8

#### RESULT 26

P82452

ID P82452 PRELIMINARY; PRT: 14 AA.

AC P82452;

DT 01-JUN-2000 (TrEMBLrel. 14, Created)

DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)

DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE 60S ribosomal protein L26 (Fragment).

OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

OX NCBI\_taxid=3562;

RN [1]

RP SEQUENCE.

RC STRAIN=cv. ALVARO; TISSUE=LEAF;

RA Yamaguchi K., Subramanian A.R.;

RT \*Nuclear factor Y activates the human xanthine oxidoreductase gene promoter.\*

RL Submitted (AF203979) to the EMBL Data Bank.

DR EMBL: AF203979; AAF15890.1;

FT NON\_TER 14 14

SQ SEQUENCE 14 AA: 1626 MW: D300FB701792F022 CRC64;

Query Match

Best Local Similarity 27.3% Score 3; DR 10; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARK 4

DB 12 ARK 11

#### RESULT 27

P04114

ID P04114 PRELIMINARY; PRT: 14 AA.

AC P04114;

DT 01-MAY-1999 (TrEMBLrel. 13, Created)

DT 01-MAY 1999 (TrEMBLrel. 13, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE 2X myosin heavy chain (fragment)

OS Rattus rattus (Rat).

OC Eukaryota; Mammalia; Eumammalia; Theria; Eutheria; Rodentia; Muridae; Muridae; Eutheria;

OC Mammalia; Eutheria; Rodentia; Muridae; Muridae; Muridae; Eutheria;

OX NCBI\_taxid=10117;

RN [1]

RP SIOFONE FROM N.A.

RC TISSUE=Brain;

EX MEDLINE=94064476; PubMed=10476074;

RA Buckdahn M., Schmitt M., Gahrz M., Sauer N.;

RT \*Type 2X myosin heavy chain is coded by a mouse fiber type slow 1a

RT and developmentally regulated gene.\*

RL Plant J. 19:269-278(1999).

DR EMBL: X72641; CAB1109.1

FT NON\_TER 14 AA: 673 MW: 67300 G: 44.6% A: 24.6% C: 14.6% T: 15.2%

SQ SEQUENCE 14 AA: 673 MW: 67300 G: 44.6% A: 24.6% C: 14.6% T: 15.2%

Query Match

Best Local Similarity 27.3% Score 3; DR 10; Length 14;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ARK 1

DB 2 ARK 1

#### RESULT 28

P04114

ID P04114 PRELIMINARY; PRT: 14 AA.

AC P04114;

DT 01-MAY-1999 (TrEMBLrel. 13, Created)

DT 01-MAY 1999 (TrEMBLrel. 13, Last sequence update)

DE 01-MAY 2001 (TrEMBLrel. 22, Last annotation update)

DE 2X myosin heavy chain (fragment)

OS Rattus rattus (Rat).

OC Eukaryota; Mammalia; Eumammalia; Theria; Eutheria; Rodentia; Muridae; Muridae; Eutheria;

OC Mammalia; Eutheria; Rodentia; Muridae; Muridae; Muridae; Eutheria;

OX NCBI\_taxid=10117;

RN [1]

RP SIOFONE FROM N.A.

RC TISSUE=Brain;

EX MEDLINE=94064476; PubMed=10476074;

RA Buckdahn M., Schmitt M., Gahrz M., Sauer N.;

RT \*Type 2X myosin heavy chain is coded by a mouse fiber type slow 1a

RT and developmentally regulated gene.\*

RL Plant J. 19:269-278(1999).

DR EMBL: X72641; CAB1109.1

FT NON\_TER 14 AA: 673 MW: 67300 G: 44.6% A: 24.6% C: 14.6% T: 15.2%

SQ SEQUENCE 14 AA: 673 MW: 67300 G: 44.6% A: 24.6% C: 14.6% T: 15.2%

[illegible][illegible]

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Alkaline phosphodiesterase I (EC 3.1.4.1) (Fragment).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Ruminantia; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=93250579; PubMed=8387170;  
 RA Maruyama E., Iwanatsu A., Takashima S.;  
 RL Biochem. Mol. Biol. Int. 29:579-586(1994).  
 SQ SEQUENCE 15 AA; 1678 MW; BE31498FEA8B7071 CRG64;

Query Match 27.3%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3  
 DB 13 ARK 15

## RESULT 34

Q8WK21 ID Q8WK21 PRELIMINARY; PRT; 15 AA;  
 AC Q8WK21;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DE Putative proteolysis tag (Fragment).  
 OS Bolidomonas sp. OL146SE.  
 CC Chloroplast.  
 CC Eukaryota; Stramenopiles; Bolidophyceae; Bolidomonas.  
 OX NCBI\_TaxID=129302;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OL146SE;  
 RT Williams K., Guillou L., Gueneau de Novoa P.;  
 RL \*Small RNAs from non-green plastidial genomes.\*;  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases  
 DR EMBL; AF169626; AAL55606.1;  
 KW Chloroplast.  
 FT NON-TER  
 SQ SEQUENCE 15 AA; 1666 MW; 0D578E9144198201 CRG64;

Query Match 27.3%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKS 4  
 DB 9 RKS 11

## RESULT 35

P82135 ID P82135 PRELIMINARY; PRT; 15 AA;  
 AC P82135;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S18 alpha (Fragment).  
 OS Spinacia oleracea (Spinach).  
 CC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 CC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3362;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC STRAIN=cv. ALVARO; TISSUE=Leaf;

RX MEDLINE=20455793; PubMed=1194077;  
 RA Yanooperi K., von Klot J., Kottmann A.R.;  
 RL The plastid ribosomal protein: Identification of all the proteins in  
 RL the small subunit of an organelle ribosome (entoroplast).  
 RL Biol. Chem. 274:24155-24156(2000).  
 CC 1 SUBCELLULAR LOCALIZATION: CHLOROPLAST.  
 CC 1 TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC 1 MISCELLANEOUS: THE ALPHA AND BETA FORMS DIFFER IN THE SUB-CELL  
 CC FORM 15 THE LEAF, BETA FORM  
 CC 1 MASS SPECTROMETRY: MW 22.0 KDa, METRIC: MALDI.  
 CC 1 MISCELLANEOUS: IN THE CHLOROPLAST, THIS MW 15.14 KDa  
 CC 1 SIMILARITY: SEQUENCES OF THE SUB-FAMILY OF RIBOSOMAL PROTEIN  
 CC Enteroplasmodium, with some sp.  
 DR Plant, P82135; Eukaryota; Streptophyta; Tracheophyta;  
 DR Proteins; P82135; Eukaryota; Streptophyta; Tracheophyta;  
 KW Ribosomal protein; Chloroplast.  
 FT NON-TER  
 SQ SEQUENCE 15 AA; 1666 MW; 0D578E9144198201 CRG64;

Query Match 27.3%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKS 4  
 DB 10 RKS 15

## RESULT 36

Q8WK21 ID Q8WK21 PRELIMINARY; PRT; 15 AA;  
 AC Q8WK21;  
 DT 01-MAY-2000 (TrEMBLrel. 20, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 20, Last annotation update)  
 DE 16 kDa alpha lactalbumin homolog (Fragment).  
 OS Mus sp.  
 CC Eukaryota; Metazoa; Chordata; Euteleostomi; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=9545477; PubMed=7636251;  
 RA Suto Y., Nagasawa H., Sasak. T., Tanami T., Iuchi T.;  
 RL "Biochemical changes during growth and regression of pregnancy  
 RL dependent mammary tumors of DEZA mice."  
 RL Proc. Soc. Exp. Biol. Med. 200:43-45(1993)  
 SQ SEQUENCE 15 AA; 1666 MW; 166A7AD707E9A4A6 CRG64;

Query Match 27.3%; Score 3; DB 11; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 11  
 DB 11 ARK 14

## RESULT 37

Q820X5 ID Q820X5 PRELIMINARY; PRT; 15 AA;  
 AC Q820X5;  
 DT 01-MAY-2000 (TrEMBLrel. 15, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 15, Last annotation update)  
 DE 10 kDa MIR-100 ribonuclease protein (Fragment).  
 OS Rattus sp.  
 CC Eukaryota; Metazoa; Chordata; Euteleostomi; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathini; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10114;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96195455; PubMed=8014308;

RA Goto S., Lord R., Kobayashi E., Vari F., Edwards Smith C., Kamada N.  
 RT "Novel immunosuppressive proteins purified from the spleen of liver-  
 RL retransplanted rats."  
 SL Transplantation 61:1147-1151(1996).  
 SQ SEQUENCE 15 AA: 1477 MW: 81089700000714P CRC64:

Query Match 27.3% Score 3; PB 11; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4, 6, 9;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 10  
 Db 8 TA 10

## RESULT 38

Q9S6D5 PRELIMINARY: PRT: 8 AA.

ID Q9S6D5  
 AC Q9S6D5  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Putative IS50 transposase (fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID:562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:A295b;  
 RX MEDLINE:9919477; PubMed:10094716;  
 RA Rahn A., Drummelsmith J., Whitfield G.  
 RT "Conserved organization in the cps gene clusters for expression of  
 RT Escherichia coli group 1 k antigens: relationship to the enterohemolysin  
 RT biosynthesis locus and the cps genes from Klebsiella pneumoniae".  
 RL J. Bacteriol. 181:2307-2314(1999).  
 DR EMBL: AF118251; AAD30008.1;  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 1011 MW: F21DC1A9D1B41406 CRC64:

Query Match 18.2% Score 2; PB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 4, 6, 9;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 9  
 Db 6 TA 7

## RESULT 39

Q45615 PRELIMINARY: PRT: 8 AA.

ID Q45615  
 AC Q45615  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE GcbB protein (fragment).  
 GN GUTR.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID:1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:168;  
 RX MEDLINE:94253000; PubMed:8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis alcohol  
 RT dehydrogenase gene."  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL: U16626; AAA20875.1;  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 927 MW: FD56C772D1A1F1A6 CRC64:

Query Match 27.3% Score 3; PB 11; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4, 6, 9;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MI 8  
 Db 1 MI 2

## RESULT 40

Q45615 PRELIMINARY: PRT: 8 AA.

ID Q45615  
 AC Q45615  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Putative IS50 transposase (fragment).  
 GN GUTR.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID:562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:A295b;  
 RX MEDLINE:9919477; PubMed:10094716;  
 RA Rahn A., Drummelsmith J., Whitfield G.  
 RT "Conserved organization in the cps gene clusters for expression of  
 RT Escherichia coli group 1 k antigens: relationship to the enterohemolysin  
 RT biosynthesis locus and the cps genes from Klebsiella pneumoniae".  
 RL J. Bacteriol. 181:2307-2314(1999).  
 DR EMBL: AF118251; AAD30008.1;  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 1011 MW: F21DC1A9D1B41406 CRC64:

Query Match 18.2% Score 2; PB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 4, 6, 9;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TA 10  
 Db 6 TA 7

## RESULT 41

Q45615 PRELIMINARY: PRT: 8 AA.

ID Q45615  
 AC Q45615  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE GcbB protein (fragment).  
 GN GUTR.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID:1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:168;  
 RX MEDLINE:94253000; PubMed:8195086;  
 RA Ye R., Wong S.L.;  
 RT "Transcriptional regulation of the Bacillus subtilis alcohol  
 RT dehydrogenase gene."  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL: U16626; AAA20875.1;  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 927 MW: FD56C772D1A1F1A6 CRC64:

Query Match 18.2% Score 2; PB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 4, 6, 9;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TK 10  
 Db 6 TK 6







Best Local Similarity 100.0%; Pred. No. B. se-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 A1 10  
   11  
Db 4 A1 5

Search completed: September 30, 2003, 10:18:17  
Job time : 35.6667 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:05 : Search time 11.8333 Seconds  
(without alignments)  
39.331 Million cpi/updates/sec

Title: US-09-787-443-22  
Perfect score: 11  
Sequence: 1 AKSRDWTAK 11

Scoring table: OLIGO  
Gapox 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 24459

Minimum DB seq length: 8  
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/UCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	8	4	US-09-451-234-1
2	4	36.4	9	2	US-08-705-660-4
3	4	36.4	9	2	US-08-146-028-402
4	4	36.4	9	2	US-08-146-028-403
5	4	36.4	9	2	US-08-146-028-404
6	4	36.4	9	2	US-08-146-028-405
7	4	36.4	9	2	US-08-146-028-406
8	4	36.4	9	2	US-08-146-028-407
9	4	36.4	9	3	US-08-989-045-4
10	4	36.4	9	3	US-08-723-425A-402
11	4	36.4	9	3	US-08-723-425A-403
12	4	36.4	9	3	US-08-723-425A-404
13	4	36.4	9	3	US-08-723-425A-405
14	4	36.4	9	3	US-08-723-425A-406
15	4	36.4	9	3	US-08-723-425A-407
16	4	36.4	9	3	US-09-112-206-402
17	4	36.4	9	3	US-09-112-206-403
18	4	36.4	9	3	US-09-112-206-404
19	4	36.4	9	3	US-09-112-206-405
20	4	36.4	9	3	US-09-112-206-406
21	4	36.4	9	3	US-09-112-206-407
22	4	36.4	10	4	US-09-258-689-1
23	4	36.4	10	4	US-09-195-179-1
24	4	36.4	11	1	US-08-185-448-5
25	4	36.4	11	2	US-08-747-137-63
26	4	36.4	11	3	US-08-696-854B-3
27	4	36.4	11	5	PCT-US91-08328-13

28	4	36.4	12	1	US-09-451-234-1
29	4	36.4	12	1	US-09-112-206-406
30	4	36.4	12	1	US-09-258-689-1
31	4	36.4	12	1	US-09-195-179-1
32	4	36.4	12	1	US-09-451-234-1
33	4	36.4	12	1	US-09-112-206-406
34	4	36.4	12	1	US-09-258-689-1
35	4	36.4	12	1	US-09-195-179-1
36	4	36.4	12	1	US-09-451-234-1
37	4	36.4	12	1	US-09-112-206-406
38	4	36.4	12	1	US-09-258-689-1
39	4	36.4	12	1	US-09-195-179-1
40	4	36.4	12	1	US-09-451-234-1
41	4	36.4	12	1	US-09-112-206-406
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46	4	36.4	12	1	US-09-258-689-1
47	4	36.4	12	1	US-09-195-179-1
48	4	36.4	12	1	US-09-451-234-1
49	4	36.4	12	1	US-09-112-206-406
50	4	36.4	12	1	US-09-258-689-1
51	4	36.4	12	1	US-09-195-179-1
52	4	36.4	12	1	US-09-451-234-1
53	4	36.4	12	1	US-09-112-206-406
54	4	36.4	12	1	US-09-258-689-1
55	4	36.4	12	1	US-09-195-179-1
56	4	36.4	12	1	US-09-451-234-1
57	4	36.4	12	1	US-09-112-206-406
58	4	36.4	12	1	US-09-258-689-1
59	4	36.4	12	1	US-09-195-179-1
60	4	36.4	12	1	US-09-451-234-1
61	4	36.4	12	1	US-09-112-206-406
62	4	36.4	12	1	US-09-258-689-1
63	4	36.4	12	1	US-09-195-179-1
64	4	36.4	12	1	US-09-451-234-1
65	4	36.4	12	1	US-09-112-206-406
66	4	36.4	12	1	US-09-258-689-1
67	4	36.4	12	1	US-09-195-179-1
68	4	36.4	12	1	US-09-451-234-1
69	4	36.4	12	1	US-09-112-206-406
70	4	36.4	12	1	US-09-258-689-1
71	4	36.4	12	1	US-09-195-179-1
72	4	36.4	12	1	US-09-451-234-1
73	4	36.4	12	1	US-09-112-206-406
74	4	36.4	12	1	US-09-258-689-1
75	4	36.4	12	1	US-09-195-179-1
76	4	36.4	12	1	US-09-451-234-1
77	4	36.4	12	1	US-09-112-206-406
78	4	36.4	12	1	US-09-258-689-1
79	4	36.4	12	1	US-09-195-179-1
80	4	36.4	12	1	US-09-451-234-1
81	4	36.4	12	1	US-09-112-206-406
82	4	36.4	12	1	US-09-258-689-1
83	4	36.4	12	1	US-09-195-179-1
84	4	36.4	12	1	US-09-451-234-1
85	4	36.4	12	1	US-09-112-206-406
86	4	36.4	12	1	US-09-258-689-1
87	4	36.4	12	1	US-09-195-179-1
88	4	36.4	12	1	US-09-451-234-1
89	4	36.4	12	1	US-09-112-206-406
90	4	36.4	12	1	US-09-258-689-1
91	4	36.4	12	1	US-09-195-179-1
92	4	36.4	12	1	US-09-451-234-1
93	4	36.4	12	1	US-09-112-206-406
94	4	36.4	12	1	US-09-258-689-1
95	4	36.4	12	1	US-09-195-179-1
96	4	36.4	12	1	US-09-451-234-1
97	4	36.4	12	1	US-09-112-206-406
98	4	36.4	12	1	US-09-258-689-1
99	4	36.4	12	1	US-09-195-179-1
100	4	36.4	12	1	US-09-451-234-1

[illegible]

247	3	27.3	11	4	US-09-104-337A-375	Sequence 375, App	329	27.3	12	3	US-09-104-337A-375	Sequence 375, App
248	3	27.3	11	4	US-09-104-337A-424	Sequence 424, App	329	27.3	12	3	US-09-104-337A-424	Sequence 424, App
249	3	27.3	11	4	US-09-104-337A-427	Sequence 427, App	329	27.3	12	3	US-09-104-337A-427	Sequence 427, App
250	3	27.3	11	4	US-09-104-337A-430	Sequence 430, App	329	27.3	12	3	US-09-104-337A-430	Sequence 430, App
251	3	27.3	11	4	US-09-104-337A-436	Sequence 436, App	329	27.3	12	3	US-09-104-337A-436	Sequence 436, App
252	3	27.3	11	4	US-09-104-337A-522	Sequence 522, App	329	27.3	12	3	US-09-104-337A-522	Sequence 522, App
253	3	27.3	11	4	US-09-810-873-2	Sequence 2, App11	329	27.3	12	3	US-09-810-873-2	Sequence 2, App11
254	3	27.3	11	4	US-08-488-446-550	Sequence 550, App	329	27.3	12	3	US-08-488-446-550	Sequence 550, App
255	3	27.3	11	4	US-08-467-344A-530	Sequence 530, App	329	27.3	12	3	US-08-467-344A-530	Sequence 530, App
256	3	27.3	11	5	PCT-US95-01721-5	Patent No. 5187155-6	329	27.3	12	3	PCT-US95-01721-5	Patent No. 5187155-6
257	3	27.3	11	6	US-07-958-083-4	Sequence 4, App11	329	27.3	12	3	US-07-958-083-4	Sequence 4, App11
258	3	27.3	12	1	US-08-031-148-22	Sequence 22, App1	329	27.3	12	3	US-08-031-148-22	Sequence 22, App1
259	3	27.3	12	1	US-08-212-433A-10	Sequence 10, App2	329	27.3	12	3	US-08-212-433A-10	Sequence 10, App2
260	3	27.3	12	1	US-08-218-025A-2	Sequence 2, App11	329	27.3	12	3	US-08-218-025A-2	Sequence 2, App11
261	3	27.3	12	1	US-08-190-788A-228	Sequence 228, App	329	27.3	12	3	US-08-190-788A-228	Sequence 228, App
262	3	27.3	12	1	US-08-313-681A-27	Sequence 27, App1	329	27.3	12	3	US-08-313-681A-27	Sequence 27, App1
263	3	27.3	12	1	US-08-260-542-24	Sequence 44, App1	329	27.3	12	3	US-08-260-542-24	Sequence 44, App1
264	3	27.3	12	1	US-08-260-542-40	Sequence 40, App1	329	27.3	12	3	US-08-260-542-40	Sequence 40, App1
265	3	27.3	12	1	US-08-257-528B-44	Sequence 44, App1	329	27.3	12	3	US-08-257-528B-44	Sequence 44, App1
266	3	27.3	12	1	US-08-241-054-41	Sequence 57, App1	329	27.3	12	3	US-08-241-054-41	Sequence 57, App1
267	3	27.3	12	1	US-08-241-054-57	Sequence 98, App1	329	27.3	12	3	US-08-241-054-57	Sequence 98, App1
268	3	27.3	12	1	US-08-241-054-57	Sequence 51, App1	329	27.3	12	3	US-08-241-054-57	Sequence 51, App1
269	3	27.3	12	1	US-08-390-156A-51	Sequence 59, App1	329	27.3	12	3	US-08-390-156A-51	Sequence 59, App1
270	3	27.3	12	1	US-08-390-156A-51	Sequence 87, App1	329	27.3	12	3	US-08-390-156A-51	Sequence 87, App1
271	3	27.3	12	1	US-08-390-156A-59	Sequence 27, App1	329	27.3	12	3	US-08-390-156A-59	Sequence 27, App1
272	3	27.3	12	1	US-08-439-817-21	Sequence 87, App1	329	27.3	12	3	US-08-439-817-21	Sequence 87, App1
273	3	27.3	12	1	US-08-439-817-47	Sequence 37, App1	329	27.3	12	3	US-08-439-817-47	Sequence 37, App1
274	3	27.3	12	1	US-08-439-817-78	Sequence 78, App1	329	27.3	12	3	US-08-439-817-78	Sequence 78, App1
275	3	27.3	12	1	US-08-460-602A-34	Sequence 31, App1	329	27.3	12	3	US-08-460-602A-34	Sequence 31, App1
276	3	27.3	12	1	US-08-383-474B-231	Sequence 6, App11	329	27.3	12	3	US-08-383-474B-231	Sequence 6, App11
277	3	27.3	12	1	US-08-467-607-6	Sequence 41, App1	329	27.3	12	3	US-08-467-607-6	Sequence 41, App1
278	3	27.3	12	1	US-08-485-508-41	Sequence 57, App1	329	27.3	12	3	US-08-485-508-41	Sequence 57, App1
279	3	27.3	12	1	US-08-485-508-57	Sequence 98, App1	329	27.3	12	3	US-08-485-508-57	Sequence 98, App1
280	3	27.3	12	1	US-08-463-966A-34	Sequence 228, App	329	27.3	12	3	US-08-463-966A-34	Sequence 228, App
281	3	27.3	12	1	US-08-463-966A-34	Sequence 44, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 44, App1
282	3	27.3	12	1	US-08-463-966A-34	Sequence 45, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 45, App1
283	3	27.3	12	1	US-08-463-966A-34	Sequence 34, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 34, App1
284	3	27.3	12	1	US-08-463-966A-34	Sequence 121, App	329	27.3	12	3	US-08-463-966A-34	Sequence 121, App
285	3	27.3	12	1	US-08-463-966A-34	Sequence 6, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 6, App1
286	3	27.3	12	1	US-08-463-966A-34	Sequence 228, App	329	27.3	12	3	US-08-463-966A-34	Sequence 228, App
287	3	27.3	12	1	US-08-463-966A-34	Sequence 41, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 41, App1
288	3	27.3	12	1	US-08-463-966A-34	Sequence 57, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 57, App1
289	3	27.3	12	1	US-08-463-966A-34	Sequence 98, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 98, App1
290	3	27.3	12	1	US-08-463-966A-34	Sequence 51, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 51, App1
291	3	27.3	12	1	US-08-463-966A-34	Sequence 59, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 59, App1
292	3	27.3	12	1	US-08-463-966A-34	Sequence 27, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 27, App1
293	3	27.3	12	1	US-08-463-966A-34	Sequence 87, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 87, App1
294	3	27.3	12	1	US-08-463-966A-34	Sequence 37, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 37, App1
295	3	27.3	12	1	US-08-463-966A-34	Sequence 78, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 78, App1
296	3	27.3	12	1	US-08-463-966A-34	Sequence 31, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 31, App1
297	3	27.3	12	1	US-08-463-966A-34	Sequence 6, App11	329	27.3	12	3	US-08-463-966A-34	Sequence 6, App11
298	3	27.3	12	1	US-08-463-966A-34	Sequence 41, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 41, App1
299	3	27.3	12	1	US-08-463-966A-34	Sequence 57, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 57, App1
300	3	27.3	12	1	US-08-463-966A-34	Sequence 98, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 98, App1
301	3	27.3	12	1	US-08-463-966A-34	Sequence 51, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 51, App1
302	3	27.3	12	1	US-08-463-966A-34	Sequence 59, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 59, App1
303	3	27.3	12	1	US-08-463-966A-34	Sequence 27, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 27, App1
304	3	27.3	12	1	US-08-463-966A-34	Sequence 87, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 87, App1
305	3	27.3	12	1	US-08-463-966A-34	Sequence 37, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 37, App1
306	3	27.3	12	1	US-08-463-966A-34	Sequence 78, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 78, App1
307	3	27.3	12	1	US-08-463-966A-34	Sequence 31, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 31, App1
308	3	27.3	12	1	US-08-463-966A-34	Sequence 6, App11	329	27.3	12	3	US-08-463-966A-34	Sequence 6, App11
309	3	27.3	12	1	US-08-463-966A-34	Sequence 41, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 41, App1
310	3	27.3	12	1	US-08-463-966A-34	Sequence 57, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 57, App1
311	3	27.3	12	1	US-08-463-966A-34	Sequence 98, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 98, App1
312	3	27.3	12	1	US-08-463-966A-34	Sequence 51, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 51, App1
313	3	27.3	12	1	US-08-463-966A-34	Sequence 59, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 59, App1
314	3	27.3	12	1	US-08-463-966A-34	Sequence 27, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 27, App1
315	3	27.3	12	1	US-08-463-966A-34	Sequence 87, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 87, App1
316	3	27.3	12	1	US-08-463-966A-34	Sequence 37, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 37, App1
317	3	27.3	12	1	US-08-463-966A-34	Sequence 78, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 78, App1
318	3	27.3	12	1	US-08-463-966A-34	Sequence 31, App1	329	27.3	12	3	US-08-463-966A-34	Sequence 31, App1
319	3	27.3	12	1	US-08-463-966A-34	Sequence 6, App11	329	27.3	12	3	US-08-463-966A-34	Sequence 6, App11



Sequence 4, Application US/08705660  
 Patent No. 5858683  
 GENERAL INFORMATION:  
 APPLICANT: KESSEE, SUSAN  
 APPLICANT: OBAR, ROBERT  
 APPLICANT: WU, YING-JYE  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
 DETECTION OF CERVICAL CANCER  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Testa, Hurwitz & Thibault  
 STREET: 125 High St.  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/705,660  
 FILING DATE:  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GREENHALGH, DUNCAN A  
 REGISTRATION NUMBER: 38,678  
 REFERENCE/DOCKET NUMBER: MTP-023 (#395/27)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 248-7000  
 TELEFAX: (617) 248-7100  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-705-660-4

Query Match 36.4% Score 4; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRDM 7  
 DB 6 SRDM 9

## RESULT 3

US-08-146-028-402  
 Sequence 402, Application US/08146028  
 Patent No. 5891640  
 GENERAL INFORMATION:  
 APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
 CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
 TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
 TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR REGUNYLATED  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 NUMBER OF SEQUENCES: 453  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/146,028  
 INFORMATION FOR SEQ ID NO: 402:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-146-028-402

Query Match 36.4% Score 4; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KRSP 5  
 DB 6 KRSP 4

## RESULT 4

US-08-146-028-404  
 Sequence 404, Application US/08146028  
 Patent No. 5891640  
 GENERAL INFORMATION:  
 APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
 CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
 TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR REGUNYLATED  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 NUMBER OF SEQUENCES: 453  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/146,028  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-146-028-404

Query Match 36.4% Score 4; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRSP 5  
 DB 6 KRSP 8

## RESULT 5

US-08-146-028-404  
 Sequence 404, Application US/08146028  
 Patent No. 5891640  
 GENERAL INFORMATION:  
 APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
 CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
 TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR REGUNYLATED  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
 NUMBER OF SEQUENCES: 453  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/146,028  
 INFORMATION FOR SEQ ID NO: 404:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids



;  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-404

Query Match 36.4%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 5  
DB 4 RKSR 7

## RESULT 6

US-08-146-028-405  
; Sequence 405, Application US/08146028  
; Patent No. 5891640

## GENERAL INFORMATION:

;  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES ARE THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146.028

; INFORMATION FOR SEQ ID NO: 405:

;  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-405

Query Match 36.4%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 5  
DB 3 RKSR 6

## RESULT 7

US-08-146-028-406  
; Sequence 406, Application US/08146028  
; Patent No. 5891640

## GENERAL INFORMATION:

;  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146.028  
; INFORMATION FOR SEQ ID NO: 406:  
; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-406

Query Match 36.4%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 5  
DB 4 RKSR 5

## RESULT 8

US-08-146-028-407  
; Sequence 407, Application US/08146028  
; Patent No. 5891640

## GENERAL INFORMATION:

;  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES ARE THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146.028

; INFORMATION FOR SEQ ID NO: 407:

;  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-407

Query Match 36.4%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 6  
DB 3 RKSR 4

## RESULT 9

US-08-999-045 4  
; Sequence 4, Application US/0899045  
; Patent No. 627542

## GENERAL INFORMATION:

;  
; APPLICANT: KESSEF, ROYAN  
; APPLICANT: GRAY, ROBERT  
; APPLICANT: WU, YING-GE  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
; TITLE OF INVENTION: DETECTION OF SERVICIAL CANCER  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: POSTAL BOX 104, Hithersville  
; STREET: 125 South St.  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Vers.06. #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/989,045  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GREENHALGH, DUNCAN A  
 REGISTRATION NUMBER: 38,674  
 REFERENCE/DOCKET NUMBER: WTP-023 (8/95/27)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 248-7000  
 TELEFAX: (617) 248-7100  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-989-045-4

Query Match 36.4% Score 4: 100.0% Seq-Id: 9  
 Best Local Similarity 100.0% Pred. No. 2.5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

Qy 4 SRDM 7  
 DB 6 SRDM 9

# RESULT 10

US-08-723-425A-402  
 Sequence 402, Application US/08723425A  
 Patent No. 6165730  
 GENERAL INFORMATION:  
 APPLICANT: DELEYS, ROBERT  
 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 TITLE OF INVENTION: ANTIBODIES OR HINT-INVOLVED PEPTIDES CORRESPONDING TO  
 NUMBER OF SEQUENCES: 453  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 CITY: Arlington  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/723,425A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SADOFF, B.J.  
 REGISTRATION NUMBER: 36,663  
 REFERENCE/DOCKET NUMBER: 1487-13  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-816-4000  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 402:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

## US-08-723-425A-402

Query Match 36.4% Score 4: 100.0% Seq-Id: 9  
 Best Local Similarity 100.0% Pred. No. 2.5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

Qy 4 SRDM 7  
 DB 6 SRDM 9

RESULT 10  
 US-08-723-425A-402  
 Sequence 402, Application US/08723425A  
 Patent No. 6165730  
 GENERAL INFORMATION:  
 APPLICANT: DELEYS, ROBERT  
 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 TITLE OF INVENTION: ANTIBODIES OR HINT-INVOLVED PEPTIDES CORRESPONDING TO  
 NUMBER OF SEQUENCES: 453  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 CITY: Arlington  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/723,425A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SADOFF, B.J.  
 REGISTRATION NUMBER: 36,663  
 REFERENCE/DOCKET NUMBER: 1487-13  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-816-4000  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 402:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

Query Match 36.4% Score 4: 100.0% Seq-Id: 9  
 Best Local Similarity 100.0% Pred. No. 2.5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

Qy 4 SRDM 7  
 DB 6 SRDM 9

RESULT 10  
 US-08-723-425A-402  
 Sequence 402, Application US/08723425A  
 Patent No. 6165730  
 GENERAL INFORMATION:  
 APPLICANT: DELEYS, ROBERT  
 TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 TITLE OF INVENTION: ANTIBODIES OR HINT-INVOLVED PEPTIDES CORRESPONDING TO

1 NUMBER OF SEQUENCES: 453  
 2 CORRESPONDENCE ADDRESS:  
 3 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 4 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 5 CITY: Arlington  
 6 STATE: VA  
 7 COUNTRY: USA  
 8 ZIP: 22201  
 9 COMPUTER READABLE FORM:  
 10 MEDIUM TYPE: Floppy disk  
 11 COMPUTER: IBM PC compatible  
 12 OPERATING SYSTEM: PC-DOS/MS-DOS  
 13 SOFTWARE: Patent in Release #1.0, Version: #1.0  
 14 CURRENT APPLICATION DATA: US/08/723,425A  
 15 APPLICATION NUMBER: US/08/723,425A  
 16 FILING DATE:  
 17 CLASSIFICATION: 435  
 18 ATTORNEY/AGENT INFORMATION:  
 19 NAME: SADOFF, B.J.  
 20 REGISTRATION NUMBER: 36,663  
 21 REFERENCE/DOCKET NUMBER: 1487-13  
 22 TELECOMMUNICATION INFORMATION:  
 23 TELEPHONE: 703-816-4000  
 24 TELEFAX: 703-816-4100  
 25 INFORMATION FOR SEQ ID NO: 404:  
 26 SEQUENCE CHARACTERISTICS:  
 27 LENGTH: 9 amino acids  
 28 TYPE: amino acid  
 29 STRANDEDNESS: single  
 30 TOPOLOGY: linear  
 31 MOLECULE TYPE: peptide  
 32 US-08-723-425A-404

Query Match 36.48; Score 4; Db: 6; Length: 9;  
 Best Local Similarity 100.0%; Pred. No: 2; Seq: 5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 HKSR 5  
 1111  
 DB 4 HKSR 7

RESULT 13  
 US-08-723-425A-405  
 1 Sequence 405, Application US/08723425A  
 2 Patent No. 6165730  
 3 GENERAL INFORMATION:  
 4 APPLICANT: DELAYS, ROBERT  
 5 TITLE OF INVENTION: PEPTIDES FOR THE DETERMINATION OF  
 6 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 7 TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 8 TITLE OF INVENTION: ANTIBODIES OR BLATTINATED PEPTIDES CORRESPONDING  
 9 NUMBER OF SEQUENCES: 453  
 10 CORRESPONDENCE ADDRESS:  
 11 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 12 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 13 CITY: Arlington  
 14 STATE: VA  
 15 COUNTRY: USA  
 16 ZIP: 22201  
 17 COMPUTER READABLE FORM:  
 18 MEDIUM TYPE: Floppy disk  
 19 COMPUTER: IBM PC compatible  
 20 OPERATING SYSTEM: PC-DOS/MS-DOS  
 21 SOFTWARE: Patent in Release #1.0, Version: #1.0  
 22 CURRENT APPLICATION DATA:  
 23 APPLICATION NUMBER: US/08/723,425A  
 24 FILING DATE:  
 25 CLASSIFICATION: 435  
 26 ATTORNEY/AGENT INFORMATION:  
 27 NAME: SADOFF, B.J.  
 28 REGISTRATION NUMBER: 36,663  
 29 REFERENCE/DOCKET NUMBER: 1487-13

1 TELECOMMUNICATION INFORMATION:  
 2 TELEPHONE: 703-816-4000  
 3 TELEFAX: 703-816-4100  
 4 INFORMATION FOR SEQ ID NO: 404:  
 5 SEQUENCE CHARACTERISTICS:  
 6 LENGTH: 9 amino acids  
 7 TYPE: amino acid  
 8 STRANDEDNESS: single  
 9 TOPOLOGY: linear  
 10 MOLECULE TYPE: peptide  
 11 US-08-723-425A-404  
 12 Query Match 36.48; Score 4; Db: 6; Length: 9;  
 13 Best Local Similarity 100.0%; Pred. No: 2; Seq: 5;  
 14 Matches 4; Conservative 0; Mismatches 0; Indels 0;

RESULT 13  
 US-08-723-425A-405  
 1 Sequence 405, Application US/08723425A  
 2 Patent No. 6165730  
 3 GENERAL INFORMATION:  
 4 APPLICANT: DELAYS, ROBERT  
 5 TITLE OF INVENTION: PEPTIDES FOR THE DETERMINATION OF  
 6 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
 7 TITLE OF INVENTION: PEPTIDES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
 8 TITLE OF INVENTION: ANTIBODIES OR BLATTINATED PEPTIDES CORRESPONDING  
 9 NUMBER OF SEQUENCES: 453  
 10 CORRESPONDENCE ADDRESS:  
 11 ADDRESSEE: NIXON & VANDERHYE, P.C.  
 12 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
 13 CITY: Arlington  
 14 STATE: VA  
 15 COUNTRY: USA  
 16 ZIP: 22201  
 17 COMPUTER READABLE FORM:  
 18 MEDIUM TYPE: Floppy disk  
 19 COMPUTER: IBM PC compatible  
 20 OPERATING SYSTEM: PC-DOS/MS-DOS  
 21 SOFTWARE: Patent in Release #1.0, Version: #1.0  
 22 CURRENT APPLICATION DATA:  
 23 APPLICATION NUMBER: US/08/723,425A  
 24 FILING DATE:  
 25 CLASSIFICATION: 435  
 26 ATTORNEY/AGENT INFORMATION:  
 27 NAME: SADOFF, B.J.  
 28 REGISTRATION NUMBER: 36,663  
 29 REFERENCE/DOCKET NUMBER: 1487-13  
 30 TELECOMMUNICATION INFORMATION:  
 31 TELEPHONE: 703-816-4000  
 32 TELEFAX: 703-816-4100  
 33 INFORMATION FOR SEQ ID NO: 404:  
 34 SEQUENCE CHARACTERISTICS:  
 35 LENGTH: 9 amino acids  
 36 TYPE: amino acid  
 37 STRANDEDNESS: single  
 38 TOPOLOGY: linear  
 39 MOLECULE TYPE: peptide  
 40 US-08-723-425A-404

Query Match 36.48; Score 4; Db: 6; Length: 9;  
 Best Local Similarity 100.0%; Pred. No: 2; Seq: 5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 HKSR 5  
 1111  
 DB 4 HKSR 7

## RESULT 15

US-08-723-425A-407

Sequence 407, Application US/08723425A

Patent No. 6165730

GENERAL INFORMATION:

APPLICANT: DELEYS, ROBERT

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT

TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF

TITLE OF INVENTION: ANTIBODIES OR BICITINYLATED PEPTIDES CORRESPONDING TO

NUMBER OF SEQUENCES: 453

CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON &amp; VANDERHUYE, P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723,425A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 1487-13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 407:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-723-425A-407

Query Match

Best Local Similarity 100.0%; Pred. No. 2 56-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 2 RKSR 5

Db 1 RKSR 4

## RESULT 16

US-09-112-206-402

Sequence 402, Application US/09112206

Patent No. 6210903

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT PEPTIDES AND THEIR

TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BICITINYLATED

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

INFORMATION FOR SEQ ID NO: 402

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US/09-112-206-402

Query Match

Best Local Similarity 100.0%; Pred. No. 2 56-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 2 RKSR 5

Db 1 RKSR 4

## RESULT 17

US-09-112-206-402

Sequence 402, Application US/09/112206

Patent No. 6210903

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT PEPTIDES AND THEIR

TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BICITINYLATED

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

INFORMATION FOR SEQ ID NO: 402

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-112-206-402

## RESULT 16

US-09-112-206-402

Sequence 402, Application US/09112206

Patent No. 6210903

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT PEPTIDES AND THEIR

TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BICITINYLATED

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIOR APPLICATION DATA:

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 404:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-404

Query Match 36.4%, Score 4, DB 3, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0;

QY 2 RKSR 5
DB 4 RKSR 7

RESULT 19
US-09-112-206-405
: Sequence 405, Application US/09112206
: Patent No. 6210503
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
: TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
: TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOGENICATED
: TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
: TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
: NUMBER OF SEQUENCES: 453
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 405:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-405

Query Match 36.4%, Score 4, DB 3, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0;

QY 2 RKSR 5
DB 3 RKSR 6

RESULT 20
US-09-112-206-406
: Sequence 406, Application US/09112206

```

```

: Patent No. 6210503
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
: TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
: TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOGENICATED
: TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
: TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
: NUMBER OF SEQUENCES: 453
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 404:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-404

Query Match 36.4%, Score 4, DB 3, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0;

QY 2 RKSR 5
DB 4 RKSR 7

RESULT 21
US-09-112-206-407
: Sequence 407, Application US/09112206
: Patent No. 6210503
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
: TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
: TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOGENICATED
: TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
: TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
: NUMBER OF SEQUENCES: 453
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA: US/09/112,206
: APPLICATION NUMBER: US/09/112,206
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/146,028
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 405:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-112-206-407

Query Match 36.4%, Score 4, DB 3, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0;

```

QY 2 RKSR 5  
 DB 1 RKSR 4

RESULT 22  
 US-09-258-689-1  
 : Sequence 1, Application US/09258689  
 : Patent No. 6451527  
 : GENERAL INFORMATION:  
 : APPLICANT: Larocca, David  
 : APPLICANT: Kassner, Paul  
 : TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR  
 : FILE REFERENCE: 760100.430C3  
 : CURRENT APPLICATION NUMBER: US/09/258.689  
 : CURRENT FILING DATE: 1999-02-26  
 : NUMBER OF SEQ ID NOS: 10  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1  
 : LENGTH: 10  
 : TYPE: PRT  
 : ORGANISM: Unknown  
 : FEATURE:  
 : OTHER INFORMATION: Description of Unknown Organism: A screened  
 : OTHER INFORMATION: peptide, from a random peptide library, that binds  
 : OTHER INFORMATION: and internalizes in a FGF receptor overproducing  
 : OTHER INFORMATION: cell line  
 US-09-258-689-1

Query Match 36.48; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.08; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 5  
 DB 7 RKSR 10

RESULT 23  
 US-09-195-379-1  
 : Sequence 1, Application US/09195379  
 : Patent No. 6472146  
 : GENERAL INFORMATION:  
 : APPLICANT: Larocca, David  
 : APPLICANT: Baird, Andrew  
 : TITLE OF INVENTION: METHODS FOR IDENTIFICATION OF TARGET CELLS  
 : FILE REFERENCE: 760100.430C1  
 : CURRENT APPLICATION NUMBER: US/09/195.379  
 : CURRENT FILING DATE: 1998-11-17  
 : NUMBER OF SEQ ID NOS: 4  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1  
 : LENGTH: 10  
 : TYPE: PRT  
 : ORGANISM: Unknown  
 : FEATURE:  
 : OTHER INFORMATION: Description of Unknown Organism: A screened  
 : OTHER INFORMATION: peptide, from a random peptide library, that binds  
 : OTHER INFORMATION: and internalizes in a FGF receptor overproducing  
 : OTHER INFORMATION: cell line  
 US-09-195-379-1

Query Match 36.48; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.08; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 5  
 DB 7 RKSR 10

DB 7 RKSR 10

RESULT 24  
 US-09-195-448-6  
 : Sequence 1, Application US/09195448  
 : Patent No. 6480747  
 : GENERAL INFORMATION:  
 : APPLICANT: Shultz, Alan W  
 : TITLE OF INVENTION: SUBSTITUTED KINASE  
 : FILE REFERENCE: 760100.430C1  
 : CURRENT APPLICATION NUMBER: US/09/195.448  
 : CURRENT FILING DATE: 1999-02-26  
 : NUMBER OF SEQ ID NOS: 10  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1  
 : LENGTH: 10  
 : TYPE: PRT  
 : ORGANISM: Unknown  
 : FEATURE:  
 : OTHER INFORMATION: Description of Unknown Organism: A screened  
 : OTHER INFORMATION: peptide, from a random peptide library, that binds  
 : OTHER INFORMATION: and internalizes in a FGF receptor overproducing  
 : OTHER INFORMATION: cell line  
 US-09-195-448-6

Query Match 36.48; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.08; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 5  
 DB 7 RKSR 10

RESULT 25  
 US-09-747-137-6  
 : Sequence 1, Application US/090747137  
 : Patent No. 6480747  
 : GENERAL INFORMATION:  
 : APPLICANT: Yen, Richard K  
 : TITLE OF INVENTION: NON-ASSIGNED PROTEIN PARTICLES FOR  
 : OTHER INFORMATION: THERAPEUTIC AND DIAGNOSTIC USE  
 : OTHER INFORMATION: cell line  
 US-09-747-137-6

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,841
FILING DATE: 01-JUN-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: App.e, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-00284005
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO.: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
US-08-747-137-63

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```

Query Match      36.48; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy      2 RKSR 5
Db      5 RKSR 8

```

```

RESULT 26
US-08-696-8548-3
Sequence 3, Application US/08696854B
Patent No. 6017878
GENERAL INFORMATION:
APPLICANT: SARAGOVIT, Uri H.
APPLICANT: Lesauteur, Lynne
APPLICANT: CUELLO, Claudio A.
TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
TITLE OF INVENTION: AND THEIR USES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: KLAUBER & JACKSON
STREET: Continental Plaza, 411 Hackensack Avenue
CITY: Hackensack
STATE: N.J.
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
NAME: App.e, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-00284005
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO.: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
US-08-747-137-63
Query Match      36.48; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      2 RKSR 5
Db      5 RKSR 8
RESULT 27
US-08-696-8548-3
Sequence 3, Application US/08696854B
Patent No. 6017878
GENERAL INFORMATION:
APPLICANT: SARAGOVIT, Uri H.
APPLICANT: Lesauteur, Lynne
APPLICANT: CUELLO, Claudio A.
TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
TITLE OF INVENTION: AND THEIR USES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: KLAUBER & JACKSON
STREET: Continental Plaza, 411 Hackensack Avenue
CITY: Hackensack
STATE: N.J.
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
NAME: App.e, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-00284005
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO.: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
US-08-747-137-63

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; CURRENT FILING DATE: 1999-11-29  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: PATENT  
 ; OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
 ; OTHER INFORMATION: The first Ala is a modified residue, it is  
 ; OTHER INFORMATION: acetylated  
 US-09-451-034-3

Query Match 36.4% Score 4; Db 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1,40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 Db 8 ARKS 11

## RESULT 32

US-09-451-034-8  
 ; Sequence 8, Application US/09451034  
 ; Patent No. 6369030  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cole, Philip et al  
 ; TITLE OF INVENTION: INHIBITORS OF HISTONE ACETYLTRANSFERASE (HATS) AND USES  
 ; FILE REFERENCE: THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/451,034  
 ; CURRENT FILING DATE: 1999-11-29  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: PATENT  
 ; OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
 ; OTHER INFORMATION: The first ala is a modified residue, it is  
 ; OTHER INFORMATION: acetylated.  
 US-09-451-034-8

Query Match 36.4% Score 4; Db 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1,40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 Db 7 ARKS 10

## RESULT 33

US-09-115-209-28  
 ; Sequence 28, Application US/09115209  
 ; Patent No. 598375  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thorgersen, Henning  
 ; APPLICANT: Madsen, Kjeld  
 ; APPLICANT: Olsen, Uffe B.  
 ; APPLICANT: Johansen, Nils L.  
 ; APPLICANT: Scheidegger, Mark  
 ; TITLE OF INVENTION: No. 5998375iceptin Analogues  
 ; FILE REFERENCE: 5285.200-US  
 ; CURRENT APPLICATION NUMBER: US/09/115,209  
 ; EARLIER FILING DATE: 1998-07-14  
 ; EARLIER APPLICATION NUMBER: 0867/97  
 ; EARLIER FILING DATE: 1997-07-15  
 ; EARLIER APPLICATION NUMBER: 60/052,862

; PATENT FILING DATE: 1998-07-14  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 28  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; OTHER INFORMATION: NO. 5998375iceptin Analogues  
 ; OTHER INFORMATION: 1998-07-14  
 ; OTHER INFORMATION: 0867/97  
 ; OTHER INFORMATION: 1997-07-15  
 ; OTHER INFORMATION: 60/052,862

Query Match 36.4% Score 4; Db 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1,40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 Db 8 ARKS 11

## RESULT 34

US-09-174-467-4  
 ; Sequence 4, Application US/09174467  
 ; Patent No. 451714  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; TITLE OF INVENTION: NO. 451714  
 ; FILE REFERENCE: THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/174,467  
 ; CURRENT FILING DATE: 1999-11-29  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: PATENT  
 ; OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
 ; OTHER INFORMATION: The first ala is a modified residue, it is  
 ; OTHER INFORMATION: acetylated.  
 US-09-174-467-4

Query Match 36.4% Score 4; Db 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1,40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 Db 8 ARKS 11

US-09-174-467-4  
 ; Sequence 4, Application US/09174467  
 ; Patent No. 451714  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; TITLE OF INVENTION: NO. 451714  
 ; FILE REFERENCE: THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/174,467  
 ; CURRENT FILING DATE: 1999-11-29  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: PATENT  
 ; OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
 ; OTHER INFORMATION: The first ala is a modified residue, it is  
 ; OTHER INFORMATION: acetylated.  
 US-09-174-467-4

Query Match 36.4% Score 4; Db 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1,40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 Db 8 ARKS 11

US-09-174-467-4  
 ; Sequence 4, Application US/09174467  
 ; Patent No. 451714  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; TITLE OF INVENTION: NO. 451714  
 ; FILE REFERENCE: THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/174,467  
 ; CURRENT FILING DATE: 1999-11-29  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: PATENT  
 ; OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
 ; OTHER INFORMATION: The first ala is a modified residue, it is  
 ; OTHER INFORMATION: acetylated.  
 US-09-174-467-4

Query Match 36.4% Score 4; Db 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1,40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 Db 8 ARKS 11

US-09-174-467-4  
 ; Sequence 4, Application US/09174467  
 ; Patent No. 451714  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; APPLICANT: KIMURA, YASUO  
 ; TITLE OF INVENTION: NO. 451714  
 ; FILE REFERENCE: THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/174,467  
 ; CURRENT FILING DATE: 1999-11-29  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: PATENT  
 ; OTHER INFORMATION: SYNTHETIC MOLECULES THAT ACT AS ENZYME INHIBITORS  
 ; OTHER INFORMATION: The first ala is a modified residue, it is  
 ; OTHER INFORMATION: acetylated.  
 US-09-174-467-4

Query Match 36.4% Score 4; Db 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1,40-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
 Db 8 ARKS 11

```

RESULT 35
US-08-145-061-13
: Sequence 13, Application US/08145061
: Patent No. 5460955
: GENERAL INFORMATION:
: APPLICANT: Mosher, Deane F.
: APPLICANT: Sottile, Jane M.
: TITLE OF INVENTION: FIBRONECTIN PURIFICATION VECTOR
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carl R. Schwartz, Charles & Brady
: STREET: 411 East Wisconsin Avenue
: CITY: Milwaukee
: STATE: Wisconsin
: COUNTRY: USA
: ZIP: 53202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/145,061
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/637,250
: FILING DATE: 03-JAN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Schwartz, Carl R.
: REGISTRATION NUMBER: 29,437
: REFERENCE/DOCKET NUMBER: 96-296-9170-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (414)277-5715
: TELEFAX: (414)277-5591
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide Fragment
US-08-145-061-13

Query Match 27.3%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAI 10
DB 5 TAI 7

RESULT 36
US-08-401-512-81
: Sequence 81, Application US/08401512
: Patent No. 5595673
: GENERAL INFORMATION:
: APPLICANT: Keating, Mark T.
: APPLICANT: Curran, Mark E.
: APPLICANT: Wang, Qing
: TITLE OF INVENTION: Long QT Syndrome Genes
: NUMBER OF SEQUENCES: 81
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Venable, Baetjer, Howard & Civiletti LLP
: STREET: 1201 New York Avenue, Suite 1000
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3917
: COMPUTER READABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/401,512
: FILING DATE: 09 MAY 1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: SARGENT, STEVEN A.
: REGISTRATION NUMBER: 29,437
: REFERENCE/DOCKET NUMBER: 96-296-9170-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-637-2400
: TELEFAX: 202-637-2400
: INFORMATION FOR SEQ ID NO: 81
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide
: HYDROPHILIC: N
US-08-401-512-81

Query Match 27.3%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAI 8
DB 6 TAI 8

RESULT 37
US-08-446-874A-3
: Sequence 3, Application US/08446874A
: Patent No. 5744247
: GENERAL INFORMATION:
: APPLICANT: Stuber, Robert
: APPLICANT: Wiscovitz, Joseph
: APPLICANT: Zisch, Robert
: TITLE OF INVENTION: BMV Specific Peptides, Agents Therefor
: TITLE OF INVENTION: BMV Specific Peptides
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Biomedical Research Corporation
: ADDRESSEE: Biomed
: STREET: 3300 Y Street, N.W., Suite 700
: CITY: Washington,
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3416
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/446,874A
: FILING DATE: 20 JUN 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/936,279
: FILING DATE: 27 AUG 1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 4412804.7
: FILING DATE: 29 AUG 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Forman, David S.
: REGISTRATION NUMBER: 33,694
: REFERENCE/DOCKET NUMBER: 05552-1210-04060
: TELECOMMUNICATION INFORMATION:

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TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 1  
 OTHER INFORMATION: /note= "xaa is Psp where ES is any  
 OTHER INFORMATION: appropriate amino acid and p is an integer from 2  
 OTHER INFORMATION: to 11."  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 8  
 OTHER INFORMATION: /note= "xaa is Psp where ES is any  
 OTHER INFORMATION: appropriate amino acid and q is an integer from 2  
 OTHER INFORMATION: to 11."  
 US-08-460-874A-3

Query Match 27.3% Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SRD 6  
 III  
 DB 3 SRD 5

RESULT 38  
 US-08-616-855-3  
 Sequence 4, Application US/08616855  
 Patent No. 5770357  
 GENERAL INFORMATION:  
 APPLICANT: Douvas, Angelina  
 APPLICANT: Ehresmann, Glenn  
 TITLE OF INVENTION: Method of Diagnosing Carcin  
 TITLE OF INVENTION: Arthritis-Encephalitis Virus Infection  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.2/5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/616,855  
 FILING DATE:  
 CLASSIFICATION: 436  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-ST 1988  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-616-855-3

Query Match 27.3% Score 3; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PKS 4  
 III  
 DB 6 PKS 8  
 RESULT 39  
 US-08-147-777-4  
 Sequence 4, Application US/08616855  
 Patent No. 5414265  
 GENERAL INFORMATION:  
 APPLICANT: Biogen, Inc.  
 APPLICANT: Biogen, Inc.  
 APPLICANT: Biogen, Inc.  
 APPLICANT: Biogen, Inc.  
 TITLE OF INVENTION: Amino Acid Derivatives of Peptides  
 TITLE OF INVENTION: Amino Acid Derivatives of Peptides  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Biogen, Inc.  
 STREET: 611 West Street  
 CITY: Westborough  
 STATE: California  
 COUNTRY: USA  
 ZIP: 01581  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: DOS/MS-DOS  
 SOFTWARE: Windows 3.11  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/147,777  
 FILING DATE:  
 CLASSIFICATION: B01  
 PRIOR APPLICATION DATA:  
 PRIOR APPLICATION DATA: International  
 PRIOR APPLICATION DATA: International  
 APPLICATION NUMBER: 02/746,000  
 FILING DATE: April 1, 1992  
 APPLICATION NUMBER: International (2004/114)  
 FILING DATE: September 29, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Walling, Robert L.  
 REGISTRATION NUMBER: 32,427  
 REFERENCE/DOCKET NUMBER: 2004/114  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 899-1111  
 TELEFAX: (213) 899-1111  
 TELETYPE: 02/746,000  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRAIN/GENES: S101  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-147-777-4

Query Match 27.0% Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKS 4  
 III  
 DB 3 PKS 5

RESULT 40  
 US-08-669-244B-3  
 Sequence 20, Application US/08669244B  
 Patent No. 694534

```

1  GENERAL INFORMATION:
2  APPLICANT: Inoue, Makoto
3  APPLICANT: Kikuchi, Kaoru
4  APPLICANT: Ishige, Yoko
5  APPLICANT: Ito, Akira
6  APPLICANT: Kimura, Toru
7  APPLICANT: Nakayama, Chikao
8  APPLICANT: No. 5939534uchi, Hiroshi
9  TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROPROTEIN FACTORS
10 NUMBER OF SEQUENCES: 35
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: SUCHRUE, MILO, ZINN, MACPHEE & SEAS
13 STREET: 2100 Pennsylvania Avenue, N.W.
14 CITY: Washington
15 STATE: D.C.
16 COUNTRY: USA
17 ZIP: 20037
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: PatentIn Release #1.0, Version #1.40
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/669,284B
26 FILING DATE: 28-JUN-1996
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: PCT/JP94/02269
29 FILING DATE: 27-DEC-1994
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: JP 06-268281
32 FILING DATE: 05-OCT-1994
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: JP 06-201504
35 FILING DATE: 02-AUG-1994
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: JP 05-350934
38 FILING DATE: 29-DEC-1993
39 ATTORNEY/AGENT INFORMATION:
40 NAME: Nakamura, Dean H.
41 REGISTRATION NUMBER: 33,981
42 REFERENCE/DOCKET NUMBER: Q-42041
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: (202)293-7060
45 TELEFAX: (202)293-7860
46 INFORMATION FOR SEQ ID NO: 20:
47 SEQUENCE CHARACTERISTICS:
48 LENGTH: 8 amino acids
49 TYPE: amino acid
50 STRANDEDNESS:
51 TOPOLOGY: linear
52 MOLECULE TYPE: peptide
53 US-08-669-284B-20
54
55 Query Match 27.38; Score 3; DB 2; Length 8;
56 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
57 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
58
59 QY 6 DMT 8
60 DB 5 DMT 7
61
62 RESULT 41
63 US-08-726-306A-181
64 Sequence 181, Application US/08726306A
65 Patent No. 5958684
66 GENERAL INFORMATION:
67 APPLICANT: van Leeuwen, Frederik Willem
68 APPLICANT: Burbach, Johannes Peter Henri
69 APPLICANT: Grosveld, Franklin G.
70 TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
71 NUMBER OF SEQUENCES: 189
72 CORRESPONDENCE ADDRESS:

```

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1  ADDRESSEE: KIMURA, AKIRA
2  STREET: 1 Fushimi 1-chome
3  CITY: Boston
4  STATE: MA
5  COUNTRY: US
6  ZIP: 02111
7  COMPUTER READABLE FORM:
8  MEDIUM TYPE: Floppy disk
9  COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/669,284B
14 FILING DATE: 28-JUN-1996
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: PCT/JP94/02269
17 FILING DATE: 27-DEC-1994
18 NAME: Nakamura, Dean H.
19 REGISTRATION NUMBER: 33,981
20 REFERENCE/DOCKET NUMBER: Q-42041
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (202)293-7060
23 TELEFAX: (202)293-7860
24 INFORMATION FOR SEQ ID NO: 20:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 8 amino acids
27 TYPE: amino acid
28 STRANDEDNESS:
29 TOPOLOGY: linear
30 MOLECULE TYPE: peptide
31 US-08-726-306A-181
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33 Query Match 27.38; Score 3; DB 2; Length 8;
34 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
35 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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37 QY 4 SEQ 6
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40 RESULT 42
41 US-08-726-306A-21
42 Sequence 21, Application US/08726306A
43 Patent No. 5958684
44 GENERAL INFORMATION:
45 APPLICANT: van Leeuwen, Frederik Willem
46 APPLICANT: Burbach, Johannes Peter Henri
47 TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
48 NUMBER OF SEQUENCES: 189
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: KIMURA, AKIRA
51 STREET: 1 Fushimi 1-chome
52 CITY: Boston
53 STATE: MA
54 COUNTRY: USA
55 ZIP: 02111
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Floppy disk
58 COMPUTER: IBM PC compatible
59 OPERATING SYSTEM: PC-DOS/MS-DOS
60 SOFTWARE: PatentIn Release #1.0
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/08/669,284B
63 FILING DATE: 28-JUN-1996
64 PRIOR APPLICATION DATA:
65 APPLICATION NUMBER: PCT/JP94/02269
66 FILING DATE: 27-DEC-1994
67 NAME: Nakamura, Dean H.
68 REGISTRATION NUMBER: 33,981
69 REFERENCE/DOCKET NUMBER: Q-42041
70 TELECOMMUNICATION INFORMATION:
71 TELEPHONE: (202)293-7060
72 TELEFAX: (202)293-7860
73 INFORMATION FOR SEQ ID NO: 20:
74 SEQUENCE CHARACTERISTICS:
75 LENGTH: 8 amino acids
76 TYPE: amino acid
77 STRANDEDNESS:
78 TOPOLOGY: linear
79 MOLECULE TYPE: peptide
80 US-08-726-306A-181

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 APPLICATION NUMBER: 08/405617  
 FILING DATE: 15-MAR-1995  
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 APPLICATION NUMBER: 08/185899  
 FILING DATE: 26-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/879495  
 FILING DATE: 07-MAY-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/744768  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: P071820101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
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 SEQUENCE CHARACTERISTICS:  
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 TYPE: Amino Acid  
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 Patent No. 6057298  
 GENERAL INFORMATION:  
 APPLICANT: Roop, Dennis R.  
 APPLICANT: Rothnagel, Joseph A.  
 APPLICANT: Greenhalgh, David A.  
 APPLICANT: Yuspa, Stuart H.  
 TITLE OF INVENTION: KERATIN K1 EXPRESSION VECTORS  
 TITLE OF INVENTION: AND METHODS OF USE  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LYON & LYON  
 STREET: 611 West Sixth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90017  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB Storage  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/452-872  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/147,777  
 FILING DATE:  
 APPLICATION NUMBER: 07/876,289  
 FILING DATE: April 30, 1992  
 APPLICATION NUMBER: Unassigned (204/144)  
 FILING DATE: October 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.

SEQUENCE INFORMATION:  
 REFERENCE/DOCKET NUMBER: P071820101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-1489  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
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 TYPE: Amino Acid  
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 Patent No. 6057298  
 GENERAL INFORMATION:  
 APPLICANT: Roop, Dennis R.  
 APPLICANT: Rothnagel, Joseph A.  
 APPLICANT: Greenhalgh, David A.  
 APPLICANT: Yuspa, Stuart H.  
 TITLE OF INVENTION: KERATIN K1 EXPRESSION VECTORS  
 TITLE OF INVENTION: AND METHODS OF USE  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LYON & LYON  
 STREET: 611 West Sixth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90017  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB Storage  
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 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/452-071-4  
 FILING DATE:  
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 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/147,777  
 FILING DATE:  
 APPLICATION NUMBER: 07/876,289  
 FILING DATE: April 30, 1992  
 APPLICATION NUMBER: Unassigned (204/144)  
 FILING DATE: October 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.

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GenCore version 5.1.1  
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425	3	27.3	10	15	US-10-116-255-56	Sequence 56, Appl	498	3	27.3	11	11	US-10-116-255-56	Sequence 56, Appl
426	3	27.3	10	15	US-10-116-255-66	Sequence 66, Appl	499	3	27.3	11	11	US-10-116-255-66	Sequence 66, Appl
427	3	27.3	10	15	US-10-062-710-186	Sequence 186, App	500	3	27.3	11	11	US-10-062-710-186	Sequence 186, App
428	3	27.3	10	15	US-10-196-107A-28	Sequence 28, Appl							
429	3	27.3	10	15	US-10-373-541-65	Sequence 55, App							
430	3	27.3	10	15	US-10-467-849-36	Sequence 36, App							
431	3	27.3	10	15	US-10-231-055-23	Sequence 23, App							
432	3	27.3	10	15	US-10-216-122-24	Sequence 24, Appl							
433	3	27.3	10	15	US-10-095-818A-3	Sequence 3, Appl							
434	3	27.3	11	9	US-08-424-550B-550	Sequence 550, App							
435	3	27.3	11	9	US-09-935-682-19	Sequence 19, Appl							
436	3	27.3	11	9	US-09-935-682-56	Sequence 56, Appl							
437	3	27.3	11	9	US-09-813-653-22	Sequence 22, Appl							
438	3	27.3	11	9	US-09-817-661-19	Sequence 19, Appl							
439	3	27.3	11	9	US-09-873-676-4	Sequence 4, Appl							
440	3	27.3	11	10	US-09-810-673-2	Sequence 2, Appl							
441	3	27.3	11	10	US-09-758-128-25	Sequence 25, App							
442	3	27.3	11	10	US-09-758-128-26	Sequence 26, App							
443	3	27.3	11	10	US-09-949-196-16	Sequence 16, Appl							
444	3	27.3	11	10	US-09-071-838-222	Sequence 222, App							
445	3	27.3	11	10	US-09-758-426-25	Sequence 25, App							
446	3	27.3	11	10	US-09-758-426-28	Sequence 28, Appl							
447	3	27.3	11	10	US-09-758-198-25	Sequence 25, Appl							
448	3	27.3	11	10	US-09-758-198-28	Sequence 28, Appl							
449	3	27.3	11	11	US-09-983-902-567	Sequence 567, App							
450	3	27.3	11	11	US-09-882-291-44	Sequence 44, Appl							
451	3	27.3	11	11	US-09-861-661-25	Sequence 25, Appl							
452	3	27.3	11	11	US-09-861-661-28	Sequence 28, Appl							
453	3	27.3	11	11	US-09-809-391-698	Sequence 698, App							

## REFERENCES

RESUBMIT 1  
 US-09-276,941A-377  
 Sequence 456, Applicant US-09-276,941A-377  
 Publication No. US-2003-023045A  
 GENERAL INFORMATION  
 APPLICANT: BELL-KASLO, INC.  
 TITLE OF INVENTION: AGENTS WITH NOVEL LOCALIZATION SIGNALS FOR SEQUENTIAL  
 TITLE OF INVENTION: AGENTS WITH NOVEL LOCALIZATION SIGNALS FOR SEQUENTIAL  
 FILE REFERENCE: P. 2002-08  
 CURRENT APPLICATION NUMBER: US-09-276,941A  
 CURRENT FILING DATE: 2001-06-08  
 PRIOR APPLICATION NUMBER: US-09-276,941A-377  
 PRIOR FILING DATE: 2001-06-08  
 NUMBER OF SEQ ID NOS: 679  
 SOFTWARE: Patenting Ver. 2.1  
 SEQ ID NO: 456  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Unknown Organism  
 FEATURE:

OTHER INFORMATION: Description of Unknown Organism: C/ERP (CCAAAT/enhancer  
US-09-876-904A-456

Query Match 45.5% Score 5: DB 11: Length 8:  
Best Local Similarity 100.0% Pred. No. 5, 1e+05:  
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

## RESULT 2

US-09-876-904A-504  
Sequence 504, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 504  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: Mouse AGP/ERP.  
US-09-876-904A-504

Query Match 45.5% Score 5: DB 11: Length 8:  
Best Local Similarity 100.0% Pred. No. 5, 1e+05:  
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

## RESULT 3

US-09-876-904A-507  
Sequence 507, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 507  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Rattus sp.  
FEATURE:  
OTHER INFORMATION: Rat LAP, a 32-kD liver-enriched transcriptional  
activator, also present in lung with 71% sequence  
similarity to C/ERP  
US-09-876-904A-507

Query Match 45.5% Score 5: DB 11: Length 8:

Best Local Similarity 100.0% Pred. No. 5, 1e+05:  
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

## RESULT 4

US-09-876-904A-507  
Sequence 520, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 520  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Rattus sp.  
FEATURE:  
OTHER INFORMATION: Human BP 115 (53-60).  
US-09-876-904A-520

Query Match 45.5% Score 5: DB 11: Length 8:  
Best Local Similarity 100.0% Pred. No. 5, 1e+05:  
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSND 6  
IIII

DB 2 RKSND 6

## RESULT 5

US-09-876-904A-520  
Sequence 520, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: KRESEFF, SUSAN  
APPLICANT: GRAB, ROBERT  
APPLICANT: WU, YIN YI  
TITLE OF INVENTION: PEPTIDE AND COMPOSITIONS FOR THE  
TITLE OF INVENTION: TREATMENT OF HEPATOCARCINOMA  
NUMBER OF SEQUENCES: 47  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 520  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Rattus sp.  
FEATURE:  
OTHER INFORMATION: Rat LAP, a 32-kD liver-enriched transcriptional  
activator, also present in lung with 71% sequence  
similarity to C/ERP  
US-09-876-904A-520

: TELEPHONE: (617) 248-7000  
 : TELEFAX: (617) 248-7100  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 9 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS:  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 : US-09-315-355-4

Query Match 36.4% Score 4.18 12 Length 9  
 Best Local Similarity 100.0% Pred. No. 5.1e+05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 SRDM 7  
 Db 6 SRDM 9

## RESULT 6

US-09-793-451-250  
 : Sequence 260, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell  
 : APPLICANT: Rene S. Hubert  
 : APPLICANT: Pia M. Challita-Eid  
 : APPLICANT: Mary Faris  
 : APPLICANT: Aya Jakobovits  
 : TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY  
 : TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 : FILE REFERENCE: 129,205U2  
 : CURRENT APPLICATION NUMBER: US/09/793,451  
 : PRIOR FILING DATE: 2001-02-26  
 : PRIOR APPLICATION NUMBER: 60/184,556  
 : PRIOR FILING DATE: 2000-02-24  
 : PRIOR APPLICATION NUMBER: 60/218,856  
 : PRIOR FILING DATE: 2000-07-13  
 : NUMBER OF SEQ ID NOS: 752  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 260  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: homo sapiens  
 : US-09-793 451-250

Query Match 36.4% Score 4.18 12 Length 9  
 Best Local Similarity 100.0% Pred. No. 5.1e+05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 Db 6 RKSR 9

## RESULT 7

US-09-793-451-329  
 : Sequence 129, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell  
 : APPLICANT: Rene S. Hubert  
 : APPLICANT: Pia M. Challita-Eid  
 : APPLICANT: Mary Faris  
 : APPLICANT: Aya Jakobovits  
 : TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY

: TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY  
 : FILE REFERENCE: 129,205U2  
 : CURRENT APPLICATION NUMBER: US/09/793,451  
 : PRIOR FILING DATE: 2001-02-26  
 : PRIOR APPLICATION NUMBER: 60/184,556  
 : PRIOR FILING DATE: 2000-02-24  
 : PRIOR APPLICATION NUMBER: 60/218,856  
 : PRIOR FILING DATE: 2000-07-13  
 : NUMBER OF SEQ ID NOS: 752  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 329  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: homo sapiens  
 : US-09-793 451-329

Query Match 36.4% Score 4.18 12 Length 9  
 Best Local Similarity 100.0% Pred. No. 5.1e+05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 Db 6 RKSR 9

## RESULT 8

US-09-793-451-429  
 : Sequence 429, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell  
 : APPLICANT: Rene S. Hubert  
 : APPLICANT: Pia M. Challita-Eid  
 : APPLICANT: Mary Faris  
 : APPLICANT: Aya Jakobovits  
 : TITLE OF INVENTION: 103P206: TISSUE SPECIFIC PROTEIN HIGHLY  
 : TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 : FILE REFERENCE: 129,205U2  
 : CURRENT APPLICATION NUMBER: US/09/793,451  
 : PRIOR FILING DATE: 2001-02-26  
 : PRIOR APPLICATION NUMBER: 60/184,556  
 : PRIOR FILING DATE: 2000-02-24  
 : PRIOR APPLICATION NUMBER: 60/218,856  
 : PRIOR FILING DATE: 2000-07-13  
 : NUMBER OF SEQ ID NOS: 752  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 429  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: homo sapiens  
 : US-09 793-451-429

Query Match 36.4% Score 4.18 12 Length 9  
 Best Local Similarity 100.0% Pred. No. 5.1e+05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 Db 6 RKSR 9

## RESULT 9

US-09-793-451-529  
 : Sequence 529, Application US/09793451  
 : Publication No. US20030157597A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Arthur B. Raitano  
 : APPLICANT: Daniel E.H. Afar  
 : APPLICANT: Gazelle S. Rastegar  
 : APPLICANT: Steve Chappell Mitchell

: APPLICANT: Rene S. Hubert  
 : APPLICANT: Pia M. Challita-Eid  
 : APPLICANT: Mary Faris  
 : APPLICANT: Aya Jakobovits  
 : TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 : EXPRESSION: IN VARIOUS CANCERS  
 : FILE REFERENCE: 129.20S02  
 : CURRENT APPLICATION NUMBER: US/09/793.451  
 : CURRENT FILING DATE: 2001-02-26  
 : PRIOR APPLICATION NUMBER: 60/184,558  
 : PRIOR FILING DATE: 2000-02-24  
 : PRIOR APPLICATION NUMBER: 60/218,856  
 : PRIOR FILING DATE: 2000-07-13  
 : NUMBER OF SEQ ID NOS: 752  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 528  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: homo sapiens  
 : ORGANISM: Homo sapiens  
 : FEATURE:

Query Match 36.4%, Score 4: PB 12: Length 9:  
 Best Local Similarity 100.0%, Pred. No. 5, 1e-05:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 DB 3 RKSR 6

## RESULT 10

US-09-866-073-1

: Sequence 1: Application US/09866073  
 : Patent No. US20020068272A1

: GENERAL INFORMATION:

: APPLICANT: Larocca, David

: APPLICANT: Baird, Andrew

: APPLICANT: Kassner, Paul

: TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR

: DETECTING AND IDENTIFYING PROTEIN INTERACTIONS

: TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION

: TITLE OF INVENTION: AND TRANSGENE EXPRESSION AND CELLS OR TISSUE

: TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING

: TITLE OF INVENTION: GENE DELIVERY VECTORS

: FILE REFERENCE: 760100.430C4

: CURRENT APPLICATION NUMBER: US/09/866.073

: CURRENT FILING DATE: 2001-05-24

: NUMBER OF SEQ ID NOS: 17

: SOFTWARE: PatentIn Ver. 2.0

: SEQ ID NO 1

: LENGTH: 10

: TYPE: PRT

: ORGANISM: Unknown

: FEATURE:

: OTHER INFORMATION: Description of Unknown Organism: A software

: OTHER INFORMATION: peptide, from a random peptide library that binds

: OTHER INFORMATION: and internalizes in a cell receptor overexpressed

: OTHER INFORMATION: cell line

: US-09-866-073-1

## Query Match

Best Local Similarity 36.4%, Score 4: PB 9: Length 10:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 DB 7 RKSR 10

## RESULT 11

US-09-572-404B-1142

: Sequence 1142: Application US/09572404B

: Publication No. US20030078374A1

: GENERAL INFORMATION  
 : APPLICANT: Patent In  
 : TITLE OF INVENTION: Compartmentalizing Peptide Ligands from the Lipid domain  
 : FILE REFERENCE: Drug Patent  
 : CURRENT APPLICATION NUMBER: 2001-02-26  
 : CURRENT FILING DATE: 2001-02-26  
 : NUMBER OF SEQ ID NOS: 4200  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1142  
 : LENGTH: 10  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : OTHER INFORMATION: Nucleotide sequence of the DNA sequence of the peptide ligand  
 : OTHER INFORMATION: Nucleotide sequence of the DNA sequence of the peptide ligand  
 : US-09-572-404B-1142

Query Match 36.4%, Score 4: PB 11: Length 10:

Best Local Similarity 100.0%, Pred. No. 5, 1e-05:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 APPS 4

DB 4 APPS 4

## RESULT 12

US-09-572-404B-1144

: Sequence 1144: Application US/09572404B

: Publication No. US20030078374A1

: GENERAL INFORMATION:

: APPLICANT: Patent In

: TITLE OF INVENTION: Compartmentalizing Peptide Ligands from the Lipid domain

: FILE REFERENCE: Drug Patent

: CURRENT APPLICATION NUMBER: 2001-02-26

: CURRENT FILING DATE: 2001-02-26

: NUMBER OF SEQ ID NOS: 4200

: SOFTWARE: PatentIn Ver. 2.0

: SEQ ID NO 1144

: LENGTH: 10

: TYPE: PRT

: ORGANISM: Homo sapiens

: FEATURE:

: OTHER INFORMATION: Nucleotide sequence of the DNA sequence of the peptide ligand

: OTHER INFORMATION: Nucleotide sequence of the DNA sequence of the peptide ligand

: US-09-572-404B-1144

## Query Match

Best Local Similarity 36.4%, Score 4: PB 11: Length 10:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 APPS 4

DB 4 APPS 4

## RESULT 13

US-09-572-404B-1144

: Sequence 1144: Application US/09572404B

: Publication No. US20030078374A1

: GENERAL INFORMATION:

: APPLICANT: Patent In

: TITLE OF INVENTION: Compartmentalizing Peptide Ligands from the Lipid domain

: FILE REFERENCE: Drug Patent

: CURRENT APPLICATION NUMBER: 2001-02-26

: CURRENT FILING DATE: 2001-02-26

: NUMBER OF SEQ ID NOS: 4200

: SOFTWARE: PatentIn Ver. 2.0

: SEQ ID NO 1144

: LENGTH: 10

: TYPE: PRT

: ORGANISM: Homo sapiens

: FEATURE:

OTHER INFORMATION: sequence located in SEQ ID NO 3890 or SEQ ID NO 3891 and may interrelate with Sequence 2993 in this patent.  
US-09-572-404B-2994

Query Match 36.4% Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKSR 5  
1111  
Db 2 RKSR 5

## RESULT 14

US-09-572-404B-3890  
Sequence 3890, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human Patent  
CURRENT APPLICATION NUMBER: US/09/572.404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 3890  
LENGTH: 10  
TYPE: PPT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in SEQ ID NO 3891 and may interrelate with Sequence 3891 in this patent.  
US-09-572-404B-3890

Query Match 36.4% Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
1111  
Db 1 ARKS 4

## RESULT 15

US-09-572-404B-3891  
Sequence 3891, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human Patent  
CURRENT APPLICATION NUMBER: US/09/572.404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 3891  
LENGTH: 10  
TYPE: PPT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in SEQ ID NO 3890 and may interrelate with Sequence 3890 in this patent.  
US-09-572-404B-3891

Query Match 36.4% Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
1111  
Db 1 ARKS 4

RESULT 16  
US-09-572-404B-3892  
Sequence 3892, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human Patent  
CURRENT APPLICATION NUMBER: US/09/572.404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 3892  
LENGTH: 10  
TYPE: PPT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in SEQ ID NO 3891 and may interrelate with Sequence 3891 in this patent.  
US-09-572-404B-3892

Query Match 36.4% Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
1111  
Db 1 ARKS 4

## RESULT 17

US-09-572-404B-3893  
Sequence 3893, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human Patent  
CURRENT APPLICATION NUMBER: US/09/572.404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 3893  
LENGTH: 10  
TYPE: PPT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: sequence located in SEQ ID NO 3892 and may interrelate with Sequence 3892 in this patent.  
US-09-572-404B-3893

Query Match 36.4% Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4  
1111  
Db 1 ARKS 4

## RESULT 18

US-09-572-404B-3894  
Sequence 3894, Application US/09572404B  
Publication No. US20030078374A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands from the human genome  
FILE REFERENCE: Human Patent  
CURRENT APPLICATION NUMBER: US/09/572.404B  
CURRENT FILING DATE: 2000-05-17  
NUMBER OF SEQ ID NOS: 4203  
SOFTWARE: ProtPatent version 1.0  
SEQ ID NO 3894



; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in PNCV OR OFQ at 131 140 and may interact with  
 ; OTHER INFORMATION: Sequence 4131 in this patent.  
 US-09-572-404B-4130

Query Match 36.4%; Score 4; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4

DB 1111

6 ARKS 9

#### RESULT 19

US-09-572-404B-4131

; Sequence 4131, Application US/09572404H

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human Patent

; CURRENT APPLICATION NUMBER: US/09/572,404H

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 4131

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in PNCV OR OFQ at 131 140 and may interact with

US-09-572-404B-4131

Query Match 36.4%; Score 4; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4

DB 1111

6 ARKS 9

#### RESULT 20

US-09-572-270A-741

; Sequence 741, Application US/09572270A

; Publication No. US20030148368A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Inter- complementary peptide listing

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/572,270A

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 1144

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 741

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Arabidopsis Thaliana

; OTHER INFORMATION: Sequence located in Unknown at 7 16 and may interact with

US-09-572-270A-741

Query Match

Best Local Similarity 36.4%; Score 4; DB 12; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4

DB 1111

1 ARKS 4

#### RESULT 21

US-09-572-270A-745

; Sequence 745, Application US/09572270A

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Inter- complementary peptide listing

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/572,270A

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 1144

; SOFTWARE: ProPatent version 1.0

; SEQ ID NO 745

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Arabidopsis Thaliana

; OTHER INFORMATION: No sequence located in Unknown at 7 16 and may interact with

US-09-572-270A-745

Query Match 36.4%; Score 4; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARKS 4

DB 1111

1 ARKS 4

#### RESULT 22

US-10-571-204-1

; Sequence 1, Application US/10571204

; Publication No. US20030148368A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; APPLICANT: Kassner, Paul

; APPLICANT: Bittel, Andrew

; APPLICANT: Bittel, Michael, Alan

; TITLE OF INVENTION: METHOD FOR AND COMPOSITIONS FOR

; FILE REFERENCE: 7601,004,300

; CURRENT APPLICATION NUMBER: US/10/571,204

; CURRENT FILING DATE: 2002-03-17

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentPro version 2.0

; SEQ ID NO 1

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of the sequence in the patent. A sequence

; OTHER INFORMATION: peptides from a random peptide library, that binds

; OTHER INFORMATION: and internalizes in a cell receptor overproduced

US-10-571-204-1

Query Match

Best Local Similarity 36.4%; Score 4; DB 12; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ARKS 5

DB 1111

7 ARKS 10

#### RESULT 23

US-10-190-682-248

; Sequence 288, Application US/10190682

; Publication No. US20030148368A1

; GENERAL INFORMATION:

; APPLICANT: Lasky, Lawrence A.

; APPLICANT: Sidhu, Sardeep S.

; APPLICANT: Held, Heike A.  
 ; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
 ; FILE REFERENCE: P1905R1  
 ; CURRENT APPLICATION NUMBER: US/10/190.082  
 ; CURRENT FILING DATE: 2002-07-03  
 ; PRIOR APPLICATION NUMBER: US 60/303,634  
 ; PRIOR FILING DATE: 2001-07-06  
 ; NUMBER OF SEQ ID NOS: 683  
 ; SEQ ID NO 288  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic  
 US-10-190-082-288

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 1 RKSR 4

RESULT 24  
 US-09-793-451-376  
 ; Sequence 376, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129,20SU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version: 4.0  
 ; SEQ ID NO 376  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-376

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 6 RKSR 9

RESULT 25  
 US-09-793-451-401  
 ; Sequence 401, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Elm M. Chailita-Eid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129,20SU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version: 4.0  
 ; SEQ ID NO 401  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-401

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 7 RKSR 10

RESULT 26  
 US-09-793-451-478  
 ; Sequence 478, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Elm M. Chailita-Eid  
 ; APPLICANT: Mary Paris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129,20SU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version: 4.0  
 ; SEQ ID NO 478  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-478

Query Match 36.4% Score 4; 18 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RKSR 5  
 Db 4 RKSR 7

RESULT 27  
 US-09-793-451-548  
 ; Sequence 548, Application US/09793451  
 ; Publication No. US20030157597A1

GENERAL INFORMATION:  
 APPLICANT: Arthur B. Raitano  
 APPLICANT: Daniel E.H. Afar  
 APPLICANT: Gazelle S. Rastegar  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Pia M. Challita-Eid  
 APPLICANT: Mary Faris  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 FILE REFERENCE: 129.20SU2 EXPRESSED IN VARIOUS CANCERS  
 CURRENT APPLICATION NUMBER: US/09/793.451  
 PRIOR FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: 60/184,558  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: 60/218,856  
 PRIOR FILING DATE: 2000-07-13  
 NUMBER OF SEQ ID NOS: 752  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 568  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-09-793-451-568

Query Match 36.4% Score 4: DB 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 Db 4 RKSR 7

RESULT 28  
 US-09-793-451-704  
 Sequence 704: Application US/09793451  
 Publication No. US20030157597A1  
 GENERAL INFORMATION:  
 APPLICANT: Arthur B. Raitano  
 APPLICANT: Daniel E.H. Afar  
 APPLICANT: Gazelle S. Rastegar  
 APPLICANT: Steve Chappell Mitchell  
 APPLICANT: Rene S. Hubert  
 APPLICANT: Pia M. Challita-Eid  
 APPLICANT: Mary Faris  
 APPLICANT: Aya Jakobovits  
 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 FILE REFERENCE: 129.20SU2 EXPRESSED IN VARIOUS CANCERS  
 CURRENT APPLICATION NUMBER: US/09/793.451  
 PRIOR FILING DATE: 2001-02-26  
 PRIOR APPLICATION NUMBER: 60/184,558  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: 60/218,856  
 PRIOR FILING DATE: 2000-07-13  
 NUMBER OF SEQ ID NOS: 752  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 704  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-09-793-451-704

Query Match 36.4% Score 4: DB 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 RKSR 5  
 Db 4 RKSR 7

RESULT 29  
 US-10-050-200-40  
 Sequence 40: Application US/05020040  
 Publication No. US20050000000A1  
 GENERAL INFORMATION:  
 APPLICANT: Raitano, Arthur  
 APPLICANT: Gazelle, Eve  
 APPLICANT: Kathleen, Raitano  
 TITLE OF INVENTION: ANTIBODIES AND PEPTIDE SUBSTRATES AND METHODS  
 FILE REFERENCE: 08/141  
 CURRENT APPLICATION NUMBER: 12/010,240  
 CURRENT FILING DATE: 2002-11-06  
 NUMBER OF SEQ ID NOS: 60  
 SOFTWARE: PatentSeq for Windows  
 SEQ ID NO 40  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURES:  
 OTHER INFORMATION: PRT OF Antigen  
 US-10-050-200-40

Query Match 36.4% Score 4: DB 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 RKSR 7  
 Db 5 RKSR 9

RESULT 30  
 US-10-040-605-12  
 Sequence 12: Application US/1004060512  
 Publication No. US20050000000A1  
 GENERAL INFORMATION:  
 APPLICANT: Raitano, Arthur  
 TITLE OF INVENTION: PEPTIDE SEQUENCES AND NOVEL HUMAN EXPRESSION CHANNEL DATA  
 FILE REFERENCE: 08/141  
 CURRENT APPLICATION NUMBER: 12/010,240  
 PRIOR FILING DATE: 2002-11-06  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentSeq for Windows  
 SEQ ID NO 12  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: homo sapiens  
 US-10-040-605-12

Query Match 36.4% Score 4: DB 12: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 2.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 RKSR 4  
 Db 5 RKSR 1

RESULT 41  
 US-09-429-549A-27  
 Sequence 27: Application US/09429549A  
 Patent No. US20020092484A1  
 GENERAL INFORMATION:  
 APPLICANT: THE UNIVERSITY OF MISSOURI  
 TITLE OF INVENTION: PHASE DISPLAY SELECTION OF ANTI-FUNERAL PROPERTIES  
 FILE REFERENCE: DMG 152.1  
 CURRENT APPLICATION NUMBER: US/09/429,549A

1 CURRENT FILING DATE: 2001-04-10  
 2 PRIOR APPLICATION NUMBER: US 60/195,785  
 3 PRIOR FILING DATE: 2000-04-10  
 4 NUMBER OF SEQ ID NOS: 48  
 5 SOFTWARE: PatentIn version 3.0  
 6 SEQ ID NO 27  
 7 LENGTH: 15  
 8 TYPE: PRT  
 9 ORGANISM: Artificial Sequence  
 10 FEATURE:  
 11 NAME/KEY: DOMAIN  
 12 LOCATION: (1)..(15)  
 13 OTHER INFORMATION: Random peptide insert  
 14 US-09-829-549A-27

Query Match 36.4%; Score 4; LB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3,400-92  
 Matches 4; Conservative 0; Mismatches 0; Indels 0

QY 7 MTAT 10  
 1111  
 Db 10 MTAT 13

RESULT 32  
 US-09-876-904A-186  
 1 Sequence 186; Application US/09876904A  
 2 Publication No. US20030072794A;  
 3 GENERAL INFORMATION:  
 4 APPLICANT: BOULIKAS, TENI  
 5 TITLE OF INVENTION: ENCAPSULATION OF PLASMIID DNA (LIPIDEMES IN) AND LIPIDATED  
 6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/POSITIVE PEPTIDE  
 7 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPIDOME COMPLEXES  
 8 FILE REFERENCE: TR-2002-06  
 9 CURRENT APPLICATION NUMBER: US/09/876,904A  
 10 CURRENT FILING DATE: 2001-06-08  
 11 PRIOR APPLICATION NUMBER: US 60/210,925  
 12 PRIOR FILING DATE: 2000-06-09  
 13 NUMBER OF SEQ ID NOS: 629  
 14 SOFTWARE: PatentIn Ver. 2.1  
 15 SEQ ID NO 186  
 16 LENGTH: 15  
 17 TYPE: PRT  
 18 ORGANISM: Homo sapiens  
 19 FEATURE:  
 20 OTHER INFORMATION: Karyophilic peptide  
 21 US-09-876-904A-186

Query Match 36.4%; Score 4; LB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3,400-62  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 1

QY 2 RKSR 5  
 1111  
 Db 9 RKSR 12

RESULT 33  
 US-10-041-030-16  
 1 Sequence 16; Application US/10041030  
 2 Publication No. US20020150934A;  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Powers, Scott  
 5 APPLICANT: Mu, David  
 6 APPLICANT: Xiang, Phil  
 7 APPLICANT: Peng, Yue  
 8 APPLICANT: Tularik Inc.  
 9 TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Maculatin  
 10 TITLE OF INVENTION: Peptide Polypeptides and Polynucleotides  
 11 FILE REFERENCE: 018781-006610US  
 12 CURRENT APPLICATION NUMBER: US/10/041,030  
 13 CURRENT FILING DATE: 2001-12-28  
 14 PRIOR APPLICATION NUMBER: US 60/259,502

1 PRIOR FILING DATE: 2001-04-10  
 2 NUMBER OF SEQ ID NOS: 48  
 3 SOFTWARE: PatentIn Ver.  
 4 SEQ ID NO 16  
 5 LENGTH: 15  
 6 TYPE: PRT  
 7 ORGANISM: Artificial Sequence  
 8 FEATURE:  
 9 NAME/KEY: DOMAIN  
 10 LOCATION: (1)..(15)  
 11 OTHER INFORMATION: Random peptide insert  
 12 US-09-829-549A-27  
 13 Query Match 36.4%; Score 4; LB 1; Length 15;  
 14 Best Local Similarity 100.0%; Pred. No. 3,400-92  
 15 Matches 4; Conservative 0; Mismatches 0; Indels 0

RESULT 34  
 US-09-802-077-10  
 1 Sequence 10; Application US/09802077A;  
 2 Publication No. US20030072794A;  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Powers, Scott  
 5 TITLE OF INVENTION: ENCAPSULATION OF PLASMIID DNA (LIPIDEMES IN) AND LIPIDATED  
 6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/POSITIVE PEPTIDE  
 7 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPIDOME COMPLEXES  
 8 FILE REFERENCE: TR-2002-06  
 9 CURRENT APPLICATION NUMBER: US/09/802,077A  
 10 CURRENT FILING DATE: 2001-06-08  
 11 PRIOR APPLICATION NUMBER: US 60/210,925  
 12 PRIOR FILING DATE: 2000-06-09  
 13 NUMBER OF SEQ ID NOS: 629  
 14 SOFTWARE: PatentIn Ver. 2.1  
 15 SEQ ID NO 186  
 16 LENGTH: 15  
 17 TYPE: PRT  
 18 ORGANISM: Homo sapiens  
 19 FEATURE:  
 20 OTHER INFORMATION: Karyophilic peptide  
 21 US-09-802-077-10

Query Match 36.4%; Score 4; LB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3,400-62  
 Matches 4; Conservative 0; Mismatches 0; Indels 0

QY 2 RKSR 4  
 1111  
 Db 9 RKSR 12

RESULT 35  
 US-10-041-030-16  
 1 Sequence 16; Application US/10041030  
 2 Publication No. US20020150934A;  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Powers, Scott  
 5 APPLICANT: Mu, David  
 6 APPLICANT: Xiang, Phil  
 7 APPLICANT: Peng, Yue  
 8 APPLICANT: Tularik Inc.  
 9 TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Maculatin  
 10 TITLE OF INVENTION: Peptide Polypeptides and Polynucleotides  
 11 FILE REFERENCE: 018781-006610US  
 12 CURRENT APPLICATION NUMBER: US/10/041,030  
 13 CURRENT FILING DATE: 2001-12-28  
 14 PRIOR APPLICATION NUMBER: US 60/259,502

; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCI/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 27  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-802-077-27

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 RKS 4  
 III  
 Db 6 RKS 8

## RESULT 36

US-09-735-995-116  
 ; Sequence 116, Application US/09735995  
 ; Patent No. US20010234024A1

; GENERAL INFORMATION:  
 ; APPLICANT: Keating, Mark T.  
 ; APPLICANT: Splawski, Igor  
 ; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF RSK3 - A LONG QT  
 ; TITLE OF INVENTION: SYNDROME GENE  
 ; FILE REFERENCE: 2323-136  
 ; CURRENT APPLICATION NUMBER: US/09/735,995  
 ; CURRENT FILING DATE: 2000-12-14  
 ; PRIOR APPLICATION NUMBER: 09/226,012  
 ; PRIOR FILING DATE: 1999-01-06  
 ; NUMBER OF SEQ ID NOS: 116  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 116  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-735-995-116

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 DMT 8  
 III  
 Db 6 DMT 8

## RESULT 37

US-09-802-096-10  
 ; Sequence 10, Application US/09802096  
 ; Patent No. US2001003839A1

; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method of Preventing the onset of Allergic Disorders (as amended)  
 ; FILE REFERENCE: P0718P2C30S  
 ; CURRENT APPLICATION NUMBER: US/09/802,096  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/405,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCI/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07

; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCI/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; PRIOR APPLICATION NUMBER: US 07/744,768  
 ; PRIOR FILING DATE: 1991-08-14  
 ; NUMBER OF SEQ ID NOS: 64

; SEQ ID NO 27  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-802-077-27

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 RKS 4  
 III  
 Db 6 RKS 8

## RESULT 38

US-09-802-096-10  
 ; Sequence 10, Application US/09802096  
 ; Patent No. US2001003839A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method of Preventing the onset of Allergic Disorders (as amended)  
 ; FILE REFERENCE: P0718P2C30S  
 ; CURRENT APPLICATION NUMBER: US/09/802,096  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/405,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCI/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SEQ ID NO 27  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-802-077-27

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 RKS 4  
 III  
 Db 6 RKS 8

## RESULT 39

US-09-802-096-10  
 ; Sequence 10, Application US/09802096  
 ; Patent No. US2001003839A1

; GENERAL INFORMATION:  
 ; APPLICANT: Jardieu, Paula M.  
 ; APPLICANT: Presta, Leonard G.  
 ; TITLE OF INVENTION: Method of Preventing the onset of Allergic Disorders (as amended)  
 ; FILE REFERENCE: P0718P2C30S  
 ; CURRENT APPLICATION NUMBER: US/09/802,096  
 ; CURRENT FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: US 08/405,617  
 ; PRIOR FILING DATE: 1995-03-15  
 ; PRIOR APPLICATION NUMBER: US 08/185,899  
 ; PRIOR FILING DATE: 1994-01-26  
 ; PRIOR APPLICATION NUMBER: PCI/US92/06860  
 ; PRIOR FILING DATE: 1992-08-14  
 ; PRIOR APPLICATION NUMBER: US 07/879,495  
 ; PRIOR FILING DATE: 1992-05-07

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? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
?   APPLICATION NUMBER: US/09/854,799
?   FILING DATE: 14-May-2001
?   CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
?   APPLICATION NUMBER: 08/392,459
?   FILING DATE: <Unknown>
?   APPLICATION NUMBER: US 07/618,066
?   FILING DATE: 14-NOV-1990
? ATTORNEY/AGENT INFORMATION:
?   NAME: King, William T.
?   REGISTRATION NUMBER: 30,954
?   REFERENCE/DOCKET NUMBER: SEQ 14542B
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: (215) 270-5015
?   TELEFAX: (215) 270-5090
? INFORMATION FOR SEQ ID NO: 52:
?   SEQUENCE CHARACTERISTICS:
?     LENGTH: 8 amino acids
?     TYPE: amino acid
?     TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-854-799-52

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Query Match      27.3% Score 3; UB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 TAI 10
DB      6 TAI 8

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RESULT 40
US-09-949-559-111
? Sequence 111: Application US/09949559
? Patent No. US20020151682A1
? GENERAL INFORMATION:
?   APPLICANT: Athwal, Diljeet Singh
?   APPLICANT: Brown, Derek Thomas
?   APPLICANT: Weir, Andrew Neil Charles
?   APPLICANT: Popplewell, Andrew George
?   APPLICANT: Chapman, Andrew Paul
?   APPLICANT: King, David John
? TITLE OF INVENTION: Biological Products
? FILE REFERENCE: Carp-0095
? CURRENT APPLICATION NUMBER: US/09/949,559
? PRIOR FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: 0013810.7GB
? PRIOR FILING DATE: 2000-06-06
? PRIOR APPLICATION NUMBER: 09/875,221
? PRIOR FILING DATE: 2001-06-06
? NUMBER OF SEQ ID NOS: 130
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 111
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: IGS cassette-1
US-09-949-559-111

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```

Query Match      27.3% Score 3; UB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      8 TAI 10
DB      4 TAI 6

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RESULT 41
US-09-949-559-114
? Sequence 114: Application US/09949559
? Patent No. US20020151682A1
? GENERAL INFORMATION:
?   APPLICANT: Athwal, Diljeet Singh
?   APPLICANT: Brown, Derek Thomas
?   APPLICANT: Weir, Andrew Neil Charles
?   APPLICANT: Popplewell, Andrew George
?   APPLICANT: Chapman, Andrew Paul
?   APPLICANT: King, David John
? TITLE OF INVENTION: Biological Products
? FILE REFERENCE: Carp-0095
? CURRENT APPLICATION NUMBER: US/09/949,559
? PRIOR FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: 0013810.7GB
? PRIOR FILING DATE: 2000-06-06
? PRIOR APPLICATION NUMBER: 09/875,221
? PRIOR FILING DATE: 2001-06-06
? NUMBER OF SEQ ID NOS: 130
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 114
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: IGS cassette-1
US-09-949-559-114

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Query Match      27.3% Score 3; UB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 TAI 10
DB      4 TAI 6

```

```

RESULT 42
US-09-949-559-117
? Sequence 117: Application US/09949559
? Patent No. US20020151682A1
? GENERAL INFORMATION:
?   APPLICANT: Athwal, Diljeet Singh
?   APPLICANT: Brown, Derek Thomas
?   APPLICANT: Weir, Andrew Neil Charles
?   APPLICANT: Popplewell, Andrew George
?   APPLICANT: Chapman, Andrew Paul
?   APPLICANT: King, David John
? TITLE OF INVENTION: Biological Products
? FILE REFERENCE: Carp-0095
? CURRENT APPLICATION NUMBER: US/09/949,559
? PRIOR FILING DATE: 2001-12-20
? PRIOR APPLICATION NUMBER: 0013810.7GB
? PRIOR FILING DATE: 2000-06-06
? PRIOR APPLICATION NUMBER: 09/875,221
? PRIOR FILING DATE: 2001-06-06
? NUMBER OF SEQ ID NOS: 130
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 117
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: IGS cassette-1
US-09-949-559-117

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```

Query Match      27.3% Score 3; UB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 5, 1e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 8 TAI 10  
 Db 4 TAI 6

## RESULT 43

US-09-949-559-120  
 ; Sequence 120, Application US/09949559  
 ; Patent No. US20020151682A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Athwal, Diljeet Singh  
 ; APPLICANT: Brown, Derek Thomas  
 ; APPLICANT: Weir, Andrew Neil Charles  
 ; APPLICANT: Popplewell, Andrew George  
 ; APPLICANT: Chapman, Andrew Paul  
 ; APPLICANT: King, David John  
 ; TITLE OF INVENTION: Biological Products  
 ; FILE REFERENCE: Carp-0095  
 ; CURRENT APPLICATION NUMBER: US/09/949,559  
 ; CURRENT FILING DATE: 2001-12-20  
 ; PRIOR APPLICATION NUMBER: 0013810.7GB  
 ; PRIOR FILING DATE: 2000-06-06  
 ; PRIOR APPLICATION NUMBER: 09/875,221  
 ; PRIOR FILING DATE: 2001-06-06  
 ; NUMBER OF SEQ ID NOS: 130  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 120  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: ICS cassette-4  
 US-09-949-559-120

Query Match 27.3% Score 3; DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAI 10  
 Db 4 TAI 6

## RESULT 44

US-09-971-980-25  
 ; Sequence 25, Application US/09971980  
 ; Patent No. US20020164349A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weiner, David B.  
 ; APPLICANT: Yang, Joo-Sung  
 ; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein from Flaviviruses  
 ; FILE REFERENCE: Upn-4105  
 ; CURRENT APPLICATION NUMBER: US/09/971,980  
 ; CURRENT FILING DATE: 2001-10-04  
 ; PRIOR APPLICATION NUMBER: 60/237,885  
 ; PRIOR FILING DATE: 2000-10-04  
 ; NUMBER OF SEQ ID NOS: 73  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 25  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: No. US20020164349A1e1 Sequence  
 US-09-971-980-25

Query Match 27.3% Score 3; DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSR 5  
 Db 111

Db 5 KSR 7

## RESULT 45

US-09-017-7440-94  
 ; Sequence 94, Application US/09017740  
 ; Patent No. US2002117761A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sadhana, Anand  
 ; APPLICANT: Sadhana, Anand  
 ; TITLE OF INVENTION: RNA Binding Properties and Their  
 ; NUMBER OF SEQUENCES: 43  
 ; PRESENT INVENTION ADDRESS:  
 ; ADDRESS: Sadhana and Associates and GROW LLP  
 ; STREET: 14, 1st Floor, Convent, Eighth Floor  
 ; CITY: South India  
 ; STATE: CA  
 ; COUNTRY: US  
 ; E-MAIL: sadhana@grow.com  
 ; COMPUTER PROGRAM FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER PROGRAM FILE:  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/017,744  
 ; FILING DATE: 01 Feb 1998  
 ; CLASSIFICATION: C12N2301  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/551,298  
 ; FILING DATE: 25 MAR 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Patent Agent  
 ; REGISTRATION NUMBER: 42,054  
 ; REFERENCE/INVENT NUMBER: 100,216,880-005  
 ; TELEPHONE: 415 676 6020  
 ; TELEFAX: 415 676 6009  
 ; INFORMATION FOR SEQ ID NO: 94:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: polypep  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 94:  
 US-09-017-7440-94

Query Match 27.3% Score 3; DB 10; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 A-K 11  
 Db 4 A-K 4

## RESULT 46

US-09-092-256-9  
 ; Sequence 9, Application US/09002256  
 ; Publication No. US200219709A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nadekar, Anupama K.  
 ; APPLICANT: Nadekar, Anupama  
 ; TITLE OF INVENTION: Expression of 5 Protein-Coupled Receptors with Altered  
 ; FILE REFERENCE: CRI-099  
 ; CURRENT APPLICATION NUMBER: US/09/092,256  
 ; CURRENT FILING DATE: 1999-03-27  
 ; NUMBER OF SEQ ID NOS: 47

1 SOFTWARE: PatentIn Ver. 2.0  
2 SEQ ID NO 9  
3 LENGTH: 8  
4 TYPE: PRT  
5 ORGANISM: Artificial Sequence  
6 FEATURE:  
7 OTHER INFORMATION: Description of Artificial Sequence: CpAI amino terminal  
8 OTHER INFORMATION: sequence motif  
9 US-09-362-286-9

Query Match 27.3%, Score 3; DB 10; Length 8;  
Best Local Similarity 100.0%, Pred. No. 5, 1e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARK 3  
Db 2 ARK 4

RESULT 47  
US-09-983-802-330  
1 Sequence 130, Application US/09983802  
2 Publication No. US20030022185A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Fischer et al.  
5 TITLE OF INVENTION: 123 Human Secreted Proteins  
6 FILE REFERENCE: P2010P1  
7 CURRENT APPLICATION NUMBER: US/09/983,802  
8 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,457  
9 PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-08  
10 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/14684  
11 PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07  
12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926  
13 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
14 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793  
15 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
16 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925  
17 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
18 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929  
19 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
20 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803  
21 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
22 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,792  
23 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
24 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931  
25 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
26 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932  
27 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
28 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916  
29 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
30 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,940  
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40 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919  
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42 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925  
43 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
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45 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-19  
46 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723  
47 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
48 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948  
49 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
50 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949  
51 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

Qy 6 PRT 4  
Db 1 1  
2 0 0 4

Query Match 27.3%, Score 3; DB 10; Length 8;  
Best Local Similarity 100.0%, Pred. No. 5, 1e-05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-983-802-330  
1 Sequence 475, Application US/09983802  
2 Publication No. US20030022185A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Fischer et al.  
5 TITLE OF INVENTION: 123 Human Secreted Proteins  
6 FILE REFERENCE: P2010P1  
7 CURRENT APPLICATION NUMBER: US/09983802  
8 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,457  
9 PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-08  
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51 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18



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2 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
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91 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,946
92 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
93 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,946
94 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
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99 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,946
100 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

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Query Match 27.3% Score 42 GR H1 Length 4
Best local Similarity 100.0% Prod No 511-094
Matches 3: Conservative 0; Mismatches 3; Indels 0; Gaps 0

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QY 9 A1K 11
DB 2 A1K 4

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## RESULT 49

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US-09-875-221A-111
Sequence 111, Application US/0987522:A
Publication No. US2003026805A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul

```

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APPLICANT: K. S. Popplewell
TITLE OF INVENTION: PATENT IN THE FIELD OF
CURRENT APPLICATION NUMBER: US/0987522:A
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/056,946
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 111
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION:
US-09-875-221A 11
QY 9 A1K 11
DB 2 A1K 4
RESULT 50
US-09-875-221A 114
Sequence 114, Application US/0987522:A
Publication No. US2003026805A1
GENERAL INFORMATION:
APPLICANT: K. S. Popplewell
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul
TITLE OF INVENTION: PATENT IN THE FIELD OF
CURRENT APPLICATION NUMBER: US/0987522:A
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/056,946
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 114
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION:
US-09-875-221A 114

```

```

Query Match 27.3% Score 42 GR H1 Length 4
Best local Similarity 100.0% Prod No 511-094
Matches 3: Conservative 0; Mismatches 3; Indels 0; Gaps 0

```

```

QY 9 A1K 11
DB 2 A1K 4

```

```

Result 49
US-09-875-221A 111
Sequence 111, Application US/0987522:A
Publication No. US2003026805A1
GENERAL INFORMATION:
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Brown, Derek Thomas
APPLICANT: Weir, Andrew Neil Charles
APPLICANT: Popplewell, Andrew George
APPLICANT: Chapman, Andrew Paul

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